

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			621 626 649 679 719 725-726 738 793 803 831 834-836 838 844 857- 858 866 879 905 913 928 963 976 1005-1006 1012 1038 1050 1116- 1117 1151 1199 1204 1226 1243 1265 1274 1324-1325 1339 1353 1374 1377 1440-1441 1447 1504 1549 1600 1618-1619 1631 1641 1644 1653 1687-1688 1691-1692 1741 1771
young liver	GIBCO	ALV001	5-8 11 20-21 46 50-51 58 65-66 75 79 82 93 97 102-103 108 110 116 139 143-144 148-149 171-172 174 187-189 194-195 198 209 214- 215 230 250 258 267-269 280-281 306 309 342 351 356 359 362 372 374 392 394 398 401 407-408 410 414 431 444 455 459 476 478 483 493 510-512 516 520 522 526 536 549 571 574-577 585 592 601-602 607 621-624 628-630 632-633 637 648 660 666-667 678 697-698 700 717 719 728 730 734 738 744-745 766 770 773 779 788 800 808 812 814 841 849-851 871 874 879 887 893 898-900 902-904 906-907 911 919 922 924 934 953 957 963 965 970 984 986 997 1001 1004 1007 1012 1029-1030 1033-1034 1052 1061 1066 1070 1076 1086 1089 1093 1099-1102 1110-1112 1116- 1117 1119 1121 1125 1136-1137 1144-1145 1156-1157 1159 1196 1199-1200 1209 1211 1219-1220 1241 1244 1262 1270 1275 1279 1283 1295 1317-1320 1332 1339 1344 1359 1362-1363 1379 1383- 1384 1403 1415 1430-1431 1437 1450 1467 1475-1476 1483-1484 1494-1495 1498 1505 1512 1516 1518-1519 1526 1529 1547 1550- 1552 1557-1559 1565 1583 1587 1597 1609 1614 1620 1631 1637 1641 1644 1654-1655 1662 1667 1669 1684 1691-1692 1702 1711 1725 1738 1741 1743-1744 1758 1760-1761 1763-1765 1769
adult liver	Invitrogen	ALV002	5-8 17 20-21 32-33 41 55 58 64 75 77 86 89 102 108 117 119 175- 176 198 200 209 231 235-236 250 272 275-276 284 306 316 321 325 333 356 359 374 376 398 401 408 414 428 430 433-435 454 476 494 503-505 517-518 528 534 544 552 561-563 567 578 581 608-609 630 632 637 644 650 661 665 672 702 707 710 721-722 750 753 778 782 794 814 820 826 834-837 847 849- 850 858 861 874 879 893 898 904 911 918 921-922 926 946 948 972 978 986 996 1020 1027 1031 1034 1053 1063 1068 1070 1073 1086 1089 1093 1097 1113 1119 1156 1159 1195 1198-1199 1208 1220 1227 1241 1261 1272-1273 1277 1285 1308 1315 1320 1324-1325 1330 1362-1363 1375 1403 1408- 1409 1415 1431-1432 1435 1467 1469 1482 1504 1524 1542 1547

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1550 1567 1578 1581 1583 1594 1597 1601-1602 1611-1612 1615 1618-1619 1621 1625 1637 1645 1647 1652 1654-1655 1660 1666 1669-1671 1684 1706 1722 1737- 1738 1742-1744 1760-1761 1763- 1765 1772 1774
adult liver	Clontech	ALV003	29 676 997 1063 1119 1536 1766
adult ovary	Invitrogen	AOV001	1 4-18 20-23 29 35-40 42-48 50- 51 53-58 61-63 65-66 68-69 73-75 77-78 80 82 85 87 89 97 100-101 103-104 106-108 110 113 115 118 122-124 126 128 133-134 136-140 142 145-147 149-157 161 166 168- 170 174 177-178 180 182-186 188- 189 192-203 207 209 211-215 219 221-224 229-230 234 242-243 246- 247 255 258 260-262 265-269 271- 272 274 277-281 284-286 288 290 295 299 301-302 304 307 309-311 313-314 316 321 323-326 330 332- 333 335-338 341 344 349 352-353 356 358 360 362 370-372 376-377 379-384 387 390-392 394 397-398 400 403 408-410 412 414-416 423- 424 426-427 430-435 439 443-446 448-449 451 453-455 462-463 468- 471 473 476-479 481-484 487 489- 494 496-497 499-501 503-505 509- 514 516-517 519-520 522 524 526 528-534 541-544 546-547 549 552 554-555 561-564 566-567 569-570 572-573 575-576 579 581 583 585- 588 590-591 593 595 597 599 601- 605 607-613 615 618-622 624-627 630 632-633 636-640 642 644-647 649-652 654-655 657-665 667-675 677-678 681 683-684 692-695 697- 710 714-721 723 725-727 729 732 734-735 743-746 750-751 753 758 763 765 767 772-773 775-778 780 783-784 786 788 790-791 794-796 800 803 805 809-811 813-815 818- 819 821-824 826 828-829 831-832 837-838 843-850 852-857 859-864 867 869 871-872 874-875 878-883 887-888 890-895 898-910 912-914 916 919-922 924 926-927 929-939 941 943-946 948-951 953 955-958 961-964 966-967 970-979 981-982 985-986 988-990 992 995-997 999- 1001 1004-1009 1011-1013 1016 1019-1020 1024-1025 1029-1031 1033-1035 1037 1039 1041-1047 1050-1051 1054-1060 1062-1064 1067-1070 1072-1073 1075-1076 1078-1079 1085-1086 1089-1090 1094-1096 1098-1103 1106-1108 1112-1117 1119-1120 1123-1127 1131-1135 1142-1143 1146-1149 1153 1156 1158 1163 1165-1166 1169-1171 1173-1175 1177-1178 1180 1183-1185 1190-1191 1195 1197-1200 1202 1205-1214 1217- 1219 1221-1226 1232-1235 1238- 1241 1243-1244 1247 1249 1252- 1254 1256-1258 1262 1265 1267- 1268 1270 1275 1278 1280-1283 1286-1289 1291 1293-1294 1298-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1299 1306 1308 1312 1317-1321 1323 1327 1329-1330 1332-1333 1338-1339 1341 1343-1351 1356 1359 1361 1365-1366 1371-1375 1377-1379 1383-1384 1386 1389 1394 1400 1404 1416-1417 1422- 1427 1429-1431 1435-1436 1439- 1443 1445-1450 1453-1454 1459 1463-1464 1466 1468 1470 1474- 1481 1484-1485 1488 1491 1493- 1494 1496-1498 1501-1504 1506- 1507 1511-1517 1519 1521-1524 1526-1527 1530-1531 1534-1536 1538-1539 1541 1546 1548-1550 1553 1555-1559 1561-1563 1566- 1567 1569-1570 1572 1574-1575 1578 1580-1581 1587-1588 1590- 1591 1595 1597-1598 1600-1606 1609 1611-1621 1623-1630 1634 1636 1638 1641 1643 1645 1647- 1657 1659-1662 1664 1667 1669- 1671 1673-1674 1676-1681 1683- 1690 1699 1702-1707 1710-1711 1713-1714 1716-1719 1723-1724 1726-1728 1731-1733 1735 1737- 1738 1740-1741 1743-1744 1748- 1751 1753 1755-1756 1760-1762 1765 1767-1768 1770-1771 1776 1778-1779 1783-1784 1786
adult placenta	Clontech	APL001	5-8 44-45 90-91 107-108 159 178 311 351 414 476 503 545 574 624 636 719 755 773 860 890-891 924 947 955-956 962 990 992 1002 1045 1202 1320 1369 1628 1686 1713-1714 1743-1744
placenta	Invitrogen	APL002	14-16 26 29 43 60-61 79-80 103 106 116 135 171 177 180 194 196 198 210 216 235-236 272 290 299 309 329 334 339 359 379-380 417 423 430 434-435 448 454 483 490- 491 517 522 631 723 725-726 728 738 746 769 818 843 854-855 857- 858 916 948 953-954 976 988-989 1005-1006 1013 1033 1036 1064 1068 1070 1086 1139 1144-1145 1160 1277 1285 1317-1320 1343 1345 1429 1435 1438 1454 1482 1486 1490 1512 1519 1532 1549 1592-1593 1602 1626 1647 1649 1664 1673 1675 1722 1727 1730 1746 1776
adult spleen	GIBCO	ASP001	3 5-8 12 15-16 19-21 24 29 34-36 44-45 57 60 82-83 87 89 94 98-99 103 106 108 117 119-121 139 141 147 152-153 155 166 169 171 174 178-180 196 198 201-206 209-211 215 219 234 253-254 256 258 264 272 280-281 290 295 302 309 312 325 333 341 349 358 372 382 386- 387 394 406 414 431 434-436 446 448 451 473 481 490-493 500 503 505 517 519 530 534 536-540 547 554 557 574-576 582 592 595 604 611-612 620-621 623 631-632 642 652 659 661 667 671 673-675 684 700 721 728 730 732 738 742-744 746 762 765 774 780 788-789 794 810-811 817 822 830 832 845 848 852-853 858 862 866 874 879 882

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			884 906-908 912 919 921-923 926- 927 934 942 949 957-958 963 977- 978 983 990 992-994 996-997 999 1005-1007 1010 1012 1031 1036 1042-1044 1046 1049 1059 1068 1070 1076 1089-1090 1094 1103 1109 1113 1115 1124 1140 1163 1170 1174 1177 1190 1196 1219- 1220 1226-1227 1229 1236 1241 1246 1258 1269 1271 1274 1295 1301 1320 1322 1330 1334-1335 1339 1349 1351 1353 1359-1360 1364 1369 1374 1386 1397 1413 1417 1434 1436-1437 1439 1468 1474 1477 1480 1485-1487 1498 1512 1522 1525 1544-1549 1553 1560 1567 1591 1600 1631 1636 1651 1654-1655 1658 1662 1670 1674 1678-1679 1684 1686 1700 1727 1733 1738 1740-1741 1760- 1761 1774 1779 1781-1782
testis	GIBCO	ATS001	5-8 10 26 30-31 47 50-51 57 68- 69 82 84-85 97 102 113 119 137 139 150 152 154 156 163 169 174 176-177 192 194 196-197 212-215 227-228 247 255 258 261 282 285 288-289 301 307 311 316 330 334 349 370-372 392 398 410 415 426- 427 430-431 433 437 446 454 461 469 473 477 481-482 493 499 502- 503 513 522 526 547 552-553 563- 564 572-573 575-576 581-582 585 599-602 605 612 615-617 620 631 637 647 649-650 656 660 665 670 674-675 712 719-721 723 728 731 738 744 746 773 780 784 788-789 802 804 809 811 814 826 831 837 843 845 848 859 866 869 877 905 913 916 919 921 926 929 937 950 960 963 971 975 977 981 990 992- 993 1007 1016 1029-1030 1034- 1035 1038-1039 1045 1059-1060 1064 1070 1072-1073 1087 1089 1097 1099-1102 1104 1108 1113 1141 1149 1161-1162 1175 1208- 1209 1222 1227 1229 1231 1235 1238-1239 1243 1253 1285 1287- 1289 1291-1293 1307 1311 1317- 1320 1330 1332 1338 1345 1369 1373-1374 1379 1389 1399-1400 1409 1423-1424 1430 1435-1437 1443 1459 1484 1486 1490 1493 1496-1497 1501 1505 1509-1513 1527 1530-1531 1533 1537 1546 1549 1563 1565 1567 1569 1571 1577 1586 1591 1599 1602 1625 1628 1630-1632 1636 1639 1642 1649 1661-1662 1666-1667 1670 1675 1684 1690 1699 1705 1712 1717 1724 1730 1737-1738 1752 1767 1779
Genomic DNA from BAC 63I18	Research Genetics (CITB BAC Library)	BAC001	686 1352 1412
Genomic DNA from BAC 393I6	Research Genetics (CITB BAC Library)	BAC002	1411-1412

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
Genomic DNA from BAC 393I6	Research Genetics (CITE BAC Library)	BAC003	1352
adult bladder	Invitrogen	BLD001	5-8 17-18 22-23 33 37-39 56-57 80 93 100 120-121 169 201 237 251-252 272 278 311 348 363 382 413 415 424 430 443 483 502 542- 543 562 564 607 616-617 626 635 652 667 671 710 727 755-756 762 773 786 788 837 840 866 893 898 909 918 929 966 977 983 1016 1025 1055 1073 1082 1140 1167 1185 1189 1199 1270 1369 1481 1536 1560 1573 1596 1614 1636- 1637 1649-1650 1654-1655 1658 1669 1671 1690 1719 1727 1731- 1732 1739 1741 1760-1761 1779
bone marrow	Clontech	BMD001	3-8 11 13 18 29-31 33 35-36 40 43-45 47-48 50-51 57 60 65-66 75 80 82 85 88-89 94 100 103 107 110 115 118-119 124-125 133-134 136-137 139-141 146 150 152-153 155 161 163 168-170 172 178-180 187 192-193 197-198 203-205 210- 213 215 217 219 222 224-226 233 235-237 242-244 255 258 260 263- 264 266 273 276 278 283 286 290 295 301-302 307 312-313 321 330 333 339 343 352 357-358 370-371 382 384-385 387 389 394 408 410 412 416 421 424-427 429-431 436- 437 439 441-442 445 447 454-456 461-462 471-472 475 477-479 481- 482 485 488 493 498 500 503-506 513 516 519 523-524 526 530 535- 540 542 544-545 549 555 565 567 569-577 581 583-586 588 593 601 603-604 608-609 613-619 621-622 632-633 636-637 642 649-650 656- 660 666 670 672 674-675 679 683 701 708 716 718-720 731 735-736 740-742 744-745 752 761 765 772- 773 775-778 780 785-786 789-791 796 798 802 810-812 823-824 826 830 832-833 837-838 843-844 848- 855 858-859 866-867 869 878-880 883 890-892 896 903 905 908 912- 914 922-924 927 930-931 937 939- 941 952-953 955-958 963 969 973 976 981 985 987 990 992 995 1000 1002 1005-1007 1013 1016 1025 1028-1031 1033 1035 1037 1039 1042 1044 1047 1050 1053-1054 1059 1061 1063 1066 1070-1071 1079 1106 1110-1113 1115-1117 1124 1126 1134-1135 1142 1144- 1145 1163 1172 1178 1197 1199- 1200 1202 1216-1217 1224 1227- 1228 1240 1246 1254 1261 1266 1270 1278 1281 1285 1287 1290- 1291 1293 1299-1301 1308 1314 1317-1320 1327 1331 1339 1343 1346 1349 1353 1356 1361 1367 1369 1372-1374 1379-1380 1394 1400 1403 1406 1408 1413 1417 1419 1423 1425-1427 1430-1431 1433 1439 1443 1446-1449 1459 1463-1464 1482 1486 1493-1494

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1506 1509 1513 1521-1522 1524 1526 1528 1531 1536-1537 1543 1546 1548-1549 1552 1554-1555 1557-1559 1571-1572 1581 1589- 1592 1597-1600 1609 1614 1621 1626-1628 1630-1632 1634 1636 1638-1639 1641 1646-1647 1651 1653-1655 1661-1662 1676-1681 1684 1686 1690 1702 1707 1711 1713-1714 1717 1720 1722-1723 1727 1737-1738 1740 1758 1767 1772 1781-1782 1785-1786
bone marrow	Clontech	BMD002	11 15-16 19 30-31 35-36 68-69 75 83-84 93 99 103 108-109 118 137 139 169-170 174 177 180 190 193 212-213 219 222 225-226 232 237 255 259 264 273-274 284 286 290- 292 295 301 303-304 307 312-313 316 324 326 330 334-335 348 352- 353 357 360 370-373 384 386-387 397 403-404 414-416 421 425-427 429-430 433-436 440 444 451 454 465-466 472 475 478 491 493 516 520 523 525 531 545 548 552 566 569-570 581 583 590-591 597-598 601 616-617 621 641 650 652 656 659 671 674-675 679 684 710 718- 719 728 734 737-738 742 761 765 774-778 790 811 814 818 830 834- 836 854-855 859 866 869 871 878- 879 884 889 892 904 922-923 932 990 992 998 1001 1004 1016 1036 1042 1048 1051 1054-1055 1058 1088-1089 1106 1112-1114 1155 1157 1192 1200 1223 1227-1228 1236-1237 1260-1261 1282-1283 1285 1287 1295 1314 1317-1321 1324-1327 1330 1333 1341 1343 1347 1350 1353 1355-1357 1367 1369-1370 1373 1377 1379 1381 1383-1384 1394 1397 1400 1406 1413 1417 1425-1427 1438 1442 1446 1459-1460 1470 1493 1505 1521 1536 1546-1549 1560 1573- 1574 1578 1598-1600 1621 1626 1631 1634 1646 1649 1653 1656 1658 1669-1670 1683-1684 1687- 1688 1690-1693 1696 1699 1702 1704 1707-1709 1711 1720 1722- 1723 1725 1727 1729 1731-1733 1738-1740 1743-1746 1752 1755 1760-1761 1767 1777 1781-1782 1786
bone marrow	Clontech	BMD004	73-74 503 922 1036 1711
bone marrow	Clontech	BMD007	95-96 866 1320 1475
adult colon	Invitrogen	CLN001	17 56-58 103 110 117 144 150 171 179 185 188-189 201 204-206 210 218-221 225-226 231 237 251 277 288 310 312 320 333 359 386 388 394 408 420 455 481 485 503 510- 512 590-591 615 635 647-648 665 672 684 697 710 725-726 743 780 786 788 826-827 848-850 854-855 858 866 872 898 918 921-923 953 976 983 993 1005-1006 1017 1020 1025 1027 1054-1055 1063 1068- 1069 1140 1153 1170 1185 1196 1199 1220 1280 1314-1315 1320 1345 1351 1355 1369 1428 1439

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1462-1464 1512 1556 1583 1587 1594 1596 1614 1625-1626 1631 1639 1645 1650 1675-1677 1687- 1688 1701 1713-1714 1724 1740 1765
Mixture of 16 tissues - mRNAs	Various Vendors	CTL016	401 1490 1686
Mixture of 16 tissues - mRNAs*	Various Vendors	CTL021	312 782 1132-1133 1403 1712 1715
adult cervix	BioChain	CVX001	1 4-8 11 13 18-21 25-26 30-31 33 37-39 43 46-47 58 61 64-66 71 73-74 82 85 94 100 103-104 113 118 122 126 130 134 140 147 153- 156 163 170 179 181 186 192 195- 196 198 201-202 218-219 222 229- 231 257 266 276-277 285-286 288 298 301-302 304 307 312-314 324 326 329-330 332 335 342 352 358 362 371-372 376 379 381-382 384 388 398 400 410 414 416 419-420 426-427 430-431 433-436 439 446 448 461-462 464 471-477 479 482- 483 491 493 496 503 506 510-513 516-517 526 530 535 542-544 546- 547 557 561 572-573 575-577 581- 582 585-586 588-589 593-594 600 602 604-605 607-609 612 615-619 623 644 650 654 657-658 662-665 670 672 680 683 691-694 698 706 708-709 711 713 720-721 727 729 731-732 737 745-747 753-754 760 765 771 774-777 780 790 793 796 798 800 803 805 818 826 828 831- 832 834-836 843 847-848 851-855 857-860 864-866 869 871 876 878- 880 882 887 890-891 897 899-902 905-908 912-913 916 918-919 922 927 932 934-938 944 948 955-956 958 963-964 967 969-970 972 976 978-979 983 985 990 992 1000 1005-1007 1016-1017 1024 1027 1033 1036 1038 1045 1047 1053- 1056 1066-1067 1071 1073 1075 1079 1082 1098 1113 1124 1129 1134 1139 1146-1149 1163 1167 1170 1173 1175 1177 1181 1197 1200 1202 1211 1214 1216 1221- 1222 1225 1227 1232-1234 1240- 1241 1243 1258 1264-1265 1268 1270 1279 1287-1290 1308 1310- 1311 1316 1320 1323 1327 1345 1349 1353-1354 1360 1372-1374 1383-1384 1386 1394 1397 1405-

* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1406 1416 1425-1427 1431 1436-1437 1442 1446 1448 1453 1459 1466 1472 1478 1482 1496 1501-1503 1506 1512 1522 1527-1528 1531 1533 1541 1547 1569 1571 1585 1589 1597-1598 1600 1608-1609 1614-1616 1620 1623-1624 1626-1628 1630 1638 1641 1643 1649 1653 1656 1662 1667 1669 1674-1675 1683 1685-1688 1699 1702 1709-1710 1715 1717 1722 1724 1729 1731-1732 1735-1739 1741 1743-1744 1748-1749 1755 1760-1762 1767 1773 1778 1785-1786
diaphragm	BioChain	DIA002	137 282 289 730 780 986 1409 1478 1599 1614
endothelial cells	Strategene	EDT001	3 5-10 13 15-21 24-26 29 34 37-39 42 44-45 50-51 53-55 57-58 60-61 65-66 68-69 73-74 77-78 80 82-83 85 87 89 93-96 101-105 108 110 112-114 116 118-122 124 128 133-134 137-142 147-150 152-153 161-163 166-172 176-179 187 190 192 194 196-201 204-207 210 212-214 220 224 229-230 233 235-236 240-241 251-252 258 261-262 265 267-269 272 276-277 279-281 284-285 288 290 295-296 301-302 310-311 313 316 321 325 329 331-333 335 340-342 351-355 360 371 375 380-382 384 387 390 392 397 400 407-408 410 412 414 416 425-427 431 434-436 439 444-445 449 454 463-464 472-475 477-479 486 488-490 497-498 500-504 510-513 516-519 522 524 526-528 532-534 536-540 542-546 548 561-563 566-567 572-576 579 581 585-586 589 593 595 597 599 603 607-612 615-617 620 622 626 630 632-634 638-641 644 647 656-660 662-664 670 673 678 680-682 692-697 707 709-710 712-713 719 730 732 734 736 738 743-746 751 759 768 771 773 775-778 783 786-789 793 800 803 805-807 810-811 814 816-818 821-822 824 826 828-829 832 834-838 842-845 848-850 854-860 862 864 869 871 874 876-879 883 885 887 890-891 894-895 898-900 903 908 910-913 916 919-922 924 926-928 930-935 939 943 948-949 951-954 957 959-961 964 969-970 973 975-978 983-984 988-990 992-993 996-997 1000 1002 1004-1013 1016-1020 1022-1025 1028 1031 1033-1034 1038-1046 1050 1055-1056 1059-1060 1062-1064 1067-1070 1072-1074 1076 1078 1082 1086-1087 1089-1090 1093-1097 1099-1103 1107 1109-1113 1116-1117 1124-1126 1128-1131 1134-1135 1138 1140 1144-1145 1148-1149 1153 1157 1160 1163 1171 1183-1184 1198-1199 1202 1205-1207 1211 1216-1217 1219 1221 1225 1229 1232-1235 1238-1241 1243-1244 1246 1250 1253 1257-1258 1261

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1265-1266 1268 1270-1271 1274- 1277 1280-1283 1285-1286 1288- 1290 1293 1295 1298 1308 1312 1317-1320 1324-1325 1327 1329- 1330 1334-1335 1338 1342-1343 1345-1347 1350 1355-1356 1359 1367 1369 1374 1376 1379 1398 1400 1406 1408 1414 1417 1419 1424-1426 1428-1431 1434-1438 1440-1442 1448 1450 1462-1466 1468 1472 1474 1478 1487-1488 1491-1493 1501-1504 1506 1509 1511 1516 1520-1521 1526 1529 1531 1536-1537 1539-1540 1546- 1547 1549 1552 1555 1557-1559 1561-1565 1568 1571 1575 1578- 1579 1581-1583 1587-1588 1590 1592 1597 1605-1606 1611 1613 1615 1618-1621 1624-1628 1630- 1631 1634 1636 1638 1641 1643- 1650 1652-1659 1664 1666-1667 1669 1671 1675-1681 1683-1688 1696-1698 1703 1711 1715-1716 1719 1722-1723 1726 1731-1733 1736 1739-1741 1743-1744 1749 1755 1760-1761 1765 1767-1768 1771-1773 1776 1779 1783-1786
Genomic clones from the short arm of chromosome 8 esophagus	Genomic DNA from Genetic Research BioChain	EPM001 ESO002	286 686 1297 1303-1304 1352 1411-1412 1754 131-132 261 289 380 503 860 892 1000 1007 1397
fetal brain	Clontech	FBR001	62-63 89 112 126 194 322 336-338 379 391 411 481 546 563 607 679 710 867 1012 1031 1055 1251 1262 1320 1407 1643 1652 1686 1731- 1732 1746 1765
fetal brain	Clontech	FBR004	68-69 90-91 139 212-213 301 331 362 374 403 436 611 645-646 659 668 670 691 785 805 845 1163 1209 1216 1232-1233 1238-1239 1387 1410 1416 1430 1496 1536 1547 1593
fetal brain	Clontech	FBR006	5-9 25 43 60 62-63 65-66 70 72 80 87 92 101 103 108 114 136 139 149 152-153 157 168 171-172 175 207-208 210 212-213 221-226 237- 238 251-253 266 272 279-281 295 301-302 307 310 317-318 321-324 330 333-334 336-338 346-347 352 357 370 373 377 379-380 382 384 391-392 397 399 402 406-408 410- 411 417 421 424 426-427 430 436- 437 440-443 454 460 464 467 473 476 483 488-489 495 497 508 510- 513 516 519-520 524 530 537-540 544 547 550 561 567 572-574 582 590-591 595 597 604 607-609 615 623 628-629 631 634 638-640 655 657-658 660 665 669 674-675 679 689 691-694 696-697 699 701 706 710 716 720 728 732 734 736 742- 744 757-760 763 775-778 780 799 806-807 810 817-818 826 839 843 858 861 864 871-872 884 890-891 894-895 898 904 915 921-923 935- 936 938 945 950 952 955-956 958- 959 961 963 967 969-971 990 992

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			999 1001 1005-1006 1008 1013 1016 1022 1024 1029-1030 1032 1035 1042 1047-1048 1052 1056 1065 1067 1070 1082 1089 1109 1114-1115 1119 1131 1143-1149 1151 1153-1156 1160 1163 1167 1172-1173 1178 1184 1186 1188 1190-1200 1211 1216 1222-1223 1226-1227 1229 1231 1236 1245 1253-1255 1258 1260 1262 1266 1270-1273 1281 1287 1308-1309 1314 1317-1320 1326 1334-1335 1339 1341 1344 1350 1356 1369- 1371 1373 1376 1379 1381-1382 1386 1392 1396-1398 1419 1423 1425-1426 1428-1429 1432 1437 1440-1441 1448 1466 1470 1482 1502-1503 1507 1511 1513 1516 1519 1536 1544 1549-1550 1557- 1559 1573 1589-1590 1598 1608 1611-1614 1619 1621 1625-1626 1640 1651 1657-1658 1676-1679 1693 1696 1703-1704 1713-1714 1718 1720 1722 1724 1726 1728 1730-1733 1735-1736 1738-1739 1742 1745 1755 1759-1761 1765 1767 1771-1772 1777 1779-1780 1786
fetal brain	Clontech	FBRs03	235-236 520 864 1068 1188 1587
fetal brain	Invitrogen	FBT002	15-18 20-21 24-25 29 34 43 61-63 77-78 98 101 103 107-108 128 130 136 146 148 165-166 171 174 181 185 196-198 204-205 208 223 230 235-236 251 253 261 268-269 280- 281 284-285 288 309-311 321 329 334 339 346-347 350 357-359 381- 383 390 407 418-419 430 434-435 438 443-444 461 464-466 483 490 494 509 516 519 522 527 557 561- 562 572-573 590-591 595 597 623 632 647-648 650 655 669-670 672 682 690-691 700-701 710 717 736 746 782 784 788-789 814-815 825 829 840-841 847 854-855 857-858 897-900 904 919 925 935-937 946 948-949 954 960-962 966 969-970 986 996 1000-1001 1005-1007 1012 1014 1022-1028 1045 1052 1055 1068 1070 1072 1078 1082 1085 1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156- 1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776 1778 1781-1782 1786
fetal heart	Invitrogen	FHR001	105 124 180 289 864 1036 1148 1229 1614 1616 1762 1785
fetal kidney	Clontech	FKD001	5-8 11 40 47 57 65-66 82 85 102 124 163 171 216 222 224 235-236

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			258 277 280-281 307 310 314 330 371 387 392 395 403 422-423 431 436 443 455 469 500 519 522 542 563 572-573 585 600 619 623 650 654 657-658 660 679 719 731 780 798 821 833 844 854-855 857 864 868 878 911 929 958 960 969 990 992 1007 1046 1087 1103 1129 1139 1285 1312 1331 1355 1369 1371 1376 1391 1422 1425-1426 1440-1441 1470 1543 1598 1601 1618 1631 1651 1654-1655 1669 1678-1679 1691-1692 1733 1785
fetal kidney	Clontech	FKD002	352 384 426-427 440 583 602 1060 1131 1324-1325 1636
fetal kidney	Invitrogen	FKD007	20-21 82 163 335 679 988-989 1000 1227 1230 1320 1554
fetal lung	Clontech	FLG001	35-36 94 323 371 398 426-427 445 473 549 560 604 616-617 626 631 649 651 719 746 786-787 832 842 849-850 864 894-895 1075 1178 1182 1200 1206 1309 1311 1345 1429 1493 1567 1576 1620 1686
fetal lung	Invitrogen	FLG003	9 15-16 29 41 47 68-69 83 88-89 102 124 137 152-153 165 196 224 229 231 249 254 256 267 291-292 300 325 333 344-345 352 373 376 379 384 408 426-427 430 432 467- 468 475 483 488 493 516 531 535 545 547 549 564 582 602 623 644 660 662-664 670 673 725-726 728 761 766-767 774 805 830 852-853 864 875 921 932 937 946 949 963 988-989 1014 1016-1017 1024 1027 1090 1097 1170 1185 1200 1215- 1216 1224 1258 1290 1309 1320 1342 1347 1355 1369 1381 1413- 1414 1431 1438 1449 1491 1512 1536 1547 1557-1560 1567 1590 1601 1636 1644 1653-1655 1662 1667 1671 1675 1680-1681 1706 1739 1760-1761 1769
fetal lung	Clontech	FLG004	103 276 334 465-466 737 843 1131 1614 1658
fetal liver- spleen	Columbia University	FLS001	3-11 13 15-21 25 30-39 41-48 50- 51 54 56-58 60-66 68-69 72 75 77-80 82-83 85 87 89 92-103 105- 110 112 116-124 126-127 130 133 135-139 141 144 147-149 152-153 157 163-165 167-172 174 176-178 180 186 188-190 193-194 196 198- 200 202-206 210-214 219 221-231 233-236 240-244 246-247 250-251 255-256 258 261-265 268-269 272 274 276-278 280-281 284-286 288 293 295 299-301 304 306-307 309 311 314 316 318 320-321 326 329- 332 342 344-345 350 352-353 356- 358 360 362 370-374 376 378-384 386-387 390 392-393 400-401 403 406 408 410-412 415 417 419 422- 437 439-442 444-445 448 452-454 456 459 461-470 472-479 481-483 487-488 490-491 493 500-501 503- 506 509-513 515-520 522-524 526- 529 531 534 536-540 542 547-549 553-554 561-562 564 567-568 571- 576 579 581 583 585-597 599-605

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			607 610-613 615-621 623-624 626 628-634 636-640 644 647-650 655- 660 665 669-670 672 674-675 678 681-682 684 690-695 697 702 708- 710 713-714 716-719 725-728 730- 731 734 736 738 740-741 743-746 748 750-751 759-766 768 772 774- 777 779 783-788 793 796 798 800- 805 808 810-812 814 818-819 821- 824 826-832 834-837 843-847 849- 867 869-876 878-883 887 889-895 897-898 902 904-914 916 919 921- 928 930-937 939 945-950 953-958 960-961 963-965 967 969 971 974- 978 980-983 986 988-990 992-993 995-997 1000-1002 1004-1008 1012 1014 1016-1019 1025-1026 1028- 1031 1033 1035-1036 1039-1044 1047 1049-1050 1053-1056 1058- 1059 1061-1064 1067-1070 1072- 1074 1076 1078 1082 1085-1087 1089-1090 1097 1099-1103 1107- 1113 1115-1119 1121-1123 1125 1127-1128 1131-1134 1136-1137 1144-1150 1153 1159-1160 1163 1170 1175 1177-1178 1188 1190- 1192 1195-1200 1202 1206 1208- 1211 1214 1216 1218 1221-1222 1225 1227 1234 1237 1241 1244 1246-1247 1251 1254 1258 1261 1266 1268 1270-1273 1277-1282 1284-1285 1287-1290 1294 1299- 1300 1306-1308 1313-1320 1324- 1325 1327 1330 1332-1333 1338 1341 1343 1345-1347 1349-1350 1353-1360 1362-1363 1365-1367 1369-1370 1372-1374 1376 1378- 1381 1383-1384 1386 1389-1391 1400 1402-1403 1405-1410 1413 1415 1417-1419 1422-1429 1431 1435-1437 1439-1442 1445-1446 1448-1449 1454 1458-1459 1466- 1470 1472 1474 1477-1478 1480 1482 1485 1491-1493 1496-1498 1501-1507 1509 1511-1512 1516- 1519 1524-1526 1529 1532 1536- 1541 1546-1547 1549-1550 1552- 1554 1562 1564 1569 1572 1574- 1575 1578 1581 1583 1587-1588 1591-1592 1594-1595 1597-1598 1600-1604 1611-1612 1614-1615 1617-1618 1620-1622 1624-1625 1627-1628 1630-1632 1634-1639 1645-1651 1653-1662 1664 1667- 1669 1671 1673-1674 1676-1688 1690 1696 1701-1703 1706-1709 1711 1713-1714 1718-1719 1722 1724-1727 1731-1733 1738 1740- 1741 1743-1744 1746 1748 1751- 1752 1754 1760-1765 1767-1773 1780 1783-1786
fetal liver- spleen	Columbia University	FLS002	3-11 13 15-21 26 29 32 35-39 42 44-45 48 50-51 54-55 57-58 61 64 68-69 73-75 78 80 82 84 87 95-98 100 103 105 107-108 110 112-113 116-119 122-125 128 130 137-138 145 147-153 155 157 159 161-163 166 168 171-172 174-175 177 181 188-189 193-194 196-198 200-203

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			206 212-215 219-221 223 225-229 231-232 240-244 246-247 250-251 258-259 262 264 268-269 272 275 277 280-281 284 286 288 290-292 295 298-299 301-304 306 308-310 318 320-321 323 325 329 331 334 342 348-349 352-353 356 359 368 371 374 376-379 381-384 386-387 392-393 397-398 400-401 403 410- 413 421 423 426-427 429-430 433- 436 438 440 443 445 448 451-452 454-455 460-463 465-467 469 471- 473 475-476 478-479 481-483 487 490-491 493-494 497 500-501 503- 505 509-513 515-517 519-520 524 526-531 534 537-542 544 547 552- 554 556 558 561-562 564-567 571- 577 583-587 590-591 593 595 597 601 604-606 608-613 616-617 619- 624 626-632 634 637-642 644 647 649-652 654-659 662-665 669-672 674-675 681-682 685 688 690 696 698 700-703 707 709-710 713 717 719-721 723-724 728 731-732 734 737-738 742-745 748 752 754 759 763-766 768 770 773-777 780 782 784 786 791 795-798 801-802 805 808 811-812 818 823-824 826-827 832 834-837 839 843 846 848-856 858-861 865 867 869 871 873-874 876 878 881-882 887 889 892 894- 898 901-902 904 906-908 913-915 919 921-924 926-932 934-935 937 939-941 943 946-947 950 953 958 961 965-967 971 973-975 977-979 981 984-985 990 992-993 995-997 999 1001 1004-1007 1009-1011 1013 1016 1020 1023 1025 1027- 1031 1033-1035 1039-1042 1044- 1045 1049 1053 1055-1056 1058- 1059 1062 1064-1065 1067-1070 1072-1074 1079 1082 1087 1089 1093 1097 1099-1103 1105-1107 1109-1114 1123 1125-1127 1132- 1134 1140 1143-1145 1148-1150 1156 1158 1160 1163 1172-1173 1177-1178 1181-1184 1190-1192 1195-1197 1199 1204 1206 1208 1211 1214 1216 1219 1227 1230 1234-1235 1237 1240-1241 1243 1245 1247 1256 1258 1260-1261 1264 1268 1270-1271 1275 1278- 1279 1284-1286 1288-1289 1299- 1301 1306 1308 1312 1314 1317- 1319 1323-1325 1327-1330 1334- 1335 1339 1343-1347 1349-1350 1354-1355 1357 1360 1362-1363 1365-1367 1369 1372 1376 1378- 1380 1386 1389-1391 1394 1400 1403 1406 1409 1416-1419 1422- 1427 1429 1435 1437-1438 1440- 1442 1446 1448-1450 1453 1460- 1461 1468 1470 1472 1474-1475 1478 1482 1486 1490-1493 1496 1498 1500-1504 1506 1508-1509 1511-1512 1516 1518-1519 1521 1524-1528 1531 1536-1538 1543 1547 1550 1554 1556 1564 1567- 1569 1580 1587-1588 1591-1592

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1597-1598 1600-1601 1611-1612 1618-1628 1630-1631 1635-1638 1641 1646-1649 1652 1654-1659 1661-1662 1664 1667-1669 1674 1676-1679 1683-1684 1686-1688 1691-1692 1699 1702 1707 1711 1713-1714 1717 1719 1722 1726- 1727 1730-1733 1738 1740 1743- 1744 1748-1752 1758 1760-1761 1763-1764 1767 1769 1772-1773 1776 1779 1783-1786
fetal liver-spleen	Columbia University	FLS003	103 300 318 321 352 372 379 381 384 392-393 403 422 424 429 434- 435 440 444 453 503 515 544 592 978 1064 1324-1325 1327 1333 1357 1369 1378 1418 1424 1622 1646 1649 1680-1681 1689-1690 1717 1743-1744 1769
fetal liver	Invitrogen	FLV001	15-16 26 34 58 61 64 70 75 78 89 98 105 112 116 120-121 123 133 151 165 176 180 194-196 198 200 204-206 210-211 220 225-226 230 235-236 239 247 259 261 267 272 277 280-281 303 310 313 317 320- 321 329 344 356 371 374 376 379- 382 395 408 412 414 419 429 434- 435 441-442 465-466 490 494 504- 506 509 522 527 534 552-553 562 567 569-570 572-574 607 631 657- 658 667 669 672 685-686 702 717 725-726 732 748 759 761 778 784 786 809 817 829 837 857 861 872- 873 875 881 889 894-895 909 911 916 954 963 967 974 977 986 988- 989 993 995 997 1000 1005-1006 1008 1014-1015 1020 1042-1043 1070 1086-1087 1089-1090 1118- 1119 1122 1144-1145 1148 1153 1157 1159 1183 1195-1196 1227 1250 1257-1258 1262 1267 1280 1285 1307 1312 1314 1317-1320 1344-1345 1349-1350 1355 1362- 1363 1403 1405 1415 1419 1425- 1426 1429 1431 1442 1448 1463- 1464 1469-1470 1489 1528 1536 1539 1549-1550 1557-1562 1577 1583 1598 1601 1611 1615 1622 1644 1649 1666 1674 1706 1721 1738 1746 1763-1765 1774 1776 1779
fetal liver	Clontech	FLV002	676 998 1719
fetal liver	Clontech	FLV004	93 133 214 301 355 374 379 555 581 601 679 837 847 859 1123 1236 1270 1313 1324-1325 1327 1355 1367 1425-1426 1536 1690 1733 1760-1761
fetal muscle	Invitrogen	FMS001	26 37-39 50-51 58 84 86 89 98 113 128 131-132 139 155 172 186 194 198 201 206 211 230-231 256 261 276 282 286 302 325 359 361 376 379 383 398 412-413 419 430 436 448 452 462-463 473 477 503 519 529 561 569-570 590-591 597 607 623 626 635 647 660 672 715 725-726 730 733 761 775-777 788 826 837 860 874 913 915 921 935 970 980 986 988-990 992 1000- 1001 1007 1014 1027 1035-1036 1045 1060 1064 1070 1083 1097

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1099-1102 1116-1117 1121 1164 1173 1198 1208 1228 1240 1258 1266 1270 1277 1298 1317-1320 1324-1325 1329 1336-1337 1369 1383-1384 1399-1400 1403 1409 1433 1505 1514 1542 1551 1554 1557-1559 1562 1589 1599 1620 1632 1644 1650 1652 1671 1675 1712 1725-1726 1743-1744 1754 1766
fetal muscle	Invitrogen	FMS002	119 221 273 402 426-427 463 547 599 736 869 1000 1033 1083 1266 1431 1440-1441 1468 1545 1599 1673 1678-1679 1687-1688 1710 1712-1714 1723 1725 1731-1733 1743-1744 1760-1761 1767
fetal skin	Invitrogen	FSK001	1 4-11 15-16 20-23 25 29 33 40 43 46 56-57 60-61 64-66 75 82 87 97-98 105 107-108 113 118-119 123 133 135-137 139 144 146 148 151-153 156 163 170 176 180 188- 189 197-198 200 202-203 210 218 222 231 246-247 261 263 265-270 277 285-286 290 293 299 301 307 311 321 325 328 330 333-335 339 341 345 351-352 355-356 358-359 362 368 370 372 376 379-382 384 388 394 404-405 408-409 411-412 419-420 424 426-427 436 441-442 445 448-449 454 462 465-466 472 476 490 493 504 506 509 515-517 519 526 531 537-540 547 549 560- 561 567 572-573 581 584 589 611- 612 615 623 630-631 635 647 649 651 657-658 660 662-665 667 669 672 676 678 681 688 701 704-705 709-710 713 717 720-721 725-726 728-729 732 748 750 753 759 764 766 770 775-777 780-781 786 788- 789 798 809 811 814 816-817 822 824-826 831 842 857 859 861 863- 864 881 894-895 908 910-911 916 918 922-923 928 932-933 935 937 946 948-949 953 960-961 966-967 970 975 977 986 990 992-993 999- 1000 1004 1007 1013 1018 1025 1027 1032 1035 1041-1043 1054 1057-1058 1060 1062-1064 1069 1072 1077 1090-1091 1097 1099- 1103 1108 1113 1119 1123 1128 1131 1134 1140 1148-1149 1152- 1153 1156 1163 1167 1178 1182 1189 1192 1195-1196 1198 1201- 1205 1208 1211-1212 1216 1219- 1220 1222 1225 1240 1243 1258 1266-1267 1274 1277 1280 1282- 1285 1299 1310 1317-1322 1324- 1325 1329-1330 1342 1344 1346 1349-1351 1354-1357 1365-1366 1369 1371 1373 1376 1378 1380 1383-1384 1387 1399-1400 1405 1410 1427 1429 1431 1433-1435 1439-1441 1448-1449 1454 1457 1468 1470 1472 1475 1480-1481 1487 1490-1491 1493 1498 1509 1512 1521 1525-1526 1529 1535- 1536 1547 1549 1557-1559 1588 1592 1595 1597-1598 1601 1603- 1604 1608 1611 1614 1618 1624-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1626 1632 1634 1636 1641 1643- 1644 1646 1654-1657 1660-1662 1665 1668 1675 1685 1687-1689 1702-1703 1709-1710 1716 1719 1724 1727 1731-1732 1737-1740 1742 1747 1749 1755 1760-1761 1765 1772 1776-1777 1779-1780 1786
fetal skin	Invitrogen	FSK002	13 286 302 307 313 321 330 335 339 341 354 370 372 385 400 402 408 414 426-427 433 436 450 454 515 544 585 598 767 810 845 939 1076 1109 1155 1317-1320 1326 1333-1335 1343 1347 1350 1369- 1371 1377-1378 1391 1397 1422 1466 1647 1656 1678-1679 1687- 1688 1693 1718 1721 1725 1731- 1732 1739 1755
fetal spleen	BioChain	FSP001	110 137 211 353 589 927 1108 1639 1771
umbilical cord	BioChain	FUC001	4-8 10 12 14 17 33-36 44-46 57 64 68-69 75 82 85 101 104 113- 114 116 119 122-124 133 137 153- 154 157 161 163 166-167 175 181- 184 186 192 197-198 200-202 212- 215 230 234 246-247 251 256 263 267 271-272 280-281 284 295 301 314 317 321 326 333-335 345 351 356 368 371-373 379-380 386 390 392 394 406 408-410 412 414 416 420 424 427 430-436 438 444-446 454 459 461 463 467 473 482-483 486 488 490 495 504 509 524 526 537-540 547 555 561 574-577 588- 591 593 606 615 620-621 632 637 645-647 650 659-660 662-664 667- 668 674-675 684 687 696 698 701 703-705 709 711 714 719-720 725- 727 732 749-750 762 765 771 775- 777 780 789-791 793 796 802-803 814-817 822 833 843 845 848 858 861 864 875 879 888 894-895 897- 900 903 906-907 911-912 925 930- 933 936 940 948 953 960 966 977 984 990 992 998 1000-1001 1005- 1007 1016 1023 1025 1037 1046- 1047 1059 1061-1063 1073 1076- 1077 1089 1094-1097 1112-1113 1115 1134 1144-1148 1151 1154 1156 1163 1171 1197 1204-1205 1208 1216 1218 1224 1234-1235 1243-1244 1246 1279 1283 1286- 1287 1298 1316 1320 1344 1346 1350 1357 1359 1371 1373 1375 1381 1398 1400 1403 1408 1414 1424 1427-1428 1431 1433 1440- 1442 1446 1454-1455 1479 1482 1484-1485 1489 1492-1493 1504- 1505 1513 1525 1527 1536 1538 1546 1565 1567 1571 1573 1575- 1576 1578-1579 1591 1595 1600- 1601 1608 1612 1615 1621 1624 1626 1636-1637 1647-1648 1651 1653 1656 1658 1661-1662 1672 1675 1682 1684 1686-1688 1690 1709-1710 1722 1727 1729 1735- 1738 1740-1741 1760-1761 1768
fetal brain	GIBCO	HFB001	4 9 11-13 17-18 22-23 25 37-39 42-47 50-51 54-55 58 60-61 65-66

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			72 75 77 80 82 85 90-91 94 100- 102 107 110 112-116 118-119 122- 123 126 128 134 136-140 147-148 153-155 157 161 165 169-172 175 181 186 188-189 197-198 204-206 208 210 215 222-223 225-226 230 235-238 240-241 247 253 256-258 260-262 267-269 276 279-281 284 286 289 298 300-302 307 310 318 321-323 325 330-331 339 341 346- 349 352 354 356-359 362 364-365 371-372 377 379-380 382 384 387 390 400 408 414-416 419 424 431 434-435 438 441-443 449 451 453- 455 457-463 470 472-473 475 477- 478 482-483 486-488 490-491 493 496 499-500 502-504 506-507 509- 512 516 519-520 522 525-526 529- 530 537-540 543-544 546-547 566- 567 569-570 572-582 585 588 590- 591 593 595 599 601 604 606-609 611-612 614-620 622-624 630 632 636 643 645-647 650-652 654 659 661 665 667-668 670-672 676 678 681 687 689 692-694 697 699 710 714 717 721 727 729-732 734 736 738 743-746 750-751 759 763 766 770 772 775-777 784 789 791 796 799 802-805 810-811 814 819-821 824 826 830 834-837 839-850 854- 856 858-860 862 864 869 871 876- 877 879 883 886-887 890-891 893- 895 898-901 905 908-910 912-916 919 922-923 925 927 930-933 935- 938 948 952-960 963-964 967 969- 972 975 978-979 981 983 986-987 990 992 995 997 999-1002 1005- 1009 1011-1013 1016 1018-1019 1023 1026 1029-1031 1033-1035 1038 1041 1047 1050 1053 1057 1059 1064 1068 1070 1072-1073 1078-1079 1081-1082 1086 1089 1094 1097 1103 1107-1109 1113- 1115 1121-1122 1127 1134-1135 1138 1140 1143 1148-1151 1153 1156-1157 1159 1167 1170 1175 1193-1194 1200 1202 1207-1209 1211 1216 1219-1220 1226-1227 1229 1232-1234 1240-1241 1243 1246 1249-1251 1253-1254 1258 1267-1268 1271 1276 1279 1282 1285-1289 1293-1294 1305 1307- 1308 1312 1316 1320 1327 1338- 1339 1341-1344 1346 1349 1355- 1357 1359 1365-1366 1369-1370 1373-1375 1379 1386 1389 1394 1398 1409 1413-1414 1416-1417 1420-1421 1425-1427 1430 1433 1437 1439 1442 1445-1452 1454- 1457 1459 1463-1464 1468 1470 1474 1477-1479 1489 1492 1494 1497-1498 1501-1503 1507 1509 1511-1513 1517 1520-1521 1524- 1526 1531-1533 1535 1537-1538 1547 1554 1556-1559 1564-1567 1571 1584 1587 1589 1594 1599- 1601 1611-1612 1614-1616 1619- 1620 1625-1628 1630-1631 1634 1637-1638 1640-1643 1645 1648-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1649 1651 1653-1655 1657-1658 1664-1665 1667 1669 1673 1678- 1679 1683-1684 1686 1693 1701 1704-1705 1709 1713-1714 1717- 1720 1724 1727-1728 1731-1733 1737-1738 1743-1744 1752 1754- 1755 1757 1760-1761 1765 1772 1779 1785
macrophage	Invitrogen	HMP001	5-8 110 204-205 503 634 678 859 878 933 988-989 1379 1448 1504
infant brain	Columbia University	IB2002	10 12-13 15-18 22-23 25 29 34 37-39 43 47 50-51 54-56 58 60-63 65-66 68-69 72-74 80 82-83 86 88-92 97 100 102-104 106-108 110 112-113 115-116 118 123 128 130 134-136 138-139 143 147-149 151- 152 154-155 163 165-167 169 172- 175 181-184 186 193-196 198 201 203-205 209-210 214-215 222 224- 226 231-232 235-236 239 246-247 252 257 260 268-269 272 276-277 279-281 286 288 291-292 295 298 300-301 304 307 310 313 321-323 330-331 333-334 339 346-347 349 352 356-357 362 371-372 377 379- 380 383-384 392 397 401 406 408 411 413-414 416 418-419 422 428 430-431 434-435 438 443 449 453- 454 461 464-466 469-470 472-473 475-476 478 482-483 487 490 492 494 497 503 507-508 510-513 516 519-520 524-526 530-534 536-540 547 550-551 561 563-564 566-567 572-576 579 581-582 584-587 590- 591 593 595-597 607-609 611-613 616-617 620 622-624 627 631 637 641 645-647 650-655 657-658 660- 665 667-675 689 691 695 697 699 703 707 713-715 717 721 728-731 733-736 739 743 745 751 755 759 763 769-770 772 778 780-781 785 788-789 793-794 799 803 808 811 814 825-826 830 834-836 840-843 845 848-850 854-855 860 862 864- 865 870 872 875-876 878 886 888 890-891 894-896 898 903-904 916- 917 919 922-925 927-928 930-932 934-936 938 941 945-946 948-950 953-954 959-962 966-969 977 979 981 986-990 992 997 999-1000 1004-1006 1014 1016 1018-1019 1024-1025 1033 1036 1047 1051- 1052 1054-1055 1057-1059 1063- 1064 1068-1070 1073 1081-1082 1085 1089 1108-1113 1118-1120 1123-1124 1130 1132-1138 1140 1149 1151 1153-1154 1163-1170 1172 1174-1175 1183-1184 1188 1190 1193-1194 1196-1197 1199 1204 1208-1209 1211 1218-1222 1226-1227 1229 1231 1234 1241 1247 1249 1251 1256 1258 1261- 1262 1269 1274 1279 1281 1283 1285 1287-1289 1294-1295 1305 1307 1313-1314 1316-1320 1329 1332 1341-1342 1345 1349 1356 1362-1363 1365-1366 1368-1370 1374 1381 1383-1384 1388 1400 1403 1406-1407 1413 1417 1420

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1423 1429-1431 1435-1436 1439-1441 1443 1447-1449 1451-1452 1454-1455 1457 1459 1463-1465 1468 1470-1471 1475 1479 1482-1483 1485 1493-1494 1496 1498-1499 1502-1503 1505-1507 1509 1522-1523 1525 1528 1531-1533 1542 1546-1547 1549-1550 1554-1555 1563 1565-1567 1569 1575 1580 1583-1586 1588 1590 1592-1593 1595 1598 1600-1601 1608-1610 1612 1614-1616 1619 1621 1624 1626-1627 1630-1633 1637 1639-1640 1642 1644 1647 1652 1654-1655 1658-1659 1664-1665 1672-1673 1676-1681 1685-1688 1693-1695 1701-1702 1704 1708 1717-1720 1723-1724 1726-1728 1733 1735-1741 1743-1744 1752 1755-1758 1762 1765 1771 1774 1777-1778 1786
infant brain	Columbia University	IB2003	17-18 20-23 29 34 43 60 68-69 78-80 88 100-101 107 110 112 118 123 128 133 135-137 146 148 152 159 166 169 174 194 198 203 215 223 225-226 229 235-236 247 260 276-281 286 290-292 295 300-301 310 322 324 331 334 339 346-347 349-350 352 357 371 376-377 382 384 403 408-409 414-415 453-455 472 476 478-479 490 503 507 516 520 530 534 536-540 551 563 572-576 585 587 590-591 593 595-596 601 606 612 616-617 620 622-624 650 652-653 661 665 670-671 674-675 678 689 715 717 727-728 730 734 759 775-777 780-781 785 796 806-807 811 824 845-846 864 869 875 882 889 894-895 898 904 917 919 921-923 932 935-936 946 950 954 962 977 979 997 999-1000 1005-1006 1009 1011 1017 1024 1033 1037 1043 1055 1057 1109 1114-1115 1120 1123 1127 1144-1145 1149 1151-1153 1160 1167 1170 1174 1193-1194 1196 1199 1202 1206 1209 1220-1221 1226 1229 1240-1241 1251 1258 1284 1288-1289 1305 1314 1327 1333 1344 1347 1350 1356-1357 1365-1366 1378-1379 1388 1400 1403 1421 1423 1431 1436 1440-1441 1446-1447 1457 1459 1471 1499 1503 1507 1509 1536 1546 1557-1559 1567 1572 1587 1595 1598 1610-1612 1615 1631 1639 1644 1647 1657-1658 1673 1678-1681 1683-1684 1701-1702 1708-1709 1713-1714 1719 1757 1760-1761 1765 1771 1778
infant brain	Columbia University	IBM002	101 113 139 152 260 279 290-292 374 377 551 563 608-609 653 659 814 954 1005-1006 1029-1030 1130 1164 1209 1258 1294 1305 1320 1327 1397 1431 1498 1507 1615 1640 1694-1695 1763-1764 1767 1779
infant brain	Columbia University	IBS001	10 12 119 175 279-281 321 334 371 446 551 563 623 652 667 669

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			671-672 819 949 966 1113 1130 1151 1188 1193-1194 1196 1229 1258 1265 1271 1287 1317-1319 1324-1325 1342 1423 1440-1441 1448 1471 1482 1525 1532 1546 1562 1569 1588 1591 1610 1618 1647 1649 1658
lung, fibroblast	Stratagene	LFB001	5-9 17 20-21 25 68-69 82 94 105 153 157 197-198 203 207-208 212- 213 223 262 266 283 302 321 326 333 356 370 427 430 436 446 462 472 493 498 503 516 519 527 535 537-540 542-544 562 565 567 586 599-600 607 615 630 647 662-664 692-694 712 719 745 748 775-777 794-796 810 837 843-847 849 854- 856 869 876 903 934 953 955-956 964 975-976 984 1000 1005-1007 1024-1025 1033 1039 1053 1064 1070 1072 1082 1112-1113 1134 1136-1138 1140 1195 1223 1232- 1233 1246 1279 1285 1295 1311 1320 1334-1335 1343 1427-1428 1446 1478 1482 1493 1504 1537 1552 1555 1567 1575 1582 1598 1620 1625 1632 1638 1645 1654- 1655 1662 1680-1681 1684 1686 1690 1696 1702 1711 1733 1741 1760-1761 1778 1785
lung tumor	Invitrogen	LGT002	5-10 18 20-21 29 33-36 40 43 52 54-55 61 65-66 68-70 73-75 80 85 88-89 93-94 100 103 106-108 112- 113 115-116 118-119 123-124 126 130-132 135-137 139-141 143-144 147-148 151-153 155-156 159 161 164 169 171 179-180 185 190 192 194 196-199 203-208 210 212-214 216-217 219 222 233 240-241 244 246 251-252 255-256 261-262 266 272 276-277 279-281 284 286 288 290 295 298 301-302 309-312 317 321 329 332 341-342 344-345 348 352 358-360 363 368 370-371 376 380-381 384 389-390 398 400 409 414 423 426-427 430 432-436 443- 444 450-451 454 462 468 472-477 480-483 487-488 490-491 493 496- 498 500 503-506 509-512 515-516 519 521-523 526 530 534 541 544 547 554 557 564 566-567 572-576 585-586 588-589 595-596 601 607 611-612 615 619 621 623 626 630 632-633 644 647 649 651 655-656 660 662-665 667 669 672 683-684 696 700 706 710 713 716 718-719 722-723 728 734-739 743 750 752 763 765-766 773-778 784-785 787- 789 791 800 802-803 809-812 814 824 826 828-829 832 838-839 841- 845 849-850 852-855 857-861 864 866 874 878-880 882 887 890-891 897-898 902 904 906-907 910 916 918-920 922 924-925 927 930-932 934-935 937 947 950 953 955-956 961 963 966-967 969 971 977-979 981 984 986-987 990 992-993 995 997 999-1001 1005-1007 1009 1012-1013 1018 1020 1022-1024 1026 1029-1030 1033 1038 1041

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1045 1047-1050 1052 1054-1055 1059 1063-1064 1067-1071 1073- 1074 1078 1085 1087 1089 1095- 1097 1104 1106-1107 1109 1112 1116-1117 1119 1126 1134-1135 1139 1141-1142 1144-1145 1148 1152-1153 1156-1158 1167 1170 1172 1178 1195-1196 1198-1200 1202 1204 1208 1214 1216 1219 1222 1227 1234 1241 1247 1252 1257-1258 1265 1267-1270 1276 1278 1280-1281 1283 1285 1288- 1289 1295 1300 1305 1308 1312 1317-1321 1329 1338-1339 1341 1344-1346 1349-1351 1353-1355 1357 1365-1366 1369 1378-1379 1383-1385 1394 1397 1400 1402- 1403 1408 1417 1419 1423-1426 1431 1433-1436 1438 1444 1446- 1448 1454-1455 1460 1466 1468 1470 1474 1480-1481 1483 1486- 1488 1490-1491 1494-1496 1506 1508-1509 1511-1512 1515-1516 1519 1523-1524 1528-1529 1536- 1540 1546 1549-1550 1555 1560- 1561 1565 1567 1569 1575 1588 1591 1593-1594 1596-1598 1600- 1602 1608 1614-1616 1618 1620 1624-1625 1627-1632 1636 1639 1644-1645 1647-1649 1652-1653 1656-1662 1664 1666-1667 1670- 1671 1673-1675 1678-1679 1683 1685-1688 1690-1692 1696-1699 1705 1709 1716-1717 1722 1727 1730 1735 1739 1741 1743-1744 1748-1749 1753 1760-1762 1765 1767 1770-1771 1773 1775-1776 1778-1779 1786
lymphocytes	ATCC	LPC001	4 11-12 18 24-25 30-31 48 50-51 56-57 68-69 80 92 98 103 105 110 126 137 152-153 157 165 172 188- 189 197 203 210 217-218 222-223 225-226 229 231 247 251 256 264 272 280-281 284 300-301 321 325- 326 339 348 352 357 371 382 384 390 400 404 412 414 421 423 426- 427 430-431 445 447-448 451 454- 455 475 503 516 526-527 530 537- 540 549 556-560 563 574 577 589 602 613 615-617 621 623 628-630 636-637 647 649 657-659 690 697 717 723 755 764 775-777 780 786 789-790 793 800 802 822 838 849 866 869 876 881-883 892 898 906- 907 911 921-923 928 975 990 992 996 1001 1004-1007 1033 1050 1054 1078 1107 1135 1140-1141 1143 1148 1158 1163 1177 1199 1205 1216 1226 1231 1236 1241 1244 1250 1258 1260 1265 1269- 1271 1290-1293 1308 1312 1317 1319-1320 1339 1345-1346 1348 1350-1351 1357 1367 1369 1379 1381 1383-1384 1386-1387 1389 1394 1397 1405 1423 1425-1428 1431 1437 1446 1448 1461 1466 1470 1472 1474 1482 1492 1506 1528 1537 1546 1549 1591 1598 1600 1603-1604 1606 1627 1636

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1638 1647-1649 1651 1658-1659 1664 1676-1677 1680-1681 1687- 1688 1699 1711 1715-1716 1726 1728 1737 1740 1746 1748 1752 1756 1758 1777 1779
leukocyte	GIBCO	LUC001	3-4 10-11 13 15-18 20-21 24-25 30-31 35-36 40 43-45 48 50-51 54-58 60-63 68-69 75 79-80 82-83 85 88-91 93-96 98 100 103-104 107-108 112 116 119 123 125-128 134-140 142 147-149 151 153 155 157 162-163 167 169-172 174 177- 179 186 190 192-199 203-207 210 212-215 217-219 222-223 229 235- 236 247 251 255-258 260 262 272 274-277 280-281 285-286 297-301 307-310 313-314 316-317 321 325- 330 333-334 340-342 348-349 352 354-358 370-371 380-385 387-388 400 405 408-410 412 414-416 421- 425 430-431 434-435 437 439 441- 442 445-451 453-454 456 459 461- 464 468-472 474-479 481 483-485 487-491 496 499-501 503-504 509- 513 516-519 522 526-527 529-531 534 536-540 542 547-549 553-559 566-567 571 574-577 579 582 584- 586 589 593 595-597 601-602 604 606-607 611-613 615-621 623 627- 629 633 636-637 642 644-650 655 659-660 662-665 667 669 674-675 678 682-684 692-696 698 700 706 708 710 716-720 725-726 729-736 738-739 743-746 749 751 753 756 759 765-766 768 770-778 780 784- 786 788-790 793 796 798 800 802- 803 810-811 814 817 819 826 828- 830 832 834-836 838 843 845-860 863-864 866-871 877-879 881-892 894-896 898 902 904-914 916 919- 925 927 930-932 935-936 941-942 945 948-949 953 955-956 958 960- 962 964 967 970-971 973 975 977 985-990 992-993 995-996 999-1002 1004-1009 1011 1014 1017-1019 1022-1023 1025 1027 1029-1031 1033-1036 1038 1041 1043 1047 1050 1053-1054 1058-1059 1061- 1062 1064 1068 1070 1072 1078 1085-1086 1089-1091 1093 1097 1106-1107 1110-1113 1115-1117 1122-1123 1125 1129 1132-1133 1135-1137 1140-1145 1152 1158 1163 1168 1170-1174 1176-1178 1180 1182-1183 1186 1195 1198- 1200 1202 1205-1206 1211 1216 1219-1221 1223-1227 1230-1236 1238-1242 1247 1252 1254 1256 1258 1261-1262 1264-1265 1269- 1270 1272-1275 1277 1280-1284 1287-1293 1299-1300 1306 1308 1312-1313 1317-1320 1322 1324- 1330 1333-1335 1339 1341 1343- 1347 1349 1353-1357 1359-1361 1365-1367 1369-1370 1373-1374 1377 1379-1381 1386-1387 1394 1400 1403 1409 1419 1423 1425- 1428 1430-1431 1433-1434 1437- 1438 1440-1442 1446-1448 1450

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1453 1458-1459 1463-1464 1468 1470-1471 1474 1477-1478 1482- 1488 1490-1493 1496-1501 1504 1506 1509 1512-1513 1516 1519 1521-1522 1524-1525 1527-1528 1531 1534 1538 1541 1545-1547 1549-1550 1553 1555-1556 1560 1565 1567 1575 1580 1589 1591 1594 1596 1598 1600-1602 1606- 1608 1611 1614 1620-1621 1624 1626-1629 1631-1632 1636 1638- 1639 1641 1644-1645 1648-1650 1653-1655 1658-1660 1662 1669- 1670 1675-1679 1684-1688 1690- 1692 1696 1700 1702 1707-1709 1711 1716-1717 1720 1723 1725- 1727 1733 1737-1738 1741 1743- 1744 1748-1749 1752 1755 1760- 1762 1765 1769 1771-1772 1781- 1784 1786
leukocyte	Clontech	LUC003	4 35-36 44-45 61 68-69 75 82 102 119 139 154 179 197 244 280-281 324 372 404 430-431 455 461 476- 477 481 503 537-540 554 575-576 581 589 608-609 621-622 624 630 632 647 662-664 669 679 698 764 773 775-777 802 848 851 856-857 879 905-907 915 949 952 990 992 1002 1113 1119 1170 1183 1216 1236-1237 1241 1275 1346 1353 1357 1359 1377 1506 1515 1534 1553 1591 1600 1613-1614 1621 1628 1670 1676-1677 1691-1692 1699 1733 1738 1772
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	25 35-36 43 80 104 126 128 150 163 166 188-189 197 210 215 220 271 277 280-281 310 317 336-338 345 351 372 380-381 383 387 412 415-416 430 445 448 454 456 467 481 490 499 503 526 528 546 548 567 575-576 588 601 613 615 647 660 665 734-735 737 759 778 787 790 800 832 845 856 859 869 878 883 887 905 914 932 934 958 976 985 990 992 999-1000 1025 1031 1038 1050 1055 1068 1074 1088 1099-1102 1107 1136-1138 1149 1156 1163 1172 1190 1195 1200 1214-1215 1217 1226-1227 1235 1238-1239 1244 1253 1278 1280 1293 1311 1320 1330 1334-1335 1345 1355 1367 1386-1387 1394 1403 1406 1414 1423 1437 1442 1465 1521 1529 1536 1539 1541 1547-1548 1582 1620 1626 1631 1638 1647 1653 1660 1667 1669- 1670 1680-1681 1696 1704 1715 1724-1725 1731-1732 1750 1760- 1761
mammary gland	Invitrogen	MMG001	5-8 10 12 14-18 20-21 24-25 29 33-39 42-43 52 55-58 60-64 68-69 71 73-74 79-80 82 89 98 100 103 106 108 112 123 128 133-137 144- 146 148 150-152 154 158-159 165- 166 170-172 174 176 178 181-185 188-190 194-198 201-206 210 217- 222 224 227-228 231 233-237 247 251 253-254 256 261-263 266-267 271 276-277 279-281 284-286 288

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			290 297 299 301 304 309-312 318 320-321 323-325 327-329 331-332 334 339 341 344-345 348 350 356 359-360 362-363 368 371 376 379- 383 388 390 393-395 397-398 405 408 412 414-415 423 430 434-437 441-444 448 451-455 462-464 474 476 479 482 485-486 488 490 494- 495 498 503 506 509-512 516-517 519-520 522 527 529 534 537-541 547 549 554 557 562 572-574 587 589-591 597 602 607 618 623 628- 629 632 634-640 644 647-648 650- 652 655 657-658 660 665 667 669- 672 674-676 679 682 688 695-696 706-707 710 713 717 720 722-730 732-734 736 738 743 747-748 750 755 759 761 766 770 780 784 786- 789 794 803 806-807 809 814 817- 822 827-829 837 842 854-858 863- 864 866 869-870 872 878 881 889 893-900 904 906-907 911 916 919 921-923 926 935-937 946 948-949 953-954 957 960-961 963 965-966 970 977-978 984-989 993-997 1000-1001 1005-1006 1008 1013- 1014 1016-1017 1023 1025 1027 1032-1033 1036 1039 1043 1045 1055 1057-1058 1063 1068-1075 1077-1078 1085 1087 1089-1091 1095-1102 1107-1108 1112-1119 1121-1123 1131-1133 1136-1137 1139-1142 1144-1145 1148-1149 1153 1159 1167 1170 1172-1173 1183-1185 1190-1192 1196-1199 1207-1208 1212 1216-1218 1222- 1223 1225 1231 1234 1240-1241 1247 1253-1254 1258-1259 1261- 1262 1270-1280 1283 1285-1286 1298 1307 1314 1316-1320 1323- 1325 1330 1334-1335 1342-1345 1349-1352 1354-1355 1359 1369- 1370 1377 1379 1381 1383-1384 1389 1405 1414 1419 1421-1423 1425-1426 1428-1429 1431 1434- 1437 1439 1448-1449 1454 1457 1460-1464 1466 1471 1480-1483 1487 1489-1491 1493 1505 1507 1512 1519 1526-1528 1532 1534 1536 1539 1542 1547 1549-1550 1554 1561-1562 1564 1567 1572 1576-1579 1581-1582 1587-1588 1592 1594 1596-1597 1601-1602 1607-1608 1610 1612-1616 1618 1621-1622 1625-1626 1631 1635- 1636 1641 1643-1644 1647 1650 1652 1654-1655 1657-1658 1660 1662 1664-1666 1669-1671 1673- 1674 1676-1677 1680-1685 1689- 1692 1701 1706 1713-1715 1719- 1720 1723-1728 1730-1732 1738 1740 1742-1744 1746-1747 1749 1751 1753 1760-1762 1765-1768 1771 1774 1776-1777 1779 1783- 1784 1786
induced neuron cells	Stratagene	NTD001	29 35-36 80 116 123 156 163 181 214 230 280-281 284-285 307 321 330 340 358 371 375 377 380 382 422 424 492 497 532-533 542 546

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			549 566 586 595 612 645-647 654 734 775-778 780 792 799 821 826 856 858 875 936 953 985 990 992 1041-1043 1055 1072 1104 1193- 1194 1206 1223 1246 1253 1274 1288-1289 1291 1294 1311 1320 1349 1359 1412 1423 1485 1620 1623 1645 1684 1705 1715 1751
retinoid acid induced neuronal cells	Stratagene	NTR001	5-8 78 268-269 277 383 431 506 623 677 731 999-1000 1199 1425- 1426 1547
neuronal cells	Stratagene	NTU001	29 65-66 80 82 110 119 146 152 166 174 181-185 198 227-228 253 284 309 325 332 334 336-338 375 391 393 406 414-416 454 465-466 470 488 503 506 510-512 519 537- 540 572-574 597 602 607 623 647 661 700 702 716 743 771 792 858 904 948 954 977 1000 1005-1006 1025 1064 1068 1122 1148 1185 1219 1226 1234 1246 1271 1283 1295-1296 1311 1317-1320 1329- 1330 1350 1355 1365-1366 1378 1383-1384 1400 1412 1445 1505 1539 1547 1578 1647 1656 1683 1690 1738 1749 1783-1784
pituitary gland	Clontech	PIT004	311 314 379 408 419 430 454 1055 1095-1096 1272-1273 1312 1320 1378 1652 1671 1720 1725 1736 1741 1755
placenta	Clontech	PLA003	5-8 124 208 277 370 843 906-907 1280 1317-1319 1369 1609 1621 1737
prostate	Clontech	PRT001	9 46 57 71 107 147 171 177 197 201 229 231 242-243 274 280-281 307 310 317 330 358 373 382-383 400 430 434-436 461-462 469 477 489 497 500 505-506 513 521 526 531-533 547 618 649 657-658 662- 664 710 729 767 771 789 820 861 871 874 890-891 905 938 945 963- 964 988-989 1002 1025 1033 1045 1061 1095-1096 1112 1125 1142 1196 1198 1202 1232-1233 1241 1258 1272-1273 1287 1295 1313 1333 1341 1344 1349 1360 1362- 1363 1367 1437 1442 1447 1475 1478-1479 1482 1489 1513 1517 1527 1531 1536 1598-1599 1628 1636 1657 1680-1681 1687-1688 1717 1738 1743-1744
rectum	Invitrogen	REC001	17-18 29 33 62-63 71 73-74 83 86 113 126 146 153 158 167-169 195 200 206 261 309 312 341 344 368 373 388 395 408 414 420 430 441- 442 446 448 464 468 483 517 537- 540 547 567 585 589 602 623 628- 629 632 645-647 651 657-658 669 717-719 721 725-726 738 748 750 756 762-763 766 770 774 790 819 825 843 849 851 881 903 909 948- 949 960 986 996 1020 1023 1033- 1034 1064 1067 1070 1075 1086 1108-1109 1113 1130 1139 1153 1159 1172 1178 1185 1187-1189 1205 1220 1225 1240 1244 1271 1317-1320 1323 1334-1335 1350- 1351 1355 1369 1373 1375 1425-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			1426 1436 1439 1469 1474 1477 1482 1546 1587-1588 1592 1596 1610 1622 1627 1644 1658 1662 1665-1666 1669 1675-1677 1749 1786
salivary gland	Clontech	SAL001	10 55 97 103 110 140 149 152 158 198 217-218 242-243 256 301 308 312 321 333 351 354 360 410 437 448 473 487 494 496 501 535 555 569-570 572-573 590-591 624 636 651 759 762 764 768 771 788 800 809 826 848 865 879 906-907 925 933 963 1016 1020 1025 1040 1046 1055 1066 1103 1150 1172 1181 1234 1281-1282 1288-1289 1298 1315 1320 1333 1336-1337 1346 1359 1373 1379 1424 1447 1449 1474 1482 1492 1494 1498 1511 1523-1524 1537 1554 1596 1626- 1627 1636 1652-1655 1658 1665 1671-1672 1691-1692
salivary gland	Clontech	SALs03	158 326 1423 1463-1464
skin fibroblast	ATCC	SFB001	1320 1400
skin fibroblast	ATCC	SFB002	262 736 1025 1253
skin fibroblast	ATCC	SFB003	709 1119 1350 1631 1653
small intestine	Clontech	SIN001	25 142 146-147 151 155 198 203 244 260 271 280-281 286 288 298 301-302 308 312 334 340 371 398 408 412 414 416 423 426-427 430 434-435 445 452 454 478 503 516 519 521 523 543 547 549 555 559 563 569-570 585 592 604 611 626 628-629 632 650 659 681 710 714 718 750 764 780 798 829 842 857 859 866 887 892 894-895 901 904 906-907 912 919 935 997-998 1000 1007-1008 1026-1028 1044 1055 1089 1097 1116-1117 1131 1148 1169 1199 1219 1234 1247 1264 1279 1316 1320 1326 1341 1343 1349 1351 1374 1387 1398 1400 1403 1407 1423 1428 1468 1498 1501 1521 1550 1556 1585 1597 1636 1638-1639 1645 1653 1656 1662 1671 1675 1684 1691-1692 1704 1711 1717 1719 1722 1725- 1726 1729 1733-1734 1743-1744 1762 1767 1780 1785
skeletal muscle	Clontech	SKM001	18 20-21 82 84 101 118 134 148 151 153 166 225-226 258 274 277 289 329 361 412 414 424 440 452 459 470 488 503-504 537-540 647 660 673-675 715 773 780 786 830 905 922 950 963 982 990 992 1020 1047 1063 1115-1117 1121 1134 1228 1268 1284 1298 1321 1329 1336-1337 1343 1409 1413-1414 1509 1599 1624 1644 1653 1712
skeletal muscle	Clontech	SKM002	168 1683 1712
skeletal muscle	Clontech	SKMs03	235-236 1409
skeletal muscle	Clontech	SKMs04	235-236
spinal cord	Clontech	SPC001	4 9 11 17 30-31 35-36 43 46 60

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			82 85 92 94 108 110 116 139 157 167 198 204-205 210 215 229 256 259 277 280-281 300-302 304 315 317 372 379 387 392 419 426-427 430 433 448 467 473 487 489 506 509 513 519 524 526 537-540 543 547 549 551 559 567 569-570 593 607 616-617 623 625 637 649-650 652 657-658 670-671 673 679 681- 682 709 711 715 719 728-729 734 749-750 753 775-777 781 789 791 809 820 832 834-836 847-849 854- 855 858 861 864 871-872 875 884 898 906-908 917 919 924 934 942 944 970 985 990 992-993 998 1013 1039 1053 1059 1065 1072 1075 1077 1082 1085 1097 1103 1109 1116-1117 1128 1134 1151 1170 1174 1192-1194 1215 1225 1241 1243 1283 1294 1307 1312 1320 1323 1327 1330 1350 1353-1354 1356 1359 1368 1375 1400 1406- 1407 1423 1429 1437 1443 1448 1454 1470 1482 1492 1501 1508 1511 1529 1538 1548-1549 1565 1571 1578 1598 1600 1614 1625 1627 1630 1639 1646 1651-1652 1670 1686 1696 1740 1751 1755 1771
adult spleen	Clontech	SPLc01	117 312 326 348 424 426-427 431 845 866 1320 1330 1333 1344 1355-1357 1371 1387 1397 1446 1538 1579 1669 1686 1739 1767
stomach	Clontech	STO001	10 15-16 61 68-69 100 117 149 197 201 227-228 231 249 273 280- 281 287 291-292 302 312 358 362 426-427 430 446 462 475 479 535 597 620 630 651 662-664 722 739 780 782 785 846 919 960 964 966- 967 976 1008 1012 1032 1042 1063 1071 1135 1170 1208 1234-1235 1259 1277 1280-1281 1322 1349 1359 1369 1449 1468 1474 1478 1487 1493 1498 1557-1559 1622 1634 1651 1653 1729
thalamus	Clontech	THA002	9 11 25 85 87 112 137 146 180 190 198 206 210 212-213 235-236 239 261 268-269 279 290 301 325 333-334 341 351 356 364-365 379 388 393 396 419-420 441-442 458 477 483 508 525 531 549 567 606 608-609 647 681 715 725-727 736 774 782 784 794 827 883 890-891 899-900 961 997 999-1001 1004 1034 1055 1097 1129 1144-1145 1150-1151 1157 1172-1173 1177 1193-1194 1208 1220 1249 1280 1305 1345 1355 1369 1434-1435 1440-1441 1454 1496 1546 1549 1562 1572 1578 1590 1594 1613- 1614 1640 1651-1652 1671 1687- 1688 1703 1743-1744 1746-1747 1753
thymus	Clontech	THM001	44-45 54 57-58 62-64 79 104 123 126 134 153 193 212-213 218 242- 243 258 274 277 279 297 301 307 327 330 333 342 351 358 371 410 430 445 465-466 468 471 483 487 493 503 506 509 517 526 535 537-

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			540 546 548 554 567 584 586 590- 591 604 612 621 638-640 645-647 649 656 660 665 670 698 710 720 728 735 739 746 759 762 766-767 775-777 780 784-785 800 802 809 824 826 828 845 851 858-859 864 866 870-871 878 884 887 892 899- 900 927 930-931 967 983 986 990 992 999 1014 1029-1030 1033 1059 1066 1073 1103 1107 1113 1116- 1117 1119 1140-1142 1158 1163 1172 1177 1195 1206 1209 1213 1216 1218-1219 1221-1222 1227 1271 1277 1282 1320 1329 1349 1367 1369 1383-1384 1417 1419 1423 1425-1427 1448 1477 1488 1493 1536 1554 1620 1644 1646 1649 1654-1655 1661-1662 1669- 1670 1674 1676-1677 1685-1688 1707 1711 1731-1732 1737
thymus	Clontech	THMc02	5-9 15-21 25 33 35-36 43-45 48 50-51 54-55 60 75 83 87 89 93 98-100 102 105 112 117 135-137 141 143 146 157 167 169 192 196 211 217-219 222 224 229 233 235- 236 240-241 244 251-252 256 261- 262 268-269 286 288 290 295 297 301-302 309-310 315-317 321 324 327 334 342 350 352-353 360 370- 373 382 384 400 403 410 414-416 424 430-431 436 445 454-456 461 464-467 470 472 474-476 483 488 497 500 504 506 513 516 519-520 524 526 530-531 534 537-540 549 554-555 565-566 569-570 572-573 575-577 586-587 595 603-604 606 612 630-632 634 636 647 650 657- 660 666-667 669 673-675 678 698 700 703 708 720 725-726 731 738- 739 743-744 750-753 757 759 763- 765 767 772-779 787 789-790 798 800 810 823 829 834-836 841 848 854-856 859 861 864 870-871 881 890-891 898 908-909 913 928 933 941 949 958 961 963 967 969 975 981 986 988-990 992 999 1007- 1008 1014 1016 1039 1041 1073- 1074 1079 1089 1097 1109 1114- 1117 1122 1131 1140-1141 1144- 1145 1163 1172 1175-1177 1186 1196 1198 1206 1211 1216 1220 1223 1227 1234-1243 1261-1262 1267 1271 1280-1281 1284 1290 1308 1317-1320 1322 1324-1325 1327 1330 1334-1335 1339 1346 1350-1351 1355 1357 1360 1370 1374 1377-1379 1386 1389-1390 1392 1397 1400 1402 1406-1407 1417 1423 1425-1427 1440-1441 1466 1474 1477 1483 1493 1498 1504 1506 1525 1536 1545 1549 1566 1594 1598-1600 1608 1611 1614 1621 1623 1625 1632 1639 1641 1644 1647 1649 1653-1656 1658 1662-1663 1671 1673 1678- 1681 1686-1688 1693 1705 1707 1711 1717-1718 1726-1727 1731- 1733 1737-1738 1743-1745 1758- 1761 1771-1772 1779 1786

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
thyroid gland	Clontech	THR001	4 9-10 20-21 37-39 48 50-51 54- 57 60-61 65-66 71 83 94-96 98- 100 102 104 110 112 115-117 119 123 127 133 136-137 140 149 152- 153 155-158 163-164 168-169 171 186 190-192 197 201-203 219-220 229 233-237 246-247 253 256 258 262 265-266 268-269 277 280-281 284-286 288-289 298-299 302 309- 311 317 321 326 332 335 341-342 344 348 350 354 358-359 363 368 371-373 382-383 385 394 398 400- 401 411 414-415 421 424 430-431 433-436 443-446 450-452 454-455 458 472-474 476-478 482 484-485 487-488 490-494 496-497 500-501 503-504 506 509-513 516-517 519 524 526-527 529 535-540 547 549 562 564 569-570 575-576 588 594- 595 601-602 604 606 610 612 615- 617 619-623 628-630 634-635 642 647 649-651 660 662-665 668 670 681 690-694 696 698 700 709 721 727-729 732 734 738 740-741 743 745 750 759 761 763 765 770 773 780 785 795-796 798 802 804 823- 824 826 828 833 838 841-845 847 849 857-860 867 874-875 878 880- 881 887-888 890-892 894-895 898 908 910-911 913-914 922-923 926- 927 929 932-934 937 939 941-942 948 953 957 961 963-964 966 978- 979 981-982 987 990 992 1001 1004-1006 1010 1014 1020 1024 1033 1038-1039 1044 1047 1050 1052-1054 1056 1058 1068 1070- 1071 1077-1079 1088 1094-1097 1105-1106 1112-1113 1116-1117 1124 1126 1128-1129 1131 1134 1136-1137 1142-1143 1146-1147 1149-1150 1156 1161-1164 1167 1170-1173 1177-1181 1190 1192 1197 1200 1204 1208-1209 1214 1217 1219 1222 1230 1232-1233 1235 1241 1245 1247 1254 1257- 1258 1260 1262 1271-1273 1283 1286-1289 1299 1306 1314 1320 1330-1332 1334-1335 1342 1345 1349 1365-1367 1370-1372 1374 1381 1394 1407 1419 1428 1436- 1437 1440-1441 1443 1446-1449 1454 1459 1461-1462 1468 1470- 1471 1475 1477 1479 1482 1491 1497-1498 1504-1505 1507 1513 1522 1524-1526 1528 1531 1534 1536-1537 1548 1550 1553 1555- 1559 1562 1567 1578 1590-1591 1597 1599-1601 1612 1614 1616 1619-1620 1622 1624-1626 1628 1631-1632 1634 1636 1639 1644- 1645 1648 1651 1653-1656 1658 1660 1662-1663 1667 1669 1671 1675 1678-1681 1683-1686 1689 1691-1692 1703 1709-1711 1717 1724-1726 1729 1734 1737-1738 1740 1743-1744 1749 1753 1759- 1761 1770 1777 1786
trachea	Clontech	TRC001	9 29-31 46 48 87 104 107 110 135 158 222 262 266 286 301 318 331

Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
			352 372 377 384 414 424 445-446 454 472 474 491 496 560 579 588 593 597 607 612 626 681 702 719 810 859 866 878 894-895 912 916 922 932 935 1046 1075 1080 1099- 1102 1113 1208 1215 1232-1233 1237 1281 1312 1385 1387 1405 1414 1424 1430 1437 1447 1505 1569 1579 1586 1600 1641 1653 1667 1671 1676-1677 1683 1691- 1692 1711 1717 1726 1772
uterus	Clontech	UTR001	17 19 25 41 46 57-58 61 89 104 108 139 152 174 198 200-201 206 263-265 274 290 387 408 420 438 446 448 452 473 491 493 499 503 506 513 519 522 526 530 542-543 560 601 610 632 659 665 720 751 773 780 833 845 857 872 877 912 929 934 937 996 1009-1011 1018 1050 1075 1107 1124 1170 1219 1258 1279 1287 1310 1320 1323 1343-1344 1375 1437 1451-1452 1478 1481 1498 1519 1521 1536 1552 1579 1597 1602 1606 1620 1626-1627 1649 1652 1661 1670 1719 1722-1723

TRADOCs:1416191.1(%CQN011.DOC)

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1	Y41736	Homo sapiens	Human PRO1114 protein sequence.	1398	100
2	Y66656	Homo sapiens	Membrane-bound protein PRO943.	2389	99
3	AF113136	Homo sapiens	IL-1 receptor-associated-kinase-M; IRAK-M	3043	100
4	AF017806	Mus musculus	Zn-15 transcription factor	6351	77
5	X02761	Homo sapiens	fibronectin precursor	10535	98
6	X02761	Homo sapiens	fibronectin precursor	8990	89
8	X02761	Homo sapiens	fibronectin precursor	12564	99
9	AJ011679	Homo sapiens	Rab6 GTPase activating protein, GAPCenA	5251	99
10	W88501	Homo sapiens	Human stomach carcinoma clone HP10415-encoded protein.	2381	100
11	AF117754	Homo sapiens	thyroid hormone receptor-associated protein complex component TRAP240	11336	98
12	Z97630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	896	100
13	Y58620	Homo sapiens	Protein regulating gene expression PRGE-13.	1894	98
14	AF213457	Homo sapiens	triggering receptor expressed on myeloid cells 2	1238	100
16	AF233453	Homo sapiens	RACK-like protein PRKCBP1	3124	99
17	AF201303	Homo sapiens	dhfr oribeta-binding protein RIP60	3130	98
18	AF064205	Homo sapiens	dynactin 1 p150 isoform	6377	100
19	U00059	Saccharomyces cerevisiae	Yhr121wp	174	26
20	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1801	99
21	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1485	99
22	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	3083	99
23	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	2300	99
24	AJ289131	Homo sapiens	chondroitin 4-O-sulfotransferase	2211	99
25	U33460	Homo sapiens	DNA-directed RNA polymerase I, largest subunit	8777	98
26	Y44488	Homo sapiens	ACRP30R2 variant protein.	1387	100
27	U43701	Homo sapiens	ribosomal protein L23a	791	100
28	U02032	Homo sapiens	ribosomal protein L23a	767	97
29	Y41324	Homo sapiens	Human secreted protein encoded by gene 17 clone HNF1Y77.	1083	99
30	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	715	90
31	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	631	82
32	AF231917	Homo sapiens	long-chain 2-hydroxy acid oxidase HAOX2	1811	100
33	Z29481	Homo sapiens	3-hydroxyanthranilic acid dioxygenase	1507	99
34	AB001451	Homo sapiens	Sck	2869	100
35	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1667	99
36	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1104	98
37	Y78795	Homo sapiens	Human antizual-2 (AZ-2) amino acid sequence.	3586	78
38	Y78795	Homo sapiens	Human antizual-2 (AZ-2) amino acid sequence.	4726	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
39	Y78795	Homo sapiens	Human antizual-2 (AZ-2) amino acid sequence.	3556	77
40	U93121	Homo sapiens	M-phase phosphoprotein-1	3747	100
41	Y42750	Homo sapiens	Human calcium binding protein 1 (CaBP-1).	795	100
42	AF282626	Homo sapiens	latexin	1189	100
43	G02150	Homo sapiens	Human secreted protein, SEQ ID NO: 6231.	384	94
44	U19617	Mus musculus	Elf-1	2724	88
45	U19617	Mus musculus	Elf-1	2062	86
46	AF100758	Homo sapiens	osteoinductive factor OIF	1538	100
47	Y87591	Homo sapiens	Human SPROUTY-1 protein, SEQ ID NO:24.	1737	99
49	X04145	Homo sapiens	T3 gamma precursor (aa -22 to 160)	942	99
51	X63547	Homo sapiens	oncogene	5845	99
52	M94043	Rattus norvegicus	rab-related GTP-binding protein	1089	96
53	L31783	Mus musculus	uridine kinase	917	71
54	X83973	Homo sapiens	transcription factor	4486	98
55	AF224741	Homo sapiens	chloride channel protein 7	4128	99
56	W74805	Homo sapiens	Human secreted protein encoded by gene 77 clone HOEAS24.	1491	100
57	Z50907	Homo sapiens	Human TBC-1 cDNA from second transcript.	4824	100
58	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	6089	99
59	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	4014	91
60	Y59738	Homo sapiens	Human normal ovarian tissue derived protein 15.	601	100
61	AB031069	Homo sapiens	protein containing CXXC domain 1	1390	100
62	Y66660	Homo sapiens	Membrane-bound protein PRO783.	2492	99
63	Y66660	Homo sapiens	Membrane-bound protein PRO783.	1709	99
64	S70011	Rattus sp.	tricarboxylate carrier	895	55
65	AF139518	Rattus norvegicus	A-Kinase anchor protein	178	24
66	W29666	Homo sapiens	Homo sapiens DH1308_1 clone secreted protein.	157	30
67	AJ245738	Homo sapiens	claudin-15	1206	100
68	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4183	87
69	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4906	86
70	Z82059	Caenorhabditis elegans	Similarity to Drosophila ring canal protein comes from this gene	1285	44
71	AF224278	Homo sapiens	PMEPA1 protein	1282	100
72	AF126426	Homo sapiens	neurotrimin	1809	100
73	Y41652	Homo sapiens	Human MEK2 protein sequence.	2065	99
74	Y41652	Homo sapiens	Human MEK2 protein sequence.	1207	100
75	AF188622	Mus musculus	selectively expressed in embryonic epithelia protein-1	1485	74
76	AE000406	Escherichia coli	putative DNA topoisomerase	950	100
77	X99302	Homo sapiens	Pop1	655	100
78	AL136538	Schizosaccharomyces pombe	similarity to S. cerevisiae kti12 protein	210	31
79	AF129756	Homo sapiens	G4	1554	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
80	AL096768	Homo sapiens	dJ858B16.2 (phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65))	2033	100
81	AL096768	Homo sapiens	dJ858B16.2 (phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65))	1220	96
82	X57351	Homo sapiens	1-8D	677	98
83	AC005594	Homo sapiens	R26984_1	2700	98
84	X73113	Homo sapiens	fast MyBP-C	5959	99
85	AF097330	Homo sapiens	H1 chloride channel; p64H1; CLIC4	1305	99
86	AB018423	Mus musculus	SH2 domain-containing protein	1360	78
87	AF272151	Homo sapiens	adaptor protein CIKS	3084	99
88	AF196329	Homo sapiens	triggering receptor expressed on monocytes 1	1214	100
89	AB016879	Arabidopsis thaliana	contains similarity to pre-mRNA splicing factor-gene_id:MRB17.2	634	36
90	AJ133721	Mus musculus	homeodomain protein	654	57
91	AJ242864	Mus musculus	phtf protein	619	61
92	A61971	unidentified	MCSP	11676	99
93	Y99365	Homo sapiens	Human PRO1250 (UNQ633) amino acid sequence SEQ ID NO:86.	3890	100
94	Y87231	Homo sapiens	Human signal peptide containing protein HSPP-8 SEQ ID NO:8.	1031	100
95	AF227741	Rattus norvegicus	protein kinase WNK1	2428	95
96	AF227741	Rattus norvegicus	protein kinase WNK1	1961	94
97	Y92513	Homo sapiens	Human OXRE-10.	1626	100
98	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related protein)	3423	100
99	AC005783	Homo sapiens	R33083_1	1974	99
100	Y95293	Homo sapiens	Human GEF containing NEK-like kinase substrate sGNK.	4092	99
101	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069))	1509	100
102	AJ006267	Homo sapiens	ClpX-like protein	3233	100
103	AF100753	Homo sapiens	ancient ubiquitous 46 kDa protein AUP1	2042	96
104	AB015982	Homo sapiens	serine/threonine kinase	4718	100
105	AF151074	Homo sapiens	HSPC240	831	64
106	M35522	Canis familiaris	GTP-binding protein (rab7)	354	50
107	R99800	Homo sapiens	NTII-1 nerve protein, facilitates regeneration of nerve cells.	2337	93
108	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	1290	93
109	AC005614	Homo sapiens	P23269_2	3369	99
110	AF064729	Homo sapiens	RAN binding protein 16	3285	100
111	X52425	Homo sapiens	interleukin 4 receptor	4496	100
112	Y41686	Homo sapiens	Human PRO274 protein sequence.	2285	100
113	W15506	Homo sapiens	Mitogen activating protein kinase ERK1.	1991	100
114	Y71071	Homo sapiens	Human membrane transport protein, MTRP-16.	1190	99
115	AL049548	Homo sapiens	dJ398G3.1 (ortholog of rat CPG2)	3497	99
116	AF189817	Mus musculus	evection-2	1124	90
117	W30891	Homo	Human cytostatin III protein.	715	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	IDENTITY
		sapiens			
118	AF116618	Homo sapiens	PRO1038	1469	100
119	Y08915	Homo sapiens	alpha 4 protein.	1748	100
120	AF098070	Drosophila melanogaster	Lis1 homolog	192	39
121	AF052432	Homo sapiens	katanin p80 subunit	181	37
122	Y70743	Homo sapiens	PSEQ-1 protein encoded by NSEQ gene associated with matrix remodelling.	2637	98
123	AF083246	Homo sapiens	HSPC028	2132	100
124	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	833	99
125	M63109	Leishmania major	glycoprotein 96-92	172	27
126	U75467	Drosophila melanogaster	Atu	935	36
127	Z68220	Caenorhabditis elegans	Similarity to Human ADP/ATP carrier protein	438	43
128	AF095927	Rattus norvegicus	protein phosphatase 2C	1927	94
129	W92958	Homo sapiens	Human zsig44 protein.	463	100
130	AF115391	Lactobacillus sakei	ribokinase RbsK	508	37
131	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	1250	100
132	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	916	87
133	W52811	Homo sapiens	Human DBI/ACBP-like protein (DBIH).	705	97
134	Y84444	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	3230	100
135	M69181	Homo sapiens	non-muscle myosin B	189	20
136	W74882	Homo sapiens	Human secreted protein encoded by gene 154 clone HE6FL83.	480	100
137	W78200	Homo sapiens	Human secreted protein encoded by gene 75 clone HHGAU81.	855	99
138	AL033520	Homo sapiens	dJ349A12.1 (similar to KIAA0701 protein)	424	39
139	AF020261	Santalum album	proline rich protein	119	30
140	X70394	Homo sapiens	zinc finger protein	1634	100
141	Y06439	Homo sapiens	Human protease HUPM-8.	936	100
142	Z68493	Caenorhabditis elegans	predicted using Genefinder	365	42
143	AB018107	Arabidopsis thaliana	ADP-ribosylation factor-like protein	596	65
144	AF161483	Homo sapiens	HSPC134	580	51
145	Y84902	Homo sapiens	A human proliferation and apoptosis related protein.	480	100
146	AB004906	Ipomoea purpurea	transposase	146	20
147	AC007357	Arabidopsis thaliana	F3F19.18	647	31
148	W75155	Homo sapiens	Human secreted protein encoded by gene 41 clone HNTME13.	1494	98
149	AF056490	Homo sapiens	cAMP-specific phosphodiesterase 8A	3710	99
150	Y58171	Homo sapiens	Human hydrolase homologue HHH-7.	785	99
151	U10397	Saccharomyces cerevisiae	Yhr148wp	515	53
152	X73478	Homo sapiens	phosphotyrosyl phosphatase activator	1719	99
153	AL049697	Homo sapiens	dJ382I10.5.1 (novel protein	2034	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			similar to arginyl-tRNA)		
154	AF169802	Homo sapiens	cytochrome b5 reductase b5R.2	1455	99
155	X94703	Homo sapiens	rab28	1126	99
156	Y25716	Homo sapiens	Human secreted protein encoded from gene 6.	1471	100
158	W77404	Homo sapiens	Secreted salivary polypeptide zsig32.	937	100
159	Y17248	Homo sapiens	Human protein kinase inhibitor-2 (PKI-2).	383	100
160	J04970	Homo sapiens	carboxypeptidase M precursor	2395	100
161	W54040	Homo sapiens	Human interferon-inducible protein, HIFI.	484	98
162	AL022724	Homo sapiens	dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)	1357	100
163	AF125535	Homo sapiens	pp21 homolog	193	45
164	G03632	Homo sapiens	Human secreted protein, SEQ ID NO: 7713.	463	97
165	AJ250839	Homo sapiens	serine/threonine protein kinase	1442	71
166	L09649	Zymomonas mobilis	zm2	173	37
167	Y73337	Homo sapiens	HTRM clone 1944530 protein sequence.	1204	100
168	W88645	Homo sapiens	Secreted protein encoded by gene 112 clone HUKFC71.	1084	100
169	AF214731	Homo sapiens	ATP-dependent RNA helicase	4402	100
170	AE000871	Methanobacterium thermoautotrophicum	conserved protein	166	27
171	Y27684	Homo sapiens	Human secreted protein encoded by gene No. 118.	821	100
172	AF226044	Homo sapiens	HSNFRK	2904	100
173	AJ245946	Homo sapiens	neuroglobin	779	100
174	D43949	Homo sapiens	This gene is novel.	3202	100
175	Y07923	Homo sapiens	GTP-binding protein	1205	100
176	W90338	Homo sapiens	Human DP1 homologue protein.	966	100
177	Y41675	Homo sapiens	Human channel-related molecule HCRM-3.	1122	100
178	Y41674	Homo sapiens	Human channel-related molecule HCRM-2.	936	99
179	AF220492	Homo sapiens	krueppel-like zinc finger protein HZF2	4100	99
180	X03084	Homo sapiens	Clq B-chain precursor	1240	100
181	U57344	Mus musculus	Meis3	1813	89
183	U57344	Mus musculus	Meis3	1743	86
184	U57344	Mus musculus	Meis3	1070	86
185	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear protein	1389	58
186	AF200357	Mus musculus	pantothenate kinase 1 beta	1605	82
187	W75058	Homo sapiens	Human secreted protein encoded by gene 2 clone HLDBG33.	1188	99
188	AJ292529	Homo sapiens	suppressor of sterile four 1	2424	100
190	X54134	Homo sapiens	protein-tyrosine phosphatase	3705	100
191	Y22203	Homo sapiens	Human calcium-binding phosphoprotein, CBPP-1, protein sequence.	1083	99
192	W63692	Homo sapiens	Human secreted protein 12.	1975	100
193	W87772	Homo sapiens	Human serum glucocorticoid-regulated kinase (H-SGK2) polypeptide.	2605	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
194	AF084259	Mus musculus	bromodomain-containing protein BP75	693	54
195	Y00752	Rattus norvegicus	serine dehydratase (AA 1 - 327)	994	61
196	W95349	Homo sapiens	Human foetal brain secreted protein fh170_7.	2596	100
197	AB028859	Homo sapiens	hDj9	1890	100
198	W95633	Homo sapiens	Homo sapiens secreted protein gene clone hm236_1.	1614	100
199	Y44277	Homo sapiens	Human nucleic acid methylase-2.	2096	99
200	AB030039	Homo sapiens	hPACPL1	2258	100
201	X54162	Homo sapiens	64 Kd autoantigen	2918	99
202	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
203	X13885	Nicotiana tabacum	extensin (AA 1-620)	185	33
204	J04204	Bos taurus	32 kd accessory protein	1837	100
205	J04204	Bos taurus	32 kd accessory protein	1101	100
207	Y87283	Homo sapiens	Human signal peptide containing protein HSPP-60 SEQ ID NO:60.	1318	100
208	Y02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	936	98
209	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	694	54
210	AF226732	Homo sapiens	NPD007	1345	76
211	X66295	Mus musculus	C1q C chain	970	73
212	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	966	100
213	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	542	98
214	AJ002030	Homo sapiens	progesterone binding protein	1163	100
215	X70649	Homo sapiens	member of DEAD box protein family	3933	100
216	AF250558	Homo sapiens	claudin-2	1169	99
217	AL021453	Homo sapiens	dJ821D11.1 (PUTATIVE protein)	259	100
218	Y08565	Homo sapiens	UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase	3331	99
219	Y94452	Homo sapiens	Human inflammation associated protein	2067	100
220	AL035521	Arabidopsis thaliana	putative protein	315	42
221	AL031786	Schizosaccharomyces pombe	putative proline-trna synthetase	811	41
222	AL109736	Schizosaccharomyces pombe	WD repeat protein	626	40
223	X52493	Glycine max	DNA-directed RNA polymerase	136	23
224	AL035659	Homo sapiens	dJ979N1.1 (dJ979N1.1)	5199	98
225	AB032401	Mus musculus	mmDj4	1761	92
226	AB032401	Mus musculus	mmDj4	1988	92
227	X83502	Saccharomyces cerevisiae	J1007	112	26
228	X83502	Saccharomyces cerevisiae	J1007	79	25
229	AF143723	Homo sapiens	heat shock protein HSP60	2557	99
230	Y66677	Homo sapiens	Membrane-bound protein PRO828.	982	100
231	AB027466	Homo sapiens	spondin 2	1756	99
232	W95634	Homo sapiens	Homo sapiens secreted protein.	1391	100
233	W00365	Homo sapiens	Human cyclin B1.	2218	99
234	Y53762	Homo sapiens	A GTP-binding polypeptide	1017	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			designated RAQ.		
235	Z50749	Homo sapiens	yeast sds22 homolog	1800	100
236	Z50749	Homo sapiens	yeast sds22 homolog	1754	98
237	AB026491	Homo sapiens	PICK1	2137	100
238	AJ270205	Entodinium caudatum	putative phosphatidylinositol-4-phosphate 5-kinase	114	37
239	AB030189	Mus musculus	contains transmembrane (TM) region and ATP binding region	710	93
240	W56538	Homo sapiens	Human hedgehog interacting protein (HIP).	3785	99
241	W56538	Homo sapiens	Human hedgehog interacting protein (HIP).	3436	99
242	AF155107	Homo sapiens	NY-REN-37 antigen	996	99
243	AF155107	Homo sapiens	NY-REN-37 antigen	1005	100
244	AL031320	Homo sapiens	dJ20N2.1 (novel protein similar to yeast and bacterial cytosine deaminase)	763	99
245	U37026	Rattus norvegicus	sodium channel beta 2 subunit	162	30
246	AL078599	Homo sapiens	dJ991C6.1 (novel protein similar to C. elegans F55A12.9 (Tr:P91086))	2391	98
247	U32274	Saccharomyces cerevisiae	Ydr386wp; CAI: 0.12	191	37
248	Y41719	Homo sapiens	Human PRO864 protein sequence.	1879	100
249	AB029434	Homo sapiens	ghrelin precursor	611	100
250	X97831	Rattus norvegicus	carnitine/acylcarnitine carrier protein	246	38
251	W80993	Homo sapiens	Human RIP-interacting factor RIF.	1724	100
252	Y94873	Homo sapiens	Human protein clone HP02632.	1876	100
253	W59878	Homo sapiens	Amino acid sequence of the cDNA clone AIF-2 (HEBGM49).	765	100
254	AL354533	Leishmania major	possible adenylate kinase	265	34
255	AF233322	Mus musculus	zinc transporter like 2	1916	95
256	Y78113	Homo sapiens	Human cytokine signal regulator CKSR-1 SEQ ID NO:1.	2247	99
257	AL035539	Arabidopsis thaliana	putative amino acid transport protein	390	27
258	W74787	Homo sapiens	Human secreted protein encoded by gene 58 clone HHFHN61.	1171	100
259	AL035689	Homo sapiens	dJ187J11.1 (novel protein similar to protein kinase C inhibitors)	974	100
260	AE000909	Methanobacterium thermoautotrophicum	serine/threonine protein kinase related protein	363	30
261	AL050131	Homo sapiens	hypothetical protein	626	100
262	AF019661	Mus musculus	zeta proteasome chain; PSMA5	1214	100
263	AL035593	Homo sapiens	dJ310J6.1 (novel protein)	821	100
264	AL022318	Homo sapiens	bK150C2.3 (PUTATIVE novel protein similar to APOBEC1)	1072	100
265	AF205940	Homo sapiens	endomucin	1289	100
266	AL023583	Homo sapiens	dJ500L14.1 (novel protein)	789	100
267	AL034548	Homo sapiens	dJ1103G7.3 (novel protein kinase domains containing protein similar to phosphoprotein C8FW)	1888	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	IDENTITY
268	AF161470	Homo sapiens	HSPC121	1884	98
269	AF161470	Homo sapiens	HSPC121	1232	96
270	X90763	Homo sapiens	HMa5 hair keratin type I intermediate filament	2190	99
271	AF207600	Homo sapiens	ethanolamine kinase	1952	100
272	M32334	Homo sapiens	intercellular adhesion molecule 2	1436	100
273	AF161483	Homo sapiens	HSPC134	663	61
274	Y53052	Homo sapiens	Human secreted protein clone df202_3 protein sequence SEQ ID NO:110.	587	100
276	Y77576	Homo sapiens	Human cytoskeletal protein (HCYT) (clone 2195418).	762	100
277	AF077042	Homo sapiens	30S ribosomal protein S7 homolog	1269	100
278	Y94907	Homo sapiens	Human secreted protein clone ca106_19x protein sequence SEQ ID NO:20.	1619	98
279	Y68788	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-20.	2801	99
280	Z75134	Canis familiaris	rod transducin	1816	100
281	Z75134	Canis familiaris	rod transducin	1718	96
282	AF249873	Homo sapiens	muscle-specific protein	1395	100
283	AL050007	Homo sapiens	hypothetical protein	405	98
284	AF201931	Homo sapiens	DC1	1859	99
285	AF156102	Homo sapiens	ELL complex EAP30 subunit	1318	99
286	Y35897	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 146.	1250	99
287	U88964	Homo sapiens	HEM45	923	100
288	AL050143	Homo sapiens	hypothetical protein	598	100
289	AJ011098	Homo sapiens	telethonin	574	100
290	Y66724	Homo sapiens	Membrane-bound protein PRO836.	2321	100
291	AF034801	Homo sapiens	liprin-alpha4	2565	98
292	AF034801	Homo sapiens	liprin-alpha4	2590	100
293	AL049851	Homo sapiens	dJ889J22B.1 (novel protein (isoform 1))	1738	100
294	Y73348	Homo sapiens	HTRM clone 839651 protein sequence.	1245	99
295	L11672	Homo sapiens	zinc finger protein	1694	44
296	AL035423	Homo sapiens	dJ2013.1 (brain mitochondrial carrier protein-1 (BMCP1))	1024	79
297	AF198532	Homo sapiens	lymphoid enhancer binding factor-1	2173	100
298	AF161417	Homo sapiens	HSPC299	1147	85
299	AF159141	Homo sapiens	breast cancer metastasis-suppressor 1	1236	99
300	U26397	Rattus norvegicus	inositol polyphosphate 4-phosphatase	160	30
301	AF036145	Homo sapiens	meningioma-expressed antigen 5	3458	100
302	Z82022	Homo sapiens	GlcNac-1-P transferase	2067	99
303	AF269232	Mus musculus	butyrophilin-like protein BUTR-1	271	50
304	AJ222644	Arabidopsis thaliana	asparaginyl-tRNA synthetase	659	50
305	AF054180	Homo sapiens	hematopoietic cell derived zinc finger protein	351	79
306	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	3056	100
308	Y44486	Homo sapiens	Human GPRW receptor polypeptide.	1721	100
309	AJ131891	Homo sapiens	DNA polymerase mu	2598	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
310	AF293335	Homo sapiens	p30 DBC	1248	92
311	AF176525	Mus musculus	F-box protein FBL12	1501	93
312	X57802	Homo sapiens	immunoglobulin lambda light chain	959	81
313	Z36715	Homo sapiens	Net	2048	98
314	AF161532	Homo sapiens	HSPC047	727	100
315	AF208068	Homo sapiens	kelch-like protein KLHL3a	3046	100
316	Y66666	Homo sapiens	Membrane-bound protein PRO1013.	1166	100
317	Y29666	Homo sapiens	Human Ras protein RAPR-1.	1253	98
318	AJ387747	Homo sapiens	sialin	2614	99
319	AF161362	Homo sapiens	HSPC099	224	40
320	Y68773	Homo sapiens	Amino acid sequence of a human phosphorylation effector FHSP-5.	2243	99
321	AJ238379	Homo sapiens	putative TH1 protein	3013	100
322	AB040812	Homo sapiens	protein kinase PAK5	3792	99
323	Y95013	Homo sapiens	Human secreted protein vc48_1, SEQ ID NO:66.	913	100
324	Y13381	Homo sapiens	Amino acid sequence of protein PRO271.	1976	100
325	Y94944	Homo sapiens	Human secreted protein clone bf157_16 protein sequence SEQ ID NO:94.	2305	98
326	Y76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	6728	99
327	AF198532	Homo sapiens	lymphoid enhancer binding factor-1	2173	100
328	Z78013	Caenorhabditis elegans	Similarity to Drosophila Cadherin-related tumor suppressor	569	33
329	AF212921	Mus musculus	MMTV receptor variant 1	484	94
330	Z75330	Homo sapiens >R65207 R65207 02-MAR-1995 27-AUG-1993 Human stromalin-1. [Homo sapiens]	nuclear protein SA-1	6492	99
331	AL008583	Homo sapiens	dJ327J16.3 (supported by GENSCAN, FGENES and GENEWISE)	2133	99
332	Y36104	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 489.	310	41
333	AJ271669	Homo sapiens	putative sialoglycoprotease	1747	100
334	AF156598	Mus musculus	p53-regulated DDA3	997	64
335	M99058	Eimeria maxima	em100 gene is homologous the Eimeria tenella gene et100	154	26
336	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
337	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	2602	94
338	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3447	98
339	Z66561	Caenorhabditis elegans	Similarity to Human rab13 protein (PIR Acc. No. A49647).	716	34
340	AB021643	Homo sapiens	gonadotropin inducible transcription repressor-3	2761	99
341	G01946	Homo sapiens	Human secreted protein, SEQ ID NO: 6027.	465	98
342	AF020591	Homo sapiens	zinc finger protein	1091	48
343	L29154	Homo sapiens	immunoglobulin heavy chain	439	84

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			VDJ region		
344	U10281	Sus scrofa	gastric mucin	279	24
345	AK000404	Homo sapiens	unnamed protein product	1177	99
346	L22557	Rattus norvegicus	calmodulin-binding protein	1949	84
347	L22557	Rattus norvegicus	calmodulin-binding protein	2363	91
348	AL049481	Arabidopsis thaliana	AIG1-like protein	316	30
350	AJ251516	Mus musculus	cysteine and histidine-rich protein	1460	99
351	AK024477	Homo sapiens	FLJ00070 protein	1773	100
352	U50133	Homo sapiens	ankyrin	502	33
353	AK000625	Homo sapiens	unnamed protein product	721	100
354	AF161420	Homo sapiens	HSPC302	2623	97
355	AJ010014	Homo sapiens	M96A protein	1269	47
356	AF151029	Homo sapiens	HSPC195	941	91
357	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	1911	100
358	W78128	Homo sapiens	Human secreted protein encoded by gene 3 clone HOSBI96.	1117	100
359	X03414	Drosophila melanogaster	Kr polypeptide	316	45
360	AF151079	Homo sapiens	HSPC245	643	100
361	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	530	41
362	AF254741	Drosophila melanogaster	Centaurin Gamma 1A	681	46
363	AF213465	Homo sapiens	dual oxidase	2016	100
364	AF181562	Homo sapiens	proSAAS	1319	100
365	AF181562	Homo sapiens	proSAAS	1024	99
366	U73200	Mus musculus	p116Rip	884	82
367	AF263744	Homo sapiens	erbB2-interacting protein ERBIN	4973	99
368	U37501	Mus musculus	laminin alpha 5 chain	5867	72
369	AF043695	Caenorhabditis elegans	similar to the protein phosphates 2c family	549	36
370	Y73440	Homo sapiens	Human secreted protein clone yj23_1 protein sequence SEQ ID NO:102.	1484	99
371	AF272833	Homo sapiens	misato	2869	97
372	AF198454	Homo sapiens	epithelial protein lost in neoplasm beta	3927	100
373	Y73345	Homo sapiens	HTRM clone 438283 protein sequence.	273	80
374	AF169017	Homo sapiens	formiminotransferase cyclodeaminase	2717	98
375	A95106	unidentified	RED ALPHA	1202	99
376	W74828	Homo sapiens	Human secreted protein encoded by gene 100 clone HLQAB52.	1012	99
377	Y32131	Homo sapiens	Human LYST-2 protein.	3556	99
378	M14912	Homo sapiens	pol	132	86
379	AF090934	Homo sapiens	PRO0518	382	100
380	X66363	Homo sapiens	serine/threonine protein kinase	2499	100
381	Y41699	Homo sapiens	Human PRO703 protein sequence.	2362	100
382	AF174498	Homo sapiens	GR AF-1 specific protein phosphatase	7008	98
383	U64608	Caenorhabditis elegans	coded for by C. elegans cDNA yk173c12.5	246	36
384	U50133	Homo sapiens	ankyrin	502	33
385	AJ238520	Homo sapiens	putative transcription factor-like nuclear regulator	4123	97

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
387	AF208845	Homo sapiens	BM-003	1375	99
389	X57821	Homo sapiens	immunoglobulin lambda light chain	797	76
390	AF182404	Homo sapiens	mitochondrial uncoupling protein 1	1670	99
391	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
393	AF178432	Homo sapiens	SH3 protein	3700	100
394	AF229928	Drosophila melanogaster	cytoplasmic protein 89BC	1616	62
395	AF181721	Homo sapiens	RU2S	2254	100
396	Y69197	Homo sapiens	Amino acid sequence of a human betaIV-spectrin protein.	1626	98
397	U48238	Mus musculus	zinc finger protein neuro-d4	749	60
398	AL390137	Homo sapiens	hypothetical protein	263	51
399	AF217525	Homo sapiens	Down syndrome cell adhesion molecule	5337	60
400	AL022599	Schizosaccharomyces pombe	WD repeat protein	447	27
401	AC004859	Homo sapiens	similar to 2-oxoglutarate dehydrogenase ; similar to Q02218 (PID:g1352618)	4176	78
402	AB010266	Mus musculus	tenascin-X	10246	62
403	AL133288	Homo sapiens	dJ671D7.1 (similar to D.melanogaster CG5986 protein)	761	100
404	Z68753	Caenorhabditis elegans	ZC518.3b	888	48
405	Z78013	Caenorhabditis elegans	Similarity to Drosophila Cadherin-related tumor suppressor	569	33
406	AB031230	Homo sapiens	protein containing CXXC domain 2	1196	97
407	AF155106	Homo sapiens	NY-REN-36 antigen	1168	100
408	Y57945	Homo sapiens	Human transmembrane protein HTPN-69.	1538	99
409	Z18361	Ovis aries	trichohyalin	184	30
410	AF249744	Homo sapiens	RhoGEF	2733	100
411	AF176529	Mus musculus	F-box protein FBX13	2072	94
412	AF210842	Homo sapiens	HARP	4880	100
413	AL031658	Homo sapiens	dJ310013.7 (novel protein similar to H. roretzi HRPET-3)	776	98
414	X57398	Homo sapiens	pm5 protein	6131	99
415	AB029826	Homo sapiens	3-methylcrotonyl-CoA carboxylase biotin-containing subunit	2961	99
416	U43503	Saccharomyces cerevisiae	Lphlp	115	42
417	AL160493	Leishmania major	possible t26f17.21	239	35
418	Y08100	Homo sapiens	Human PRO331 protein.	330	29
419	U15131	Homo sapiens	p126	2228	54
420	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	2363	100
421	AF190635	Drosophila melanogaster	ankyrin 2	755	30
422	AF302150	Homo sapiens	phosphoinositol 3-phosphate-binding protein-2	1962	100
423	AL137530	Homo sapiens	hypothetical protein	433	94
424	X63753	Homo sapiens	son-a	7269	100
425	AB027249	Homo sapiens	MAPKK like protein kinase	1693	100
426	AF279144	Homo sapiens	tumor endothelial marker 7 precursor	1084	55

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
427	AF279144	Homo sapiens	tumor endothelial marker 7 precursor	1259	56
428	AE003683	Drosophila melanogaster	CG8312 gene product	149	29
429	Y07829	Homo sapiens	RING finger protein	2201	99
430	AF096897	Drosophila melanogaster	pushover	4442	47
431	U41387	Homo sapiens	Gu protein	4021	99
432	AF023674	Homo sapiens	nephrocystin	3783	100
433	AF146760	Homo sapiens	septin 2-like cell division control protein	2284	100
434	AB006697	Arabidopsis thaliana	cleft lip and palate associated transmembrane protein-like	886	42
437	Y94247	Homo sapiens	Human calcium binding protein hCBP.	1704	100
438	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase	1075	63
439	AF105228	Bos taurus	tuftelin	285	33
440	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	3073	99
441	X14971	Mus musculus	alpha-adaptin (A) (AA 1-977)	4897	98
442	X53773	Rattus norvegicus	alpha-c large chain (AA 1-938)	3979	81
443	Y66689	Homo sapiens	Membrane-bound protein PRO1136.	3299	99
444	AC067754	Arabidopsis thaliana	unknown protein; 20348-23707	114	33
445	AF229032	Mus musculus	pIL	2077	93
446	AF056035	Rattus norvegicus	s-nexilin	2662	85
447	AF132484	Mus musculus	unknown	478	51
448	W89024	Homo sapiens	Polypeptide fragment encoded by gene 156.	528	45
449	AF161445	Homo sapiens	HSPC327	1606	100
450	Z68753	Caenorhabditis elegans	ZC518.3b	951	49
451	W39160	Homo sapiens	Human partial complement factor H protein fragment 3.	155	32
452	W85727	Homo sapiens	Novel protein (Clone BM46_10).	2799	99
453	Y53629	Homo sapiens	A bone marrow secreted protein designated BMS115.	2810	100
454	D87438	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	4069	100
455	AF240468	Homo sapiens	nicastatin	3687	100
456	Z15005	Homo sapiens	CENP-E	13305	99
457	M59216	Homo sapiens	gamma-aminobutyric acid receptor beta-1 subunit	2477	100
458	Y73467	Homo sapiens	Human secreted protein clone yd61.1 protein sequence SEQ ID NO:156.	966	100
459	W67824	Homo sapiens	Human secreted protein encoded by gene 18 clone HSLFM29.	535	100
460	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	279	19
461	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	9196	99
462	G04044	Homo sapiens	Human secreted protein, SEQ ID NO: 8125.	486	93
463	AC002398	Homo sapiens	F25965_1	1018	100
464	AF064856	Rattus sp.	7acomp protein	1845	84
465	AF223408	Homo sapiens	B99	3686	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
466	AF223408	Homo sapiens	B99	2878	87
467	AF104415	Mus musculus	gene trap locus-13	6336	91
468	U53450	Rattus norvegicus	Jun dimerization protein 1 JDP-1	196	49
469	AL031297	Homo sapiens	dJ97220.1 (novel gene)	3564	99
470	AF257077	Homo sapiens	eukaryotic translation initiation factor EIF2B subunit 3	1274	95
471	L28125	Podospora anserina	beta transducin-like protein	284	38
472	Y84903	Homo sapiens	A human proliferation and apoptosis related protein.	2337	100
473	AF144237	Homo sapiens	LOMP protein	252	44
474	Y71213	Homo sapiens	Human irritable bowel disease related polypeptide IMX39.	838	100
475	Y95006	Homo sapiens	Human secreted protein ve13_1, SEQ ID NO:52.	3411	100
476	D38549	Homo sapiens	hal025 is new	6533	99
477	AF241230	Homo sapiens	TAK1-binding protein 2	3656	100
478	AL031534	Schizosaccharomyces pombe	putative asparagine synthase	482	40
479	L28125	Podospora anserina	beta transducin-like protein	233	26
480	AF161544	Homo sapiens	HSPC059	434	77
481	AJ238248	Homo sapiens	centaurin beta2	3986	99
482	Z38061	Saccharomyces cerevisiae	mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	295	23
483	AF161381	Homo sapiens	HSPC263	1404	100
484	AF223468	Homo sapiens	AD021 protein	1314	100
486	X57527	Homo sapiens	alpha 1(VIII) collagen	4166	99
487	Y19062	Homo sapiens	39k3 protein	2475	100
488	Y73373	Homo sapiens	HTRM clone 921803 protein sequence.	555	56
489	AL021918	Homo sapiens	b34f8.1 (Kruppel related Zinc Finger protein 184)	4184	100
490	X53773	Rattus norvegicus	alpha-c large chain (AA 1-938)	4675	97
491	U52426	Homo sapiens	GOK	1459	59
492	AL359773	Leishmania major	possible threonine synthase	702	45
493	AF226614	Homo sapiens	ferroportin1	2929	100
494	Z93241	Homo sapiens	dJ222E13.1 (novel protein with some similarity to Drosophila KRAKEN)	513	96
495	AF036977	Homo sapiens	unknown	1812	100
496	U93564	Homo sapiens	p40	133	45
497	Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.	357	100
498	AF069781	Drosophila melanogaster	Bem46-like protein	653	43
499	Y16601	Homo sapiens	Human cell-cycle phosphoprotein CECYP-2.	1658	98
500	X70944	Homo sapiens	PTB-associated splicing factor	3883	100
501	AF027503	Mus musculus	putative membrane-associated guanylate kinase 1	205	36
502	AF282874	Homo sapiens	nectin 3; PRR3	2856	99
503	AJ249732	Homo sapiens	G8 protein	669	100
504	AF208861	Homo sapiens	BM-019	1629	100
505	L09708	Homo sapiens	complement component C2	4022	100
507	X66285	Mus musculus	HCl ORF	115	43
508	D00189	Rattus norvegicus	Na ⁺ ,K ⁺ -ATPase alpha-subunit	5227	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
509	Y94971	Homo sapiens	Human secreted protein clone fa171_1 protein sequence SEQ ID NO:148.	2176	100
510	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	781	77
511	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1347	100
512	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1520	99
513	X84908	Homo sapiens	phosphorylase kinase	5729	99
514	X52851	Homo sapiens	peptidylprolyl isomerase	650	76
515	AF186084	Homo sapiens	epidermal growth factor repeat containing protein	3046	99
516	G03602	Homo sapiens	Human secreted protein, SEQ ID NO: 7683.	505	99
517	U04706	Bos taurus	50 kDa protein	1749	77
518	G00653	Homo sapiens	Human secreted protein, SEQ ID NO: 4734.	530	100
519	AF161475	Homo sapiens	HSPC126	1368	100
520	Y99366	Homo sapiens	Human PRO1475 (UNQ746) amino acid sequence SEQ ID NO:88.	3394	97
521	AF266852	Homo sapiens	PTPLA	1295	100
522	AE000995	Archaeoglobus fulgidus	chromosome segregation protein (smc1)	153	20
523	AF062249	Homo sapiens	immunoglobulin heavy chain variable region	605	97
524	AJ223830	Rattus norvegicus	ARE1	2950	98
525	W01535	Homo sapiens	Cellular homologue of the SV40 large T antigen.	1276	83
526	AF145658	Drosophila melanogaster	BcDNA.GH10229	320	33
527	AF112213	Homo sapiens	putative Rab5-interacting protein	524	79
528	D49387	Homo sapiens	NADP dependent leukotriene b4 12-hydroxydehydrogenase	1616	100
529	Y30819	Homo sapiens	Human secreted protein encoded from gene 9.	328	32
530	AL079335	Homo sapiens	dJ132F21.3 (72.1 KDa protein (DKFZP564A032, SBB188) similar to mouse IFN-gamma induce MG11.)	1059	99
531	Y91506	Homo sapiens	Human secreted protein sequence encoded by gene 56 SEQ ID NO:179.	1159	98
532	X76116	Caenorhabditis elegans	carrier protein (c2)	576	50
533	X76116	Caenorhabditis elegans	carrier protein (c2)	506	50
534	X12966	Homo sapiens	3-oxoacyl-CoA thiolase propeptide (424 AA)	1972	100
535	Y09267	Homo sapiens	flavin-containing monooxygenase 2	2486	100
536	Z11773	Homo sapiens	SRE-ZBP	2201	99
537	D84224	Homo sapiens	methionyl tRNA synthetase	4741	99
538	D84224	Homo sapiens	methionyl tRNA synthetase	3887	99
539	D84224	Homo sapiens	methionyl tRNA synthetase	2933	96
540	D84224	Homo sapiens	methionyl tRNA synthetase	4529	99
541	J03244	Bos taurus	H+ ATPase 31kDa subunit (EC 3.6.1.3)	848	77
542	Y92514	Homo sapiens	Human OXRE-11.	2301	99
543	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	2151	61
544	AE000919	Methanobacterium thermoautotrophicum	conserved protein	207	38
545	A06669	synthetic construct	preTGF-beta1	2070	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
546	Y02698	Homo sapiens	Human secreted protein encoded by gene 49 clone HTPCS60.	854	98
547	AF112205	Homo sapiens	WSB-1 protein	2275	100
548	X60271	Mus musculus	c-rel	2264	74
549	AC016827	Arabidopsis thaliana	putative GTPase	810	42
550	Y70400	Homo sapiens	Human cell-signalling protein-2.	429	68
551	AB048365	Homo sapiens	NEDD4-like ubiquitin ligase 1	8290	99
552	Y57880	Homo sapiens	Human transmembrane protein HTPMN-4.	1112	95
553	AF119855	Homo sapiens	PRO1847	265	67
554	M17236	Homo sapiens	MHC HLA-DQ alpha precursor	1332	100
555	AL078468	Arabidopsis thaliana	putative protein	540	40
556	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	515	44
557	AK024487	Homo sapiens	FLJ00086 protein	1623	98
558	M12140	Homo sapiens	pol gene protein; Xxx	117	48
559	W74825	Homo sapiens	Human secreted protein encoded by gene 97 clone HAQBF73.	225	56
560	X56681	Homo sapiens	jund protein	373	88
561	AF003136	Caenorhabditis elegans	contains weak similarity to an AMP-binding motif	2926	54
562	AL109839	Homo sapiens	dJ1069P2.3.1 (novel PABPC1 (poly(A)-binding protein)	877	100
563	AF181640	Drosophila melanogaster	BcDNA.GH09817	289	42
564	AF052723	Feline leukemia virus	gag-pol precursor polyprotein gPr80	1547	43
565	AF161472	Homo sapiens	HSPC123	439	44
566	Y28817	Homo sapiens	pt326_4 secreted protein.	3338	100
567	U09848	Homo sapiens	zinc finger protein	1738	100
569	AF155113	Homo sapiens	NY-REN-55 antigen	3603	93
570	AF155113	Homo sapiens	NY-REN-55 antigen	3951	99
571	AL032821	Homo sapiens	dJ55C23.1 (vanin 1)	1821	98
572	M69181	Homo sapiens	non-muscle myosin B	7350	99
573	M69181	Homo sapiens	non-muscle myosin B	7311	98
574	Y59678	Homo sapiens	Secreted protein 108-008-5-0-E6-FL.	772	100
575	AL365234	Arabidopsis thaliana	putative protein	788	40
576	AL365234	Arabidopsis thaliana	putative protein	788	40
577	X06745	Homo sapiens	DNA polymerase alpha-subunit (AA 1 - 1462)	7619	99
578	AB041642	Homo sapiens	PAR-6	1342	100
579	D86984	Homo sapiens	similar to yeast adenylate cyclase (S56776)	2446	100
580	AF165124	Homo sapiens	gamma-aminobutyric acid A receptor gamma 2	2499	99
581	W88812	Homo sapiens	Polypeptide fragment encoded by gene 58.	2339	99
582	U82319	Homo sapiens	novel ORF	342	100
583	P92219	Homo sapiens (human)	CR1 protein.	11425	99
584	AJ223948	Homo sapiens	RNA helicase	6608	99
585	Y08612	Homo sapiens	88kDa nuclear pore complex protein	3874	99
586	Y42384	Homo sapiens	Amino acid sequence of lv310_7.	1007	37
587	AF129756	Homo sapiens	BAT4	1873	98

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
588	AF131775	Homo sapiens	Unknown	1929	99
589	AJ250865	Homo sapiens	TESS 2	2348	100
591	Z98885	Homo sapiens	dJ522J7.2 (bromodomain-containing 1 (similar to peregrin, BR140))	4167	100
592	L76571	Homo sapiens	nuclear hormone receptor	1355	100
593	AF091622	Homo sapiens	PHD finger protein 3	9054	100
594	X56807	Homo sapiens	desmocollin type 2a	4443	100
595	AL137802	Homo sapiens	dJ798A10.1 (novel protein)	212	55
596	AL022329	Homo sapiens	bK407F11.2 (adrenergic, beta, receptor kinase 2)	3653	100
597	AF226048	Homo sapiens	GL003	2009	99
598	AJ278112	Homo sapiens >Y49635 Y49635 21-OCT-1999 15-APR-1998 Human sdp3.5 protein. [Homo sapiens]	putative cell cycle control protein	335	23
599	Y59741	Homo sapiens	Human normal ovarian tissue derived protein 18.	1574	99
600	L36531	Homo sapiens	integrin alpha 8 subunit	5386	99
601	Y38458	Homo sapiens	Human secreted protein encoded by gene No. 20.	895	100
602	AF218584	Homo sapiens	GGA1	3265	100
603	Y13115	Homo sapiens	serine/threonine protein kinase	5071	99
604	AL132776	Homo sapiens	dJ393D12.1 (KIAA0776)	2413	99
605	AL034452	Homo sapiens	dJ682J15.1 (novel Collagen triple helix repeat containing protein)	1979	100
606	Y14494	Homo sapiens	aralar1	3465	99
607	AJ001981	Homo sapiens	OXAL1	2603	100
608	X86098	Homo sapiens	binds directly to adenovirus type 5 E1A protein	3069	100
610	AF163572	Homo sapiens	Forssman glycolipid synthetase	1865	99
611	AF161503	Homo sapiens	HSPC154	1261	97
612	L41834	Ensis minor	nuclear protein	345	30
613	Y91954	Homo sapiens	Human cytoskeleton associated protein 9 (CYSKP-9).	3668	100
614	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	361	94
615	X85786	Homo sapiens	binding regulatory factor	3203	100
616	Y08319	Homo sapiens	kinesin-2	3487	99
617	DL2644	Mus musculus	KIF2 protein	3609	97
618	U28789	Mus musculus	PACT	5936	89
619	Y35914	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 163.	1684	99
620	AB046382	Mus musculus	testis-abundant finger protein	199	23
621	Y00062	Homo sapiens	precursor polypeptide (AA -23 to 1120)	3440	99
622	AF068286	Homo sapiens	HDCMD38P	861	100
623	X98248	Homo sapiens	sortilin	4436	99
624	X61100	Homo sapiens	75 kDa subunit NADH dehydrogenase precursor	3734	99
625	S58544	Homo sapiens	75 kDa infertility-related sperm protein	2125	99
626	AF151027	Homo sapiens	HSPC193	582	93
627	X14968	Homo sapiens	R11-alpha subunit (AA 1-404)	2079	100
628	Y50911	Homo sapiens	Human fetal brain cDNA clone vb7_1 derived protein	1983	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
629	Y50911	Homo sapiens	Human fetal brain cDNA clone vb7.1 derived protein	1694	100
630	AF098786	Homo sapiens	17 beta-hydroxysteroid dehydrogenase type VII	1754	100
631	AL034555	Homo sapiens	dJ134O19.3 (zinc finger protein 151 (pHZ-67))	4273	100
632	W74826	Homo sapiens	Human secreted protein encoded by gene 98 clone HAQBT94.	794	96
633	AF288288	Homo sapiens	HPT protein	2236	100
634	AF041429	Homo sapiens	pRGR1	823	99
635	X66357	Homo sapiens	serine/threonine protein kinase	1589	100
636	Y11284	Homo sapiens	AFX1	2571	98
637	AB004884	Homo sapiens	PKU-alpha	3718	99
638	AJ002303	Homo sapiens	synaptogyrin 1c	1020	100
639	AJ002304	Homo sapiens	synaptogyrin 1b	1002	100
640	AJ002303	Homo sapiens	synaptogyrin 1c	933	94
641	D87682	Homo sapiens	similar to a C.elegans protein encoded in cosmid T26A5.	2676	100
642	M14660	Homo sapiens	ISG-K54	2473	99
643	X06661	Homo sapiens	calbindin (AA 1-261)	1358	100
644	AF119900	Homo sapiens	PRO2822	185	76
645	AB031048	Drosophila melanogaster	microtubule associated-protein orbit	738	27
646	AF250842	Drosophila melanogaster	multiple asters	834	29
647	X86691	Homo sapiens	M1-2 protein	10110	99
648	U67934	Homo sapiens	44.9 kDa protein C18B11 homolog	827	96
649	AF236061	Oryctolagus cuniculus	RING-finger binding protein	3830	91
650	AL034553	Homo sapiens	dJ914P20.2 (KIAA0784 protein similar to Mus musculus activity-dependent neuroprotective protein (Adnp))	5708	100
653	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2388	99
654	AC004614	Homo sapiens	similar to f-spondin proteins AB006086 (PID:g2529225)	3026	99
655	Y57908	Homo sapiens	Human transmembrane protein HTMPN-32.	608	99
656	Z34975	Homo sapiens	ldlCp	3733	100
658	AL050306	Homo sapiens	dJ475B7.2 (novel protein)	1942	99
659	W76734	Homo sapiens	Human mDia Rho targeting protein.	781	34
660	AF202724	Homo sapiens	Sad1 unc-84 domain protein 1	2172	100
661	Z21966	Homo sapiens	mPOU homeobox protein	1529	100
662	AJ242954	Mus musculus	dysferlin	4752	59
663	AF182316	Homo sapiens	myoferlin	6232	99
665	AL161516	Arabidopsis thaliana	hypothetical protein	209	30
667	X59303	Homo sapiens	valyl-tRNA synthetase	3393	99
668	Y13355	Homo sapiens	Amino acid sequence of protein PRO220.	3692	100
669	AB010692	Arabidopsis thaliana	contains similarity to endo-beta-N-acetylglucosaminidase gene	611	52
671	X56123	Mus musculus	talin	4474	76
672	AB039371	Homo sapiens	mitochondrial ABC transporter 3	2902	99
673	AF269223	Homo sapiens	TCP11	806	42
674	AF229633	Mus musculus	groucho-related protein 4	4053	99
675	L14463	Rattus	transducin	3619	92

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		norvegicus			
676	AC005757	Homo sapiens	R32611_1	2779	100
677	S61069	Homo sapiens	reverse transcriptase homolog=pol {retroviral element}	252	65
678	AF271388	Homo sapiens	CMP-N-acetylneuraminic acid synthase	2273	100
679	X79066	Homo sapiens	ERF-1	1783	100
680	AF118566	Mus musculus	hematopoietic zinc finger protein	769	50
681	Y51415	Homo sapiens	Human wild type pKe83 protein.	2621	99
682	AL133545	Homo sapiens	bA386N14.1 (novel protein similar to a dual specificity phosphatase)	700	68
683	Y86214	Homo sapiens	Nuclear transport protein clone hfb341 protein sequence.	5888	99
684	Y94952	Homo sapiens	Human secreted protein clone fh116_11 protein sequence SEQ ID NO:110.	354	98
685	AL021878	Homo sapiens	dJ257I20.4 (transcription factor 20 (AR1) (KIAA0292) (isoform 2))	154	67
686	AE000198	Escherichia coli	orf, hypothetical protein	628	100
687	M58378	Homo sapiens	synapsin I	3730	99
688	AF039697	Homo sapiens	antigen NY-CO-31	508	98
689	U09355	Oryctolagus cuniculus	protein phosphatase 2A1 B gamma subunit	2356	99
690	AF155106	Homo sapiens	NY-REN-36 antigen	265	50
691	AC004774	Homo sapiens	DLX-5	1542	100
692	X90530	Homo sapiens	ragB	1926	99
693	X90530	Homo sapiens	ragB	1405	99
694	X90530	Homo sapiens	ragB	1590	85
695	G01563	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
696	AC011810	Arabidopsis thaliana	Putative methionine aminopeptidase	669	52
697	AJ250425	Rattus norvegicus	Collybistin I	2455	98
698	AB037901	Homo sapiens	gene amplified in squamous cell carcinoma-1	5364	99
699	Y99401	Homo sapiens	Human PRO1327 (UNQ687) amino acid sequence SEQ ID NO:218.	1386	100
701	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	6705	100
702	X83573	Homo sapiens	ARSE	3184	99
703	AJ243274	Homo sapiens	AP-2rep protein	2078	99
704	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchm1.	1697	94
705	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchm1.	1736	99
706	Y41257	Homo sapiens	Amino acid sequence of long human FAIM.	1060	100
707	AL022237	Homo sapiens	bK1191B2.3 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1))	2030	100
708	AJ006266	Homo sapiens	AND-1 protein	5942	100
709	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
710	Y08698	Homo sapiens	ranbp3	2849	98
711	Y68770	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-2.	754	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
712	U93574	Homo sapiens	putative p150	799	59
713	AC004531	Homo sapiens	Gene with similarity to DEAD box helicases	2715	99
714	D89016	Homo sapiens	Neuroblastoma	538	48
715	Y92175	Homo sapiens	Human cardiovascular system associated protein tyrosine phosphatase 2.	734	98
716	AL137013	Homo sapiens	bA311P8.3 (probable uracil phosphoribosyltransferase)	862	100
717	AB035123	Mus musculus	GDI alpha/GT1a alpha/GQ1b alpha synthase	1696	93
718	Y96290	Homo sapiens >P40254 P40254 25-OCT-1984 09-APR-1983 Human IgD. [Homo sapiens]	Human IGFAM-2 immunoglobulin.	2345	85
719	X07979	Homo sapiens	integrin beta 1 subunit precursor	4347	99
720	AJ224819	Homo sapiens	tumor suppressor	2149	99
721	Y07595	Homo sapiens	transcription factor TFIIH	2373	100
722	W41565	Homo sapiens >W41564 W41564 08-OCT-1997 05-APR-1996 Human calpain. [Homo sapiens]	Human calpain.	1591	99
723	AF161341	Homo sapiens	HSPC078	1097	98
724	AF187318	Homo sapiens	F-box protein Fbx2	1607	100
725	AC006708	Caenorhabditis elegans	contains similarity to Saccharomyces cerevisiae pre-mRNA splicing protein PRP31 (GB:Z72876)	1143	46
726	AC006708	Caenorhabditis elegans	contains similarity to Saccharomyces cerevisiae pre-mRNA splicing protein PRP31 (GB:Z72876)	988	46
727	AC024818	Caenorhabditis elegans	contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3	950	44
728	AJ005897	Homo sapiens	JM5	831	47
729	Y45377	Homo sapiens	Human secreted protein fragment encoded from gene 27.	908	97
730	G03931	Homo sapiens	Human secreted protein, SEQ ID NO: 8012.	578	100
731	AB012720	Oncorhynchus masou	GTP-binding protein	3865	76
732	W73404	Homo sapiens	Human secreted protein encoded by Gene No. 8.	862	97
733	G02650	Homo sapiens	Human secreted protein, SEQ ID NO: 6731.	644	97
734	AC024813	Caenorhabditis elegans	Hypothetical protein Y54F10AL.a	152	24
735	AL035461	Homo sapiens	dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)	1562	98
736	U00033	Caenorhabditis elegans	similar to S. cerevisiae YJU2 protein	605	41
737	AF079098	Homo sapiens	arginine-tRNA-protein transferase 1-1p; ATE1-1p	2733	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
738	AJ131712	Homo sapiens	nucleolar RNA-helicase	2793	100
739	AJ133115	Homo sapiens	TSC-22-like protein	2054	99
740	X98258	Homo sapiens	M-phase phosphoprotein 9	953	100
741	X98258	Homo sapiens	M-phase phosphoprotein 9	564	74
742	U97191	Caenorhabditis elegans	strong similarity to the YPT1 sub-family of RAS proteins	960	85
743	X76057	Homo sapiens	phosphomannose isomerase	2191	100
744	G03209	Homo sapiens	Human secreted protein, SEQ ID NO: 7290.	496	98
745	X97064	Homo sapiens	Sec23 protein	4034	99
746	W93946	Homo sapiens	Human regulatory molecule HRM-2 protein.	994	100
747	Y73388	Homo sapiens	HTRM clone 3376404 protein sequence.	1565	99
748	M19529	Sus scrofa	folliculin A	1906	98
749	AJ249457	Trichomonas vaginalis	centrin, putative	183	28
750	AC004410	Homo sapiens	fos39554.1	2094	100
751	AF074968	Homo sapiens	p47ING3 protein	2167	100
752	AF252284	Homo sapiens	transcription specificity factor Sp1	4005	100
753	AB049629	Homo sapiens	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	1375	99
754	D79205	Homo sapiens	ribosomal protein L39	160	77
755	AB008430	Homo sapiens	CDEP	142	29
758	L32162	Homo sapiens	transcription factor	574	80
759	AF037204	Homo sapiens	RING zinc finger protein	295	54
760	Y44250	Homo sapiens	Human cell signalling protein-13.	625	100
761	AF218586	Homo sapiens	Cide-b	1136	100
762	U38934	Gallus gallus	histone H2A	625	97
763	AF226053	Homo sapiens	HSKM-B	606	32
764	X13403	Homo sapiens	Oct-1 protein (AA 1 - 743)	3626	100
765	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	568	38
766	AL023828	Caenorhabditis elegans	Y17G7B.14	200	27
767	Y82777	Homo sapiens	Human chordin related protein (Clone dw665_4).	2551	99
768	X92475	Homo sapiens	ITBA1	1429	100
769	Y42752	Homo sapiens	Human calcium binding protein 3 (CaBP-3).	1426	100
770	X51416	Homo sapiens	hormone receptor hERR1 (AA 1-521)	2641	97
771	AJ006591	Homo sapiens	cysteine-rich protein	1793	100
772	A08695	Homo sapiens	rap2	935	100
773	Z12173	Homo sapiens	N-acetylglucosamine-6-sulphatase	2970	100
774	Y91950	Homo sapiens	Human cytoskeleton associated protein 5 (CYSKP-5).	565	43
776	AL023799	Homo sapiens	dJ322P7.1 (zinc finger)	855	56
777	AL023799	Homo sapiens	dJ322P7.1 (zinc finger)	855	56
778	G01880	Homo sapiens	Human secreted protein, SEQ ID NO: 5961.	849	98
779	AJ012590	Homo sapiens	glucose 1-dehydrogenase	4155	99
780	AL078582	Homo sapiens	dJ130E4.2 (KIAA0796)	1321	68
781	Z75955	Caenorhabditis elegans	similar to mitochondrial carrier protein	384	34
782	AL109965	Homo sapiens	dJ1121G12.2 (SCAN domain-containing 1 protein)	900	100
783	AF061262	Mus musculus	semaF cytoplasmic domain associated protein 2	1316	83
784	G03873	Homo sapiens	Human secreted protein, SEQ	649	95

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 7954.		
785	Y84441	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	2074	100
786	Y00918	Homo sapiens	Human Rab protein, RABP-1, protein sequence.	1048	99
787	Z97029	Homo sapiens	ribonuclease HI large subunit	1548	99
788	AB035384	Homo sapiens	SRp25 nuclear protein	962	94
789	AF024631	Homo sapiens	ANG2	2644	100
790	AJ006710	Rattus norvegicus	phosphatidylinositol 3-kinase	4508	97
792	V00638	bacteriophage lambda	reading frame ea10	600	100
793	AF049103	Homo sapiens	Huntingtin interacting protein	819	100
795	Z26317	Homo sapiens	desmoglein 2	4810	99
796	Y76884	Homo sapiens	Retinoblastoma binding protein-7 sequence.	5080	99
797	U15155	Gallus gallus	trypsinogen	372	37
798	U97189	Caenorhabditis elegans	strong similarity to the P13/P14 family of kinases	227	28
799	AF112201	Homo sapiens	neuronal protein NP25	1053	100
800	AF234765	Rattus norvegicus	serine-arginine-rich splicing regulatory protein SRRP86	958	63
801	AF267852	Homo sapiens	placental protein 13-like protein	743	99
802	AF208851	Homo sapiens	BM-009	766	80
803	Z81097	Caenorhabditis elegans	Similarity to Human retinoblastoma-binding protein RBAP46 yk662d12.5 comes from this gene	152	27
804	G02113	Homo sapiens	Human secreted protein, SEQ ID NO: 6194.	496	98
805	AL121673	Homo sapiens	ba305P22.1 (novel protein)	1160	100
806	AC013483	Arabidopsis thaliana	putative GTPase activator protein	264	30
807	AC013483	Arabidopsis thaliana	putative GTPase activator protein	264	30
808	AB013885	Homo sapiens	beta-ureidopropionase	1494	100
809	AF078842	Homo sapiens	HOTTL protein	1581	99
810	AF161421	Homo sapiens	HSPC303	2134	96
811	AF261689	Homo sapiens	DNA polymerase epsilon p17 subunit	734	100
812	Z74029	Caenorhabditis elegans	Similarity to C.elegans alcohol dehydrogenase comes from this gene	610	71
813	Z73497	Homo sapiens	cU240C2.2 (Core histone H2A/H2B/H3/H4)	324	100
814	W87689	Homo sapiens	Human HTXFT19 polypeptide.	1484	99
815	X16282	Homo sapiens	zinc finger protein (217 AA) (1 is 2nd base in codon)	1109	99
816	Z92539	Mycobacterium tuberculosis	pth	300	36
818	AB030483	Mus musculus	B9	197	27
819	AL117555	Homo sapiens	hypothetical protein	321	94
820	AC005328	Homo sapiens	R26660_2, partial CDS	865	97
821	G03951	Homo sapiens	Human secreted protein, SEQ ID NO: 8032.	700	99
822	I34807	Musca domestica	transposase	174	20
823	G02928	Homo sapiens	Human secreted protein, SEQ ID NO: 7009.	558	78
824	Z99531	Schizosaccharomyces pombe	caffeine-induced death	184	29

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		romyces pombe	protein 1		
825	AJ006692	Homo sapiens	ultra high sulfur keratin	693	68
826	U23037	Oryctolagus cuniculus	eIF-2Bepsilon	3406	90
827	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
828	Y30827	Homo sapiens	Human secreted protein encoded from gene 17.	113	44
829	Y32199	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379.	1012	100
830	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
832	AB011542	Homo sapiens	MEGF9	2097	100
833	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	223	70
834	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1574	100
835	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1144	89
836	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1448	94
837	X12517	Homo sapiens	C protein (AA 1-159)	918	100
838	U32865	Drosophila melanogaster	linotte protein	164	24
839	AF067730	Homo sapiens	TLS-associated protein TASR-2	631	56
840	U27831	Homo sapiens	striatum-enriched phosphatase	2840	98
841	AF286366	Homo sapiens	CamKI-like protein kinase	1796	100
842	G02309	Homo sapiens	Human secreted protein, SEQ ID NO: 6390.	278	98
843	AE003615	Drosophila melanogaster	ade3 gene product	113	48
844	G01350	Homo sapiens	Human secreted protein, SEQ ID NO: 5431.	629	100
845	U27838	Mus musculus	glycosyl-phosphatidyl-inositol-anchored protein homolog	3305	96
847	Y87788	Homo sapiens	Human RBP-26 protein.	2026	100
848	AF164794	Homo sapiens	Diff33 protein homolog	2398	100
849	U41315	Homo sapiens	ZNF127-Xp	2458	93
850	AF192784	Homo sapiens	makorin 1	2062	97
851	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1548	100
852	Z22968	Homo sapiens	M130 antigen	6205	100
853	Z22971	Homo sapiens	M130 antigen extracellular variant	6380	100
854	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	330	96
855	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	203	100
856	AF285118	Homo sapiens	CGI-203	452	100
857	AC006069	Arabidopsis thaliana	putative cleavage and polyadenylation specificity factor	1383	55
858	AL021546	Homo sapiens	Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1)	593	100
859	L02956	Xenopus laevis	ribonucleoprotein	1664	85
860	AF201947	Homo sapiens	MEK binding partner 1	616	100
861	L31783	Mus musculus	uridine kinase	1266	92
862	AF161472	Homo sapiens	HSPC123	602	73
863	Z49068	Caenorhabditis elegans	mitochondrial carrier protein	370	43
864	AF154108	Homo sapiens	tumor necrosis factor type 1	3559	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			receptor associated protein		
865	AE001530	Helicobacter pylori J99	putative	230	32
866	X57807	Homo sapiens	immunoglobulin lambda light chain	699	91
867	AL031673	Homo sapiens	dJ694B14.1 (PUTATIVE novel KRAB box protein with 18 C2H2 type Zinc finger domains)	4066	99
868	Y11652	Homo sapiens	phosphate cyclase	238	100
869	AF192968	Homo sapiens	high-glucose-regulated protein 8	3041	99
870	AB020648	Homo sapiens	KIAA0841 protein	3237	99
871	AL031427	Homo sapiens	dJ167A19.1 (novel protein)	1608	100
872	AF151534	Homo sapiens	core histone macroH2A2.2	1866	100
873	AL021331	Homo sapiens	dJ366N23.1 (putative C. elegans UNC-93 (protein 1, C46F11.1) LIKE protein)	1129	100
874	X14608	Homo sapiens	propionyl-CoA carboxylase	3579	100
875	AL117334	Homo sapiens	dJ687F11.1 (novel protein (part of translation of cDNA DKFZp434N061, Em:AL110249))	306	100
876	X79489	Saccharomyces cerevisiae	E-925 protein	446	35
877	Y53001	Homo sapiens	Human secreted protein clone dn834_1 protein sequence SEQ ID NO:8.	811	100
878	AF281064	Homo sapiens	CHMP1.5	957	100
879	X79417	Sus scrofa	40S ribosomal protein S12	687	100
880	AF001317	Saccharomyces cerevisiae	Soilp	478	28
881	Y87275	Homo sapiens	Human signal peptide containing protein HSPP-52 SEQ ID NO:52.	2547	100
882	M14036	Homo sapiens	C1-inhibitor	598	77
883	AB041261	Homo sapiens	calcium-independent phospholipase A2	2903	100
884	AF020313	Mus musculus	proline-rich protein 48	999	84
885	Y10936	Homo sapiens	hypothetical protein	1104	99
886	AF073997	Mus musculus	myotubularin related protein 1	866	36
887	Y57893	Homo sapiens	Human transmembrane protein HTPN-17.	1099	94
888	AL117635	Homo sapiens	hypothetical protein	929	99
889	AF210317	Homo sapiens	facilitative glucose transporter family member GLUT9	2046	99
890	Y36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	583	100
891	Y36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	192	57
892	AF237631	Homo sapiens	ubiquitous tropomodulin U-Tmod	1798	100
893	AF090929	Homo sapiens	PRO0477p	653	99
894	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1))	3196	100
895	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1))	2825	96
896	AF171102	Homo sapiens	retinal degeneration B beta	1302	95
897	AE003551	Drosophila melanogaster	CG18176 gene product	633	33

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
898	AJ237946	Homo sapiens	DEAD Box Protein 5	2443	100
899	Z97184	Homo sapiens	HKE2	624	100
900	Z97184	Homo sapiens	HKE2	409	98
901	AJ245587	Homo sapiens	Kruppel-type zinc finger	1942	100
902	AF091034	Homo sapiens	GTP-binding protein RAE22A	1011	100
903	R95953	Homo sapiens	Eukaryotic cell growth inhibiting factor.	414	96
904	L04733	Homo sapiens	kinesin light chain	1936	72
905	AE003540	Drosophila melanogaster	CG10984 gene product	446	33
906	M55542	Homo sapiens	guanylate binding protein isoform I	2993	98
907	M55542	Homo sapiens	guanylate binding protein isoform I	2901	96
908	W84085	Homo sapiens	Human membrane fusion protein WDProl.	1889	100
909	AF168676	Homo sapiens	TNF intracellular domain-interacting protein	647	100
910	AB029150	Homo sapiens	KRAB zinc finger protein HFB101L	2196	100
911	G02871	Homo sapiens	Human secreted protein, SEQ ID NO: 6952.	521	100
912	G03162	Homo sapiens	Human secreted protein, SEQ ID NO: 7243.	387	87
913	AJ243721	Homo sapiens >Y92508 Y92508 13-APR-2000 06-OCT-1998 Human OXRE-5. [Homo sapiens	dTDP-4-keto-6-deoxy-D-glucose 4-reductase	1710	100
914	U24189	Caenorhabditis elegans	hypothetical protein 1207-1; Method: conceptual translation supplied by authors	244	41
915	Y02591	Homo sapiens	A human progesterone receptor complex p23-like protein.	843	99
916	AE000984	Archaeoglobus fulgidus	dinitrogenase reductase activating glycohydrolase (draG)	171	26
918	M23159	Cricetus cricetus	DHFR-coamplified protein	163	30
919	L12018	Caenorhabditis elegans	putative	1232	41
920	AF102177	Homo sapiens	tumor antigen SLP-8p	1260	97
921	AL096712	Homo sapiens	dJ744I24.2 (similar to a novel human gene mapping to Activator)	1017	78
922	AL161495	Arabidopsis thaliana	putative WD-repeat protein	866	42
923	AL161495	Arabidopsis thaliana	putative WD-repeat protein	442	36
924	U97001	Caenorhabditis elegans	similar to Schizosaccharomyces pombe	605	51
925	X71978	Mus musculus	Fif	1503	95
926	M92288	Drosophila melanogaster	beta-spectrin	290	51
927	Y27575	Homo sapiens	Human secreted protein encoded by gene No. 9.	1392	100
928	Y22499	Homo sapiens	Human secreted protein sequence clone mh703_1.	2249	100
930	AJ224326	Homo sapiens	ribulose-5-phosphate-epimerase	912	100
931	U28991	Caenorhabditis	coded for by C. elegans cDNA	660	55

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		is elegans	cm21c7		
932	AL080065	Homo sapiens	hypothetical protein	210	25
933	G01884	Homo sapiens	Human secreted protein, SEQ ID NO: 5965.	767	98
934	AJ276485	Homo sapiens	integral membrane transporter protein	1200	100
935	AL035681	Homo sapiens	dJ756G23.3 (novel protein similar to drosophila transcriptional repressor)	1142	80
936	AB026808	Mus musculus	synaptotagmin XI	2142	95
937	AB015345	Homo sapiens	HRIHFB2216	2601	99
938	X65724	Homo sapiens	ORF2	498	100
939	W89024	Homo sapiens	Polypeptide fragment encoded by gene 156.	1487	100
940	G04047	Homo sapiens	Human secreted protein, SEQ ID NO: 8128.	117	100
941	AF094583	Homo sapiens	putative HIV-1 infection related protein	452	100
942	AC024200	Caenorhabditis elegans	contains similarity to several zinc finger proteins but not to the zinc finger domains	350	69
943	AF129756	Homo sapiens	G5c	273	100
944	M23765	Rattus norvegicus	alpha-tropomyosin	133	96
945	AC009917	Arabidopsis thaliana	Contains similarity to	583	47
946	AF223468	Homo sapiens	AD021 protein	551	44
947	AF055473	Homo sapiens	GAGE-8	273	51
948	X75756	Homo sapiens	protein kinase C mu	2019	68
949	AF143956	Mus musculus	coronin-2	2300	93
950	Y36729	Homo sapiens	Human PGI protein sequence.	1861	99
951	W49041	Homo sapiens	Human low density lipoprotein binding protein LBP-2.	282	67
952	AB016881	Arabidopsis thaliana	gene_id:MXC17.7-	203	46
953	Y01785	Homo sapiens	Human ubiquitin-conjugating enzyme >Y25341 Y25341 01-JUL-1999 12-AUG-1998 Human NCE-2 protein.	365	100
954	AF145615	Drosophila melanogaster	BcDNA.GH03377	823	46
955	U09410	Homo sapiens	zinc finger protein ZNF131	2483	99
956	U09410	Homo sapiens	zinc finger protein ZNF131	1853	99
957	AF195623	Homo sapiens	cholinephosphotransferase 1 alpha	2126	99
958	X94917	Drosophila melanogaster	head-elevated expression in 0.9 kb	155	32
959	U54807	Rattus norvegicus	GTP-binding protein	1167	97
960	AF058807	Bos taurus	GTP-binding protein rah	606	97
961	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	471	100
962	AF078850	Homo sapiens	steroid dehydrogenase homolog	583	40
963	AP001754	Homo sapiens	transient receptor potential-related channel 7, a novel putative Ca2+ channel protein	317	30
964	AL035419	Homo sapiens	dJ1100H13.1 (putative novel protein)	1129	100
965	X61381	Rattus rattus	interferon-induced protein	202	46
966	D38169	Homo sapiens	inositol 1,4,5-trisphosphate 3-kinase isoenzyme	3278	100
967	AL031432	Homo sapiens	dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1)	893	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
968	U79275	Homo sapiens	unknown	611	100
969	AJ011306	Homo sapiens	guanine nucleotide exchange factor (long isoform)	2752	99
970	AF281134	Homo sapiens	exosome component Rrp46	1186	100
971	U53336	Caenorhabditis elegans	weak similarity over a short region to myosin heavy chain	536	23
972	AC018749	Leishmania major	L8840.12	589	53
973	AF188504	Mus musculus	LNV	544	85
974	U25801	Homo sapiens	Tax1 binding protein	852	98
975	AP049523	Homo sapiens	huntingtin-interacting protein HYPA/FBP11	1390	97
976	AF161530	Homo sapiens	HSPC182	1040	100
977	G04020	Homo sapiens	Human secreted protein, SEQ ID NO: 8101.	626	100
978	AF164797	Homo sapiens	ribosomal protein L17 isolog	908	100
979	U94991	Xenopus laevis	transcription factor XLM01	795	97
980	S73775	Homo sapiens	calmitine; calsequestrine	2029	100
981	Y94888	Homo sapiens	Human protein clone HP01462.	2501	100
982	AJ243191	Homo sapiens	heat shock protein	827	96
983	X65020	Bos taurus	PSST subunit of the NADH: ubiquinone oxidoreductase complex	964	85
984	AJ249207	Rhodococcus sp. AD45	putative racemase	351	43
985	Z30093	Homo sapiens	basic transcription factor 2, 35 kD subunit	1576	99
986	AB030835	Homo sapiens	contains two glutamine rich domains, three zinc-finger domains, and matrin 3 homologous domain 3 (MH3)	4697	99
987	AF227258	Bos taurus	RPGR-interacting protein-1	1262	38
988	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	4048	99
989	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	2321	99
990	AF161426	Homo sapiens	HSPC308	448	92
991	AF161426	Homo sapiens	HSPC308	448	92
992	AF161426	Homo sapiens	HSPC308	453	92
993	AL023859	Schizosaccharomyces pombe	trna-splicing endonuclease subunit	172	42
994	AL049631	Homo sapiens	dJ513M9.1 (novel Homeobox domain protein)	241	47
995	AC005253	Homo sapiens	R26445_1	902	100
996	AF265206	Homo sapiens	MOG1 isoform A	974	100
997	AJ248285	Pyrococcus abyssi	sarcosine oxidase, subunit beta (soxB)	195	28
998	AE003641	Drosophila melanogaster	BG:DS00941.3 gene product	218	58
999	W69343	Homo sapiens	Secreted protein of clone CR930_1.	1340	98
1000	AY007135	Homo sapiens	similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1	1543	100
1001	Y73381	Homo sapiens	HTRM clone 1877278 protein sequence.	1668	100
1002	AF208844	Homo sapiens	BM-002	428	100
1003	AE004944	Pseudomonas aeruginosa	hypothetical protein	134	35
1004	AL031431	Homo sapiens	dJ462023.2 (novel protein)	2058	100
1005	S45367	Canis familiaris	centractin	1949	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1006	S45367	Canis familiaris	centractin	1315	98
1007	AB022158	Mus musculus	chaperonin containing TCP-1 epsilon subunit	2649	96
1008	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	1282	97
1009	AB011414	Homo sapiens	Kruppel-type zinc finger protein	1671	58
1010	Z68218	Caenorhabditis elegans	K01H12.1	269	67
1011	AB011414	Homo sapiens	Kruppel-type zinc finger protein	1671	58
1012	Z14000	Homo sapiens	RING1	2017	100
1013	G02841	Homo sapiens	Human secreted protein, SEQ ID NO: 6922.	332	93
1014	AF145659	Drosophila melanogaster	BcDNA.GH10333	1244	52
1015	Y02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	664	67
1016	Y02591	Homo sapiens	A human progesterone receptor complex p23-like protein.	772	97
1017	Y99448	Homo sapiens	Human PRO1759 (UNQ832) amino acid sequence SEQ ID NO:374.	2323	100
1018	X67250	Rattus norvegicus	n-chimaerin	1710	97
1019	AF183417	Homo sapiens	microtubule-associated proteins 1A/1B light chain 3	631	100
1020	AF164795	Homo sapiens	sex-regulated protein janus-a	674	100
1021	AF190625	Coturnix coturnix	qdg1-1	638	96
1022	AL133363	Arabidopsis thaliana	putative protein	155	37
1023	AB034912	Homo sapiens	WD-repeat like sequence	2483	100
1024	AY007091	Homo sapiens	similar to Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA with Ge	2243	100
1025	X69910	Homo sapiens	P63 protein	2958	99
1026	U80736	Homo sapiens	CAGF9	1657	100
1027	AB029333	Halocynthia roretzi	HrPET-1	1048	54
1028	AB032931	Homo sapiens	ubiquitin-conjugating enzyme isolog	1045	100
1029	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98
1030	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98
1031	AF193795	Homo sapiens	vacuolar sorting protein VPS29/PEP11	960	100
1032	AJ222968	Mus musculus	L-periaxin	120	30
1033	Z81317	Schizosaccharomyces pombe	DNA2-NAM7 helicase family protein	685	31
1034	Y41519	Homo sapiens	Fragment of human secreted protein encoded by gene 75.	1321	99
1035	AJ276004	Mus musculus	Paxneb protein	1709	77
1036	AF025459	Caenorhabditis elegans	H14A12.3 gene product	190	30
1037	U37251	Homo sapiens	Description: KRAB zinc finger protein; this is a splicing supplied by author	196	43
1038	W74580	Homo sapiens	Human membrane protein BA0306.	1921	97
1039	U88173	Caenorhabditis elegans	weak similarity to Arabidopsis thaliana ubiquitin-like protein 8	331	80

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1040	AF290204	Homo sapiens	blood group carrier molecule DOK1	1637	99
1041	Y96730	Homo sapiens	PRO539, a Costal-2 homologue.	162	22
1042	AF140683	Mus musculus	F-box protein FWD2	2397	98
1043	AF151023	Homo sapiens	HSPC189	1104	100
1044	AF181631	Drosophila melanogaster	BcDNA.GH04929	204	37
1045	Y77985	Homo sapiens	Human collectin amino acid sequence.	1940	100
1046	AJ243972	Homo sapiens	6-phosphogluconolactonase	1317	100
1047	AB035863	Homo sapiens	ATP specific succinyl CoA synthetase beta subunit precursor	2324	99
1048	AL034550	Homo sapiens	dJ1184F4.2 (novel protein similar to nucleolar protein 4 (NOL4) (NOLP))	981	92
1049	AF163825	Homo sapiens	pre-B lymphocyte protein 3	634	100
1050	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	868	100
1051	AF190624	Mus musculus	mdg1-1	236	85
1052	AE003529	Drosophila melanogaster	CG6151 gene product	160	44
1053	G01191	Homo sapiens	Human secreted protein, SEQ ID NO: 5272.	646	98
1054	AL162756	Neisseria meningitidis	Glu-tRNA(Gln) amidotransferase subunit A	682	44
1055	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	1525	99
1056	U89649	Chlamydomonas reinhardtii	Mr19,000 outer arm dynein light chain	244	34
1057	AF159141	Homo sapiens	breast cancer metastasis-suppressor 1	663	53
1058	AF230929	Homo sapiens	keratinocyte annexin-like protein pemphaxin	1710	99
1059	AJ270952	Homo sapiens	putative membrane protein	1363	100
1060	AF224263	Heterodontus francisci	HoxD8	742	83
1061	X63417	Homo sapiens	IRLB	1037	100
1062	AL079345	Streptomyces coelicolor A3(2)	hypothetical protein	143	27
1063	Y71112	Homo sapiens	Human Hydrolase protein-10 (HYDRL-10).	2547	100
1064	AF263614	Homo sapiens	acetyl-CoA synthetase	3493	99
1065	Y13356	Homo sapiens	Amino acid sequence of protein PRO221.	1363	100
1066	AC006153	Homo sapiens	similar to Aquifex aeolicus GTP-binding protein; similar to AE000771 (PID:g2984292)	662	98
1067	Y18930	Sulfolobus solfataricus	hypothetical protein	162	29
1068	R65969	Homo sapiens T98G	Glioblastoma-derived polypeptide.	887	100
1069	Y07964	Homo sapiens	Human secreted protein fragment	863	96
1070	AF177476	Rattus norvegicus	CDK5 activator-binding protein	1995	86
1071	AF245505	Homo sapiens	adlcan	3109	99
1072	U92794	Mus musculus	alpha glucosidase II, beta subunit	147	36
1073	G03889	Homo sapiens	Human secreted protein, SEQ ID NO: 7970.	698	98
1074	U15779	Homo sapiens	p70	380	28
1075	Y13392	Homo sapiens	Amino acid sequence of	1271	91

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			protein PRO328.		
1076	AF161457	Homo sapiens	HSPC339	571	100
1077	Y79509	Homo sapiens	Human carbohydrate-associated protein CRBAP-5.	2151	98
1078	AF223466	Homo sapiens	HT015 protein	831	66
1079	AL132965	Arabidopsis thaliana	putative WD-40 repeat-protein	286	29
1080	AB024937	Homo sapiens	LUNX	1284	100
1081	Y14768	Homo sapiens	V-ATPase G-subunit like protein	579	100
1082	AF016416	Caenorhabditis elegans	F29A7.4 gene product	141	31
1083	L13291	Homo sapiens	ADP-ribosylarginine hydrolase	802	45
1084	AB041541	Mus musculus	unnamed protein product	151	44
1085	G01922	Homo sapiens	Human secreted protein, SEQ ID NO: 6003.	202	97
1086	AB030814	Homo sapiens	H-REV107 protein homolog	833	100
1087	AF151638	Homo sapiens	phosphatidylcholine transfer protein	1142	100
1088	Y84432	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	2783	100
1089	Y94867	Homo sapiens	Human protein clone HP10563.	613	100
1090	AK023982	Homo sapiens	unnamed protein product	130	49
1091	AB041586	Mus musculus	unnamed protein product	1103	81
1092	Y71277	Homo sapiens	Human Zlipo3 protein.	606	100
1093	U34973	Mus musculus	protein tyrosine phosphatase-like	1131	95
1094	Y66677	Homo sapiens	Membrane-bound protein PRO828.	522	56
1095	Y87276	Homo sapiens	Human signal peptide containing protein HSPP-53 SEQ ID NO:53.	1029	99
1096	Y87276	Homo sapiens	Human signal peptide containing protein HSPP-53 SEQ ID NO:53.	863	98
1097	AF161455	Homo sapiens	HSPC337	742	98
1098	U80029	Caenorhabditis elegans	similar to thioredoxin	242	39
1099	AJ005866	Homo sapiens	Sqv-7-like protein	1321	99
1100	AJ005866	Homo sapiens	Sqv-7-like protein	1118	99
1101	AJ005866	Homo sapiens	Sqv-7-like protein	891	99
1102	AJ005866	Homo sapiens	Sqv-7-like protein	1016	99
1103	AL110244	Homo sapiens	hypothetical protein	299	31
1104	AF242194	Drosophila melanogaster	brakeless-B	147	52
1105	AL031010	Homo sapiens	dJ422F24.1 (PUTATIVE novel protein similar to C. elegans C02C2.5)	968	100
1106	U28016	Mus musculus	parathion hydrolase (phosphotriesterase)-related protein	1624	87
1107	AJ278150	Homo sapiens	putative lipid kinase	2207	99
1108	G03733	Homo sapiens	Human secreted protein, SEQ ID NO: 7814.	495	98
1109	AF217287	Drosophila melanogaster	G protein RhoBTB	834	54
1110	Y28921	Homo sapiens	Human regulatory protein HRGP-7.	941	48
1111	Y28921	Homo sapiens	Human regulatory protein HRGP-7.	1331	51
1112	AF176704	Homo sapiens	F-box protein FBX9	2027	99
1113	AF182076	Homo sapiens	glioma tumor suppressor candidate region protein 2	2418	100
1114	G04039	Homo sapiens	Human secreted protein, SEQ	475	96

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			ID NO: 8120.		
1115	AF229439	Mus musculus	zinc finger protein 289	1697	91
1116	L40357	Homo sapiens	thyroid receptor interactor	509	100
1117	L40357	Homo sapiens	thyroid receptor interactor	404	85
1118	A12155	Homo sapiens	Human X5L cDNA.	1673	100
1119	AL161542	Arabidopsis thaliana	isomerase like protein	607	53
1120	AL023754	Homo sapiens	dJ272L16.1 (Rat Ca2+/Calmodulin dependent Protein Kinase LIKE protein)	2341	98
1121	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	321	36
1122	Z14122	Xenopus laevis	XLCL2	455	77
1123	AF225418	Homo sapiens	lipase	1531	97
1124	Y06518	Homo sapiens	Zen GTPase interacting protein ZIP.	3227	100
1125	AL035690	Homo sapiens	dJ202I21.1 (novel protein)	952	100
1126	AJ000217	Homo sapiens	CLIC2	1286	99
1127	AB030505	Mus musculus	UBE-1c2	1069	79
1128	Y73375	Homo sapiens	HTRM clone 1427838 protein sequence.	874	100
1129	Y78941	Homo sapiens	Cyclophilin-type peptidyl prolyl cis/trans isomerase amino acid sequence.	877	100
1130	AL023553	Homo sapiens	dJ347H13.4 (novel protein)	557	100
1131	Y91945	Homo sapiens	Human chaperone protein 6 (HCHP-6).	1408	100
1132	Z68197	Schizosaccharomyces pombe	putative nuclear pore protein	596	39
1133	Z68197	Schizosaccharomyces pombe	putative nuclear pore protein	389	35
1134	AF180681	Homo sapiens	guanine nucleotide exchange factor	3597	100
1135	AF079765	Mus musculus	enhancer of polycomb	264	41
1136	M62419	Mus musculus	clathrin-associated protein	2189	99
1137	AJ006219	Drosophila melanogaster	clathrin-associated protein	1254	78
1138	Y76218	Homo sapiens	Human secreted protein encoded by gene 95.	440	98
1139	W88104	Homo sapiens	A Rab protein designated HRAB-2.	1065	99
1140	Y13401	Homo sapiens	Amino acid sequence of protein PRO339.	3979	98
1141	W85026	Chimeric - Homo sapiens	Green fluorescent protein-Zap70 fusion product.	3309	100
1142	Y13402	Homo sapiens	Amino acid sequence of protein PRO310.	1694	99
1143	G03875	Homo sapiens	Human secreted protein, SEQ ID NO: 7956.	660	99
1144	Y12917	Homo sapiens	Amino acid sequence of a human secreted peptide.	750	98
1145	Y12917	Homo sapiens	Amino acid sequence of a human secreted peptide.	1096	100
1146	AL022157	Homo sapiens	SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	1233	100
1147	AL022157	Homo sapiens	SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	1233	100
1148	G02548	Homo sapiens	Human secreted protein, SEQ ID NO: 6629.	370	98
1149	Y73338	Homo sapiens	HTRM clone 2019742 protein sequence.	1492	100
1150	W74841	Homo sapiens	Human secreted protein encoded by gene 113 clone	228	55

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			HEAAR60.		
1151	AF044201	Rattus norvegicus	neural membrane protein 35; NMP35	1570	92
1152	AF156774	Homo sapiens	lysophosphatidic acid acyltransferase-gamma1	1855	99
1153	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069))	872	64
1154	AF131852	Homo sapiens	Unknown	473	100
1155	Y41705	Homo sapiens	Human PR0352 protein sequence.	1381	97
1156	G04036	Homo sapiens	Human secreted protein, SEQ ID NO: 8117.	607	99
1157	AF112444	Lupinus luteus	L-asparaginase	287	43
1158	AF151848	Homo sapiens	CGI-90 protein	232	32
1159	AJ272267	Homo sapiens	choline dehydrogenase	2449	100
1160	AB001773	Clona savignyi	PEM-6	196	33
1161	Y87330	Homo sapiens	Human signal peptide containing protein HSPP-107 SEQ ID NO:107.	746	83
1162	Y87330	Homo sapiens	Human signal peptide containing protein HSPP-107 SEQ ID NO:107.	746	83
1163	AF113534	Homo sapiens	HP1-BP74 protein	2723	96
1164	AF232226	Danio rerio	Deddl	191	41
1165	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069))	1051	71
1166	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069))	945	76
1167	AF187733	Homo sapiens	syntaphilin	831	42
1168	AB019435	Homo sapiens	phospholipase	951	55
1169	AF064604	Homo sapiens	KE03 protein	324	33
1170	Y01164	Homo sapiens	Polypeptide fragment encoded by gene 6.	1191	100
1171	L03188	Saccharomyces cerevisiae	putative	180	22
1172	AF113751	Mus musculus	nuclear pore membrane glycoprotein POM210	3941	81
1173	AJ245417	Homo sapiens	G5b protein	794	100
1174	AL022238	Homo sapiens	dJ1042K10.3 (novel protein)	1285	100
1175	U41278	Caenorhabditis elegans	F33G12.3 gene product	332	28
1176	M35617	Homo sapiens	T-cell receptor V-alpha-J-alpha region	284	83
1177	ACC12680	Arabidopsis thaliana	putative protein phosphatase 2C; 55455-56414	209	37
1178	G01345	Homo sapiens	Human secreted protein, SEQ ID NO: 5426.	692	99
1179	AL096767	Homo sapiens	dJ579N16.3 (novel protein similar to worm, Arabidopsis and pine proteins)	1342	100
1180	AF039716	Caenorhabditis elegans	similar to ATP synthase B chain	496	55
1181	Y11710	Homo sapiens	collagen type XIV	1048	97
1182	X82240	Homo sapiens >R94974 R94974 09-MAY-1996 27-OCT-1994 Human TCL-1 polypeptide.	T cell leukemia/lymphoma 1	617	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		[Homo sapiens			
1183	U42841	Caenorhabditis elegans	short region of weak similarity to collagen	161	33
1185	AJ131613	Homo sapiens	dicarboxylate carrier protein	1470	99
1186	L27645	Danio rerio	growth-associated protein	130	36
1187	Y02738	Homo sapiens	Human secreted protein encoded by gene 89 clone HLHFP03.	636	100
1188	AF217544	Xenopus laevis	ornithine decarboxylase-2	1459	60
1189	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	182	33
1190	X89602	Homo sapiens	rTSbeta	197	100
1191	U32828	Haemophilus influenzae Rd	ribosomal protein S6 modification protein (rimK)	268	31
1192	AF154831	Rattus norvegicus	PV-1	1403	60
1193	Y50926	Homo sapiens	Human fetal brain cDNA clone vcl6.1 derived protein.	918	100
1194	AF026530	Rattus norvegicus	stathmin-like-protein splice variant RB3''	1093	97
1195	U35244	Rattus norvegicus	vacuolar protein sorting homolog r-vps33a	2981	96
1196	Y70470	Homo sapiens	Human p53 target molecule, PRG3 protein.	1680	100
1197	AF157318	Homo sapiens	AD-017 protein	912	47
1198	AF125443	Caenorhabditis elegans	contains similarity to S. pombe phosphatidyl synthase (GB:228295)	460	39
1199	AF201934	Homo sapiens	DC12	1649	88
1200	AL031775	Homo sapiens	dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4)	1902	100
1201	M21103	Ovis aries	BIIIB4 high-sulfur keratin	484	82
1202	Z85986	Homo sapiens	dJ108K11.3 (similar to yeast suppressor protein SRP40)	1143	75
1203	U18762	Rattus norvegicus	retinol dehydrogenase type I	890	52
1204	U35730	Mus musculus	jerky	2235	76
1205	AB002327	Homo sapiens	KIAA0329	151	24
1206	AB019233	Arabidopsis thaliana	ubiquinone/menaquinone biosynthesis methyltransferase-like	762	56
1207	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	742	100
1208	AF207989	Homo sapiens	orphan G-protein coupled receptor	2326	100
1209	Z97630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	181	44
1210	U21549	Mus musculus	Ac39/physophilin	1280	68
1211	Y27700	Homo sapiens	Human secreted protein encoded by gene No. 12.	1267	100
1212	AF117814	Mus musculus	odd-skipped related 1 protein	945	66
1213	AF277233	Naegleria fowleri	calcineurin B	222	39
1214	D14849	Mus musculus	meiosis-specific nuclear structural protein 1	1950	77
1215	G03022	Homo sapiens	Human secreted protein, SEQ ID NO: 7103.	590	100
1216	Z72510	Caenorhabditis	similarity to yeast UTR3	634	49

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		is elegans	protein (Swiss Prot accession yk677h11.5 comes from this gene		
1217	Z49703	Saccharomyces cerevisiae	unknown	134	22
1218	AC013430	Arabidopsis thaliana	F3F9.18	199	29
1219	L10910	Homo sapiens	splicing factor	1026	71
1220	Z70750	Caenorhabditis elegans	similar to vanadate resistance protein transmembranous comes from this gene	965	58
1221	AL163815	Arabidopsis thaliana	putative protein	653	61
1222	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
1223	J05071	Bos taurus	GTP-binding regulatory protein gamma-6 subunit	356	100
1224	Y73364	Homo sapiens	HTRM clone 2765991 protein sequence.	1169	99
1225	AL050170	Homo sapiens	hypothetical protein	714	100
1226	X64002	Homo sapiens	RAP74	2661	99
1227	X04085	Homo sapiens	catalase	2846	100
1228	AJ005620	Mus musculus	skeletal muscle-specific gene	1416	90
1229	AF045564	Rattus norvegicus	development-related protein	1715	93
1230	X97571	Mus musculus	HCMV-interacting protein	479	96
1231	L08239	Homo sapiens	located at OATL1	2274	100
1232	AF121863	Homo sapiens	sorting nexin 14	1964	100
1233	AF121863	Homo sapiens	sorting nexin 14	1203	84
1234	AC024805	Caenorhabditis elegans	contains similarity to TR:004595	744	31
1235	AC006634	Caenorhabditis elegans	contains similarity to Saccharomyces cerevisiae probable membrane protein YLR418c (GB:U20162)	357	33
1236	Y18101	Mus musculus	macrophage actin-associated-tyrosine-phosphorylated protein	1559	87
1237	AB042646	Homo sapiens	TGIF2	1224	100
1238	AB026264	Homo sapiens	IMPACT	1694	100
1239	AB026264	Homo sapiens	IMPACT	1123	100
1240	G00429	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	324	100
1241	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1363	53
1242	AL035602	Arabidopsis thaliana	putative protein	499	28
1243	X76483	Gallus gallus	Yes-associated protein (65kDa)	574	48
1244	AF220186	Homo sapiens	uncharacterized hypothalamus protein HT012	503	100
1245	AL021453	Homo sapiens	dJ821D11.3 (PUTATIVE protein)	856	100
1246	AJ276003	Homo sapiens	GAR1 protein	1216	100
1247	Y57910	Homo sapiens	Human transmembrane protein HTPN-34.	1369	98
1248	AC004874	Homo sapiens	similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:g1171989)	957	100
1249	AF199597	Homo sapiens	A-type potassium channel modulatory protein 1	1139	100
1250	Y13148	Rattus norvegicus	PAG608	1350	88
1251	M24852	Rattus norvegicus	neuron-specific protein PEP-19	124	46

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1252	AF146738	Rattus norvegicus	testis specific protein	771	83
1253	G02725	Homo sapiens	Human secreted protein, SEQ ID NO: 6806.	419	97
1254	W44375	Homo sapiens	Human ubiquitin-conjugating enzyme polypeptide.	1045	99
1255	AC006538	Homo sapiens	BC41195_1	831	78
1256	AB004316	Bos taurus	mitochondrial methionyl-tRNA transformylase	1556	88
1257	Z35094	Homo sapiens	SURF-2	1354	97
1258	Y13362	Homo sapiens	Amino acid sequence of protein PRO214.	2383	100
1259	AC006014	Homo sapiens	similar to RFP transforming protein; similar to P14373 (PID:g132517)	1299	100
1260	AC005099	Homo sapiens	match to AI222572 (NID:g3804775)	469	100
1261	V00507	Homo sapiens	coding sequence of DHFR (1 is 1st base in codon) (561 is 3rd base in codon)	984	100
1262	X15443	Rattus sp.	gamma-glutamyltranspeptidase (AA 1-568)	697	32
1263	AF173871	Mus musculus	neuronal PAS3	977	94
1264	AF178983	Homo sapiens	Ras-associated protein Rap1	433	97
1265	Y70473	Homo sapiens	Human cyclic nucleotide-associated protein-1 (CNAP-1).	2785	99
1266	Y41738	Homo sapiens	Human PRO541 protein sequence.	1622	100
1267	AF061346	Mus musculus	Edp1 protein	1077	64
1268	U97006	Caenorhabditis elegans	C13F10.4 gene product	154	23
1269	AF233582	Mus musculus	GTPase Rab37	942	95
1270	AF195951	Homo sapiens	signal recognition particle 68	3127	98
1271	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1150	55
1272	AF201933	Homo sapiens	DC11	650	100
1273	AF201933	Homo sapiens	DC11	346	98
1274	AL021710	Arabidopsis thaliana	putative protein	348	49
1275	AC004449	Homo sapiens	R33683_3	556	100
1276	Y86295	Homo sapiens	Human secreted protein HL2AG87, SEQ ID NO:210.	1920	100
1277	Y71111	Homo sapiens	Human Hydrolase protein-9 (HYDRL-9).	1576	99
1278	S94421	Homo sapiens	T cell receptor eta-exon	478	100
1279	Y66695	Homo sapiens	Membrane-bound protein PRO1344.	1909	100
1280	AF161380	Homo sapiens	HSPC262	772	100
1281	Y48610	Homo sapiens	Human breast tumour-associated protein 71.	779	100
1282	AC015446	Arabidopsis thaliana	Similar to AIG1 protein	406	35
1283	AK024432	Homo sapiens	FLJ00022 protein	403	35
1284	W96153	Homo sapiens	Human FADD-interacting protein (FIP).	1825	81
1285	AJ001019	Homo sapiens	ring finger protein	1301	100
1286	AE003823	Drosophila melanogaster	CG13178 gene product	195	29
1287	AF178632	Homo sapiens	FEM-1-like death receptor binding protein	3261	100
1288	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)	1195	100
1289	AC006033	Homo sapiens	similar to MLN 64; similar to I38027 (PID:g2135214)	668	93
1290	AB023811	Homo sapiens	TU3A	351	54

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1291	Z73424	Caenorhabditis elegans	C44B9.1	235	36
1292	Y94871	Homo sapiens	Human protein clone HP02551.	1222	100
1293	AF180425	Homo sapiens	retinoblastoma-associated protein RAP140	489	29
1294	G03856	Homo sapiens	Human secreted protein, SEQ ID NO: 7937.	538	99
1295	AF133670	Mus musculus	ARL-6 interacting protein-2	367	51
1296	AJ249735	Homo sapiens	claudin-6	1142	100
1297	X57560	Escherichia coli	pspE protein	535	100
1298	AF169284	Homo sapiens	LIM and cysteine-rich domains protein 1	1997	100
1299	U41023	Caenorhabditis elegans	coded for by C. elegans cDNA yk61f1.3; coded for by C. yk109h8.5	324	29
1300	AB024523	Homo sapiens	basic kruppel like factor	1206	100
1301	X55989	Homo sapiens	eosinophil cationic-related protein	737	99
1302	AF007151	Homo sapiens	unknown	1481	100
1303	X52904	Escherichia coli	open reading frame (AA 1-65)	359	100
1304	U19577	Escherichia coli	galactonate dehydratase	242	93
1305	AF266508	Mus musculus	NELF protein	1409	97
1306	Y57901	Homo sapiens	Human transmembrane protein HTPN-25.	932	100
1307	U58750	Caenorhabditis elegans	similar to the mitochondrial carrier family	365	54
1308	AF044774	Homo sapiens	breakpoint cluster region protein 2	2681	99
1309	AL078593	Homo sapiens	dJ210B1.1 (KIAA0680)	267	34
1310	X82693	Homo sapiens	E48 antigen	620	96
1311	Z82263	Caenorhabditis elegans	C47A4.1	283	35
1312	AF131218	Homo sapiens	chromosome 16 open reading frame 5	1493	100
1313	Y41763	Homo sapiens	Human PR0938 protein sequence.	1636	100
1314	AF196972	Homo sapiens	JM24 protein	2239	100
1315	AF053356	Homo sapiens	insulin receptor substrate like protein	228	97
1316	Y66695	Homo sapiens	Membrane-bound protein PRO1344.	1909	100
1317	AF153127	Gallus gallus	SAPK interacting protein	2442	89
1318	AF153127	Gallus gallus	SAPK interacting protein	1477	83
1319	AF153127	Gallus gallus	SAPK interacting protein	1651	86
1320	X56932	Homo sapiens	23 kD highly basic protein	1044	100
1321	AF174605	Homo sapiens >Y83086 Y83086 09-MAR-2000 28-AUG-1998 F-box protein FBP-18. [Homo sapiens]	F-box protein Fbx25	467	70
1322	M61732	Trypanosoma cruzi	neuraminidase	214	24
1323	Y17013	porcine endogenous	pol	304	64

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		retrovirus			
1324	AL138655	Arabidopsis thaliana	putative protein	1174	37
1325	AL138655	Arabidopsis thaliana	putative protein	946	35
1326	AL133215	Homo sapiens	bA108L7.2 (novel protein similar to rat tricarboxylate carrier)	1322	99
1327	AF161541	Homo sapiens	HSPC056	1357	99
1328	Y73346	Homo sapiens	HTRM clone 619699 protein sequence.	785	96
1329	L10910	Homo sapiens	splicing factor	912	82
1330	AF146568	Homo sapiens	MIL1 protein	1936	100
1331	W87772	Homo sapiens	Human serum glucocorticoid-regulated kinase (H-SGK2) polypeptide.	232	39
1332	Y41741	Homo sapiens	Human PR0704 protein sequence.	1860	100
1333	AF295096	Homo sapiens	zinc-finger protein ZBRK1	411	91
1334	Z82271	Caenorhabditis elegans	Similarity to Mouse kinensin-like protein KIF4 comes from this gene	578	44
1335	AE000810	Methanobacterium thermoautotrophicum	conserved protein	290	43
1336	Y68779	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-11.	1019	91
1337	AE027003	Mus musculus	protein phosphatase	378	84
1338	U64856	Caenorhabditis elegans	weak similarity to TPR domains	215	40
1339	AE001394	Plasmodium falciparum	protein of the YMR7 family	170	29
1340	X76717	Homo sapiens	MT-11 protein	204	89
1341	AC011914	Arabidopsis thaliana	putative-mutT protein; 68398-67881	289	45
1342	AJ276171	Homo sapiens	ASPIC	2122	100
1343	AF187016	Homo sapiens	myosin regulatory light chain interacting protein MIR	2303	99
1344	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	894	35
1345	AF257466	Homo sapiens	N-acetylneuraminic acid phosphate synthase	1880	99
1346	Y25896	Homo sapiens	Human secreted protein fragment encoded from gene 64.	1148	100
1347	AJ272073	Torpedo marmorata	male sterility protein 2-like protein	1664	58
1348	AF161548	Homo sapiens	HSPC063	1018	98
1349	W78128	Homo sapiens	Human secreted protein encoded by gene 3 clone HOSBI96.	1117	100
1351	G02144	Homo sapiens	Human secreted protein, SEQ ID NO: 6225.	418	100
1352	D90869	Escherichia coli	similar to	2047	100
1353	A12029	Homo sapiens	MRP-14	613	100
1354	AC005328	Homo sapiens	R26660_1, partial CDS	870	74
1355	AC024876	Caenorhabditis elegans	contains similarity to SW:RPB1_CRIGR	829	61
1356	AF077226	Homo sapiens	copine III	1876	64
1359	AF217188	Mus musculus	YIP1B	801	63
1360	AC074331	Homo sapiens	ZNF234	3869	100
1361	AL163279	Homo sapiens	homolog to cAMP response	5035	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
			element binding and beta transducin family proteins		
1362	Z48475	Homo sapiens	glucokinase regulator	3160	99
1363	Z48475	Homo sapiens	glucokinase regulator	2682	97
1364	AF195764	Homo sapiens	megakaryocyte-enhanced gene transcript 1 protein; MEGT1 protein	2055	99
1365	AF116609	Homo sapiens	PRO0915	581	100
1366	AF116609	Homo sapiens	PRO0915	581	100
1367	AL117352	Homo sapiens	dJ876B10.3 (novel protein similar to C. elegans T19B10.6 (Tr:Q22557))	2581	99
1368	Y34124	Homo sapiens	Human potassium channel K+Hnov15.	1342	100
1369	AJ245621	Homo sapiens	CTL2 protein	3728	99
1370	AF008220	Bacillus subtilis	YtaG	429	45
1371	X05562	Homo sapiens	alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon)	5908	99
1372	Z98048	Homo sapiens	dJ408N23.4 (novel DnaJ domain protein)	1296	99
1373	AF154415	Homo sapiens	FLASH	10253	100
1374	U20286	Rattus norvegicus	lamina associated polypeptide 1C	1567	69
1375	U53445	Homo sapiens	DOC1	1645	46
1376	AL117337	Homo sapiens	bA393J16.1 (zinc finger protein 33a (KOX 31))	250	60
1377	AC005328	Homo sapiens	R26660_1, partial CDS	1126	100
1378	U35113	Homo sapiens	metastasis-associated gene	1823	69
1379	L15313	Caenorhabditis elegans	putative	858	58
1380	Y25756	Homo sapiens	Human secreted protein encoded from gene 46.	1508	100
1381	AB037360	Homo sapiens	ANKHZN	5734	95
1382	AB037360	Homo sapiens	ANKHZN	959	97
1383	AF237676	Mus musculus	G beta-like protein GBL	1721	96
1384	AF237676	Mus musculus	G beta-like protein GBL	1043	70
1385	Y58793	Homo sapiens	Human calcium regulatory protein CaREG-1.	715	100
1386	AF212162	Homo sapiens	ninein	10369	99
1387	AL031685	Homo sapiens	dJ963K23.2 (novel protein)	337	33
1388	AC004890	Homo sapiens	similar to zinc finger proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein.	542	86
1389	AF187989	Homo sapiens	zinc finger protein ZNF223	2665	99
1390	AC035150	Homo sapiens	Zinc finger protein ZNF221	3459	100
1391	AF287894	Homo sapiens	PIST	1410	97
1392	AF282265	Homo sapiens	inner centromere protein INCENP	1794	99
1393	X90840	Homo sapiens	axonal transporter of synaptic vesicles	4584	99
1394	AF076249	Homo sapiens	zinc finger protein SBBIZ1	3208	99
1395	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	299	75
1396	AC004809	Arabidopsis thaliana	Similar to	130	34
1398	AF242519	Homo sapiens	zinc finger protein SBZF3	181	66
1399	AL133396	Homo sapiens	dJ1066H6.4 (prion protein like protein doppel)	962	100
1400	Y48611	Homo sapiens	Human breast tumour-associated protein 72.	817	99
1401	AC004472	Homo sapiens	Pl.11659_5	280	54
1402	X91489	Saccharomyces cerevisiae	putative HMG box	164	27

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1403	Y79222	Homo sapiens	Human transferase TRNSFS-14.	2842	100
1404	X81058	Mus musculus	tex261	1010	99
1405	AB012084	Mus musculus	ITM	194	29
1406	AB030251	Homo sapiens	GTPase activating protein	3233	99
1407	AJ010585	Rattus rattus	PTB-like protein	2684	99
1408	X75760	Drosophila melanogaster	LRR47	364	29
1409	U76618	Mus musculus	N-RAP	804	48
1410	AC005578	Homo sapiens	P20887_1, partial CDS	835	63
1411	AE000284	Escherichia coli	orf, hypothetical protein.	360	100
1412	X01563	Escherichia coli	L5 (rplE) (aa 1-179)	911	100
1413	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
1414	AB031051	Homo sapiens	organic anion transporter OATP-E	3832	100
1415	M17466	Homo sapiens	coagulation factor XII	3455	100
1416	AF097994	Homo sapiens	L-kynurenine/alpha-aminoadipate aminotransferase	2202	99
1417	AF151077	Homo sapiens	HSPC243	1262	99
1418	Y09945	Rattus norvegicus	putative integral membrane transport protein	1098	61
1419	U13152	Mesocricetus auratus	guanine nucleotide-binding protein beta 5	2179	76
1420	AL162458	Homo sapiens	BA465L10.5 (KIAA1176 (novel protein, presumed ortholog of mouse K-Cl cotransporter KCC2))	5696	100
1421	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	152	29
1422	Y94923	Homo sapiens	Human secreted protein clone qs14_3 protein sequence SEQ ID NO:52.	4039	99
1423	AF177388	Homo sapiens	cancer-amplified transcriptional coactivator ASC-2	10748	99
1424	Y48517	Homo sapiens	Human breast tumour-associated protein 62.	1851	99
1425	AF208848	Homo sapiens	BM-006	1454	89
1426	AF208848	Homo sapiens	BM-006	853	79
1427	AF112886	Bos taurus	differentiation enhancing factor 1	4693	95
1428	U41387	Homo sapiens	Gu protein	1372	63
1429	AF161534	Homo sapiens	HSPC049	2853	78
1430	AF125043	Mus musculus	bisphosphate 3'-nucleotidase	275	30
1431	Y66718	Homo sapiens	Membrane-bound protein PRO1106.	1886	100
1432	AF193613	Homo sapiens	cell recognition molecule Caspr2	568	100
1433	AB044560	Mus musculus	Gliacolin	192	34
1434	R99800	Homo sapiens	NTII-1 nerve protein, facilitates regeneration of nerve cells.	707	51
1435	AF220530	Homo sapiens	myo-inositol 1-phosphate synthase A1	2904	100
1436	X70944	Homo sapiens	PTB-associated splicing factor	1261	72
1437	AF271732	Homo sapiens	bridging integrator-3	1282	100
1438	Y30811	Homo sapiens	Human secreted protein encoded from gene 1.	595	98
1439	AJ293659	Homo sapiens	mucolipidin	628	97
1440	AF219138	Homo sapiens	GGA3 long isoform	3083	100
1441	AF219138	Homo sapiens	GGA3 long isoform	3346	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1442	AB039669	Homo sapiens	ALEX3	1944	100
1443	AF237711	Drosophila melanogaster	Diablo	191	27
1444	AJ011896	Homo sapiens	Naf1 beta protein	439	39
1445	X73874	Homo sapiens	phosphorylase kinase	6233	98
1446	AF214114	Homo sapiens	breast carcinoma-associated antigen BCAA	3999	99
1447	AF003924	Homo sapiens	ANC_2H01	2645	99
1448	AF003136	Caenorhabditis elegans	contains weak similarity to an AMP-binding motif	2843	52
1449	AF155112	Homo sapiens	NY-REN-50 antigen	1184	89
1450	Y95004	Homo sapiens	Human secreted protein vc54_1, SEQ ID NO:48.	985	100
1451	AF107203	Homo sapiens	ataxin 2-binding protein	688	57
1452	AF107203	Homo sapiens	ataxin 2-binding protein	456	78
1453	Z38011	Mus musculus	DMR-N9	882	56
1454	X90568	Homo sapiens	Protein sequence and annotation available soon via LABELIT@EMBL-Heidelberg.DE	510	28
1455	AL035409	Homo sapiens	dJ564M11.3 (similar to sialyltransferase)	1356	100
1456	D44480	Mus musculus	MATH-2 protein	272	100
1458	AF141326	Homo sapiens	RNA helicase HDB/DICE1	478	45
1459	AF242552	Gallus gallus	retinovin	945	34
1460	U11036	Homo sapiens	Ibd1	724	84
1461	AB025258	Mus musculus	granuphilin-a	545	39
1462	Y08134	Homo sapiens	acid sphingomyelinase-like phosphodiesterase	2428	99
1463	AC004997	Homo sapiens	match to ESTs 243979 (NID:g573097), R19699 (NID:g774333)	869	98
1464	AC004997	Homo sapiens	match to ESTs 243979 (NID:g573097), R19699 (NID:g774333)	869	98
1465	U32743	Haemophilus influenzae Rd	fucose operon protein (fucU)	315	50
1466	Y09022	Homo sapiens	Not56-like protein	2342	100
1467	AC003034	Homo sapiens	Homolog of rat kidney-specific (KS) gene	1072	99
1468	AF071544	Spinacia oleracea	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I	333	26
1469	Y57930	Homo sapiens	Human transmembrane protein HTMPN-54.	1053	100
1470	AF032666	Rattus norvegicus	rsec5	4504	93
1471	Y70467	Homo sapiens	Human membrane channel protein-17 (MECHP-17).	452	74
1472	AL031033	Homo sapiens	C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein)	1694	100
1473	AF177292	Homo sapiens	genethonin 3	4026	98
1474	S45936	Homo sapiens	HTS1	1101	50
1475	Y86241	Homo sapiens	Human secreted protein HOABR60, SEQ ID NO:156.	1879	98
1476	AJ010317	Fugu rubripes	Sand	1278	68
1477	U42831	Caenorhabditis elegans	coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157)	846	44
1478	X62447	Homo sapiens	PR 264	543	61
1479	X82209	Homo sapiens	MN1	7116	100
1480	U10536	Pan paniscus	MHC class I A	675	84

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
1481	AL078599	Homo sapiens	dJ991C6.1 (novel protein similar to C. elegans F55A12.9 (Tr:P91086))	1274	65
1482	Z98977	Schizosaccharomyces pombe	putative vacuolar protein	256	29
1483	AB005662	Mus musculus	JNK/SAPK-associated protein-1	4968	92
1484	AL050120	Homo sapiens	hypothetical protein	716	100
1485	M27878	Homo sapiens	DNA binding protein	1006	53
1486	Y69161	Homo sapiens	Amino acid sequence of a partial protein kinase.	575	99
1487	X84156	Saccharomyces cerevisiae	ATH1	341	29
1488	AF038963	Homo sapiens	RNA helicase	446	34
1489	U56966	Caenorhabditis elegans	coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3	620	42
1490	AE000989	Archaeoglobus fulgidus	enoyl-CoA hydratase (fad-4)	533	46
1491	M80633	Rattus norvegicus	adenylyl cyclase type IV	707	95
1492	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	3513	99
1493	Y17220	Homo sapiens	Human secreted protein (clone fj283-11).	462	37
1494	AF133670	Mus musculus	ARL-6 interacting protein-2	701	97
1495	Y94697	Homo sapiens	Human protein clone HP10574.	1371	100
1496	AL049699	Homo sapiens	dJ747H23.2 (novel protein)	1550	100
1497	AF037447	Homo sapiens	ribosomal S6 protein kinase	2427	100
1498	AL445067	Thermoplasma acidophilum	putative target YPL207w of the HAP2 transcriptional complex related protein	269	35
1499	AB039947	Homo sapiens	X11L-binding protein 51	227	36
1500	AJ277750	Homo sapiens	UBASH3A protein	3509	100
1501	AL050333	Homo sapiens	dJ93K22.1 (novel protein (contains DKFZP564B116))	2439	100
1502	AF179896	Homo sapiens	TAL homeobox protein Meis2b	1140	100
1503	AF178948	Homo sapiens	TAL homeobox protein Meis2a	1177	100
1504	Y53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	1442	99
1505	X82494	Homo sapiens	fibulin-2	3580	99
1506	X98296	Homo sapiens	ubiquitin hydrolase	783	42
1507	AL034548	Homo sapiens	dJ1103G7.6 (novel protein)	1098	100
1508	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1736	100
1509	AF220182	Homo sapiens	uncharacterized hypothalamus protein HT008	1181	98
1510	U64601	Caenorhabditis elegans	Gene probably begins in the next cosmid	415	58
1511	AL356192	Neurospora crassa	related to MDM1 protein	196	29
1512	D17629	Homo sapiens	N-acetylgalactosamine 6-sulfate sulfatase (GALNS)	1829	100
1513	AF168717	Homo sapiens	x 009 protein	694	99
1514	AJ243531	Homo sapiens	nM15 protein	735	100
1515	AC003672	Arabidopsis thaliana	putative C3HC4-type RING zinc finger protein	407	30
1516	AF115435	Rattus norvegicus	syntaxin 17	1374	90
1517	AF003140	Caenorhabditis elegans	C44E4.5 gene product	274	31
1518	AB002584	Rattus norvegicus	beta-alanine-pyruvate aminotransferase	2238	82
1519	AL121764	Schizosaccharomyces	yeast atp12 protein precursor	270	30

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		romyces pombe	homolog		
1520	AF255910	Homo sapiens	vascular endothelial junction-associated molecule	547	100
1521	D31764	Homo sapiens	KIAA0064	170	27
1522	Y66634	Homo sapiens	Membrane-bound protein PRO190.	985	100
1523	Y94450	Homo sapiens	Human inflammation associated protein	250	43
1524	AC000107	Arabidopsis thaliana	F17F8.22	277	37
1525	AF109377	Mus musculus	IdlBp	1277	83
1526	AL031427	Homo sapiens	dJ167A19.4 (novel protein)	1432	99
1527	Y08135	Mus musculus	acid sphingomyelinase-like phosphodiesterase	1496	79
1528	AK024423	Homo sapiens	FLJ00012 protein	611	100
1529	AF154502	Homo sapiens	quiescent cell proline dipeptidase	679	100
1530	AF205598	Homo sapiens	transposase-like protein	1368	100
1531	AF251039	Homo sapiens	putative zinc finger protein	1420	50
1532	W74805	Homo sapiens	Human secreted protein encoded by gene 77 clone HOEAS24.	493	57
1533	AF039023	Homo sapiens	Ran-GTP binding protein; RanBP6	5707	99
1534	AC007190	Arabidopsis thaliana	F23N19.9	374	37
1535	AB027564	Homo sapiens	DINB1	4482	100
1536	Y36178	Homo sapiens	Human secreted protein	377	87
1537	Y50907	Homo sapiens	Human fetal brain cDNA clone vb3_1 derived protein.	3693	99
1538	AF017368	Mus musculus	faciogenital dysplasia protein 2	177	47
1539	AF266756	Homo sapiens	sphingosine kinase	2011	99
1540	Z48804	Homo sapiens	OAL	2238	100
1541	AF000195	Caenorhabditis elegans	Contains similarity to Pfam domain: PF00169 (PH), Score=20.6, E-value=1.9e-05, N=1	379	42
1542	Y71159	Homo sapiens	Human phosphodiesterase interacting protein, myomegalin.	9415	99
1543	X76092	Homo sapiens	DNA binding protein RFX3	3327	100
1544	AB015330	Homo sapiens	HRIHFB2007	631	50
1545	AF198487	Homo sapiens	transcription factor LBP-1b	2822	100
1546	AF016417	Caenorhabditis elegans	Similar to BZIP transcription factor	518	42
1547	X55885	Homo sapiens	KDEL receptor	1106	100
1548	AB035495	Carassius auratus	ubiquitin-activating enzyme E1	836	42
1549	AL021707	Homo sapiens	dJ508I15.4 (KIAA0668)	3688	100
1550	AJ223978	Bacillus subtilis	YvqK protein	292	42
1551	AF145615	Drosophila melanogaster	BcDNA.GH03377	822	44
1552	AL157734	Schizosaccharomyces pombe	putative mannosyltransferase involved in N-glycosylation	435	37
1553	AF079527	Mus musculus	IER5	691	63
1554	AB026291	Rattus norvegicus	acetoacetyl-CoA synthetase	1099	88
1555	Y44722	Homo sapiens	Human immune system molecule, ISMO-3.	1780	99
1556	AF116553	Drosophila melanogaster	antennal-specific short-chain dehydrogenase/reductase	277	32
1557	Y71056	Homo sapiens	Human membrane transport	1975	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	% IDENTITY
			protein, MTRP-1.		
1558	Y71056	Homo sapiens	Human membrane transport protein, MTRP-1.	1975	99
1559	Y71056	Homo sapiens	Human membrane transport protein, MTRP-1.	1894	97
1560	AF092050	Mus musculus	beta-1,3-N-acetylglucosaminyltransferase	262	44
1561	AL109827	Homo sapiens	dJ309K20.2 (acrosomal protein ACR55 (similar to rat sperm antigen 4 (SPAG4)))	1607	97
1562	AJ131890	Homo sapiens	DNA polymerase lambda	3002	100
1563	AL035424	Homo sapiens	dA22D12.1 (novel protein similar to Drosophila Kelch proteins)	3015	100
1564	AC002400	Homo sapiens	Gene product with similarity to Ubiquitin binding enzyme	2790	100
1565	AC005306	Homo sapiens	R27216_1	919	82
1566	AF000195	Caenorhabditis elegans	Contains similarity to Pfam domain: PF00169 (PH), Score=20.6, E-value=1.9e-05, N=1	550	45
1567	AB033281	Homo sapiens	F-box and WD-repeats protein beta-TRCP2 isoform C	2879	100
1568	D49473	Mus musculus	truncated form of Sox17	1047	78
1569	AK025270	Homo sapiens	unnamed protein product	210	91
1570	X75756	Homo sapiens	protein kinase C mu	4797	99
1571	AF145713	Homo sapiens	SCHIP-1	2388	100
1572	AE003831	Drosophila melanogaster	CG18445 gene product	180	31
1573	AF074603	Streptomyces griseus subsp. griseus	NonF	205	38
1574	U28993	Caenorhabditis elegans	F22D3.3 gene product	144	27
1575	AF129507	Homo sapiens	transcription factor ICBP90	287	68
1576	X64878	Homo sapiens	oxytocin receptor	2002	100
1577	AF237711	Drosophila melanogaster	Diablo	421	54
1578	G00975	Homo sapiens	Human secreted protein, SEQ ID NO: 5056.	480	100
1579	AF248744	Cryptosporidium parvum	thrombospondin-related adhesive protein	123	33
1580	AL121782	Homo sapiens	dJ585114.2 (novel protein (translation of cDNA Em:AK000219))	663	100
1581	AF041853	Homo sapiens	kinesin family member protein KIF3A	345	33
1582	AF025441	Homo sapiens	Opa-interacting protein OIP5	1198	100
1583	AE001803	Thermotoga maritima	glycerate kinase, putative	349	34
1584	AF252283	Homo sapiens	Kelch-like 1 protein	3973	100
1585	AF169675	Homo sapiens	leucine-rich repeat transmembrane protein FLRT1	3494	99
1586	AF118274	Homo sapiens	DNB-5	2628	97
1587	X79440	Homo sapiens	NADP+-dependent malic enzyme	3167	99
1588	X99802	Homo sapiens	ZYG homologue	3966	99
1589	AF169803	Homo sapiens	flavohemoprotein b5+b5R	2563	100
1590	Y29861	Homo sapiens	Human secreted protein clone cb98_4.	181	47
1591	Z25535	Homo sapiens	nuclear pore complex protein hnup153	7567	99
1592	X13293	Homo sapiens	B-myb protein (AA 1-700)	3678	99
1593	M74027	Homo sapiens	mucin	242	27
1594	AL139314	Schizosaccharomyces	hypothetical protein	235	54

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		pombe			
1595	W78324	Homo sapiens	Fragment of human secreted protein encoded by gene 81.	1318	98
1596	Y94906	Homo sapiens	Human secreted protein clone rb649_3 protein sequence SEQ ID NO:18.	2236	98
1597	AF174605	Homo sapiens	F-box protein Fbx25	1408	99
1598	AB032254	Homo sapiens	bromodomain adjacent to zinc finger domain 2A	9676	98
1599	X73114	Homo sapiens	slow MyBP-C	5568	95
1600	X82200	Homo sapiens	gpStaf50	2305	100
1601	Y00876	Homo sapiens	Human LAPH-1 protein sequence.	1149	98
1602	AJ223351	Homo sapiens	HIRA-interacting protein 3	2821	99
1603	AJ222801	Homo sapiens	neutral sphingomyelinase	2268	99
1604	AJ222801	Homo sapiens	neutral sphingomyelinase	1601	99
1605	AF185576	Mus musculus	POZ/zinc finger transcription factor ODA-8	3435	97
1606	AF093744	Homo sapiens	unknown	131	100
1607	A12142	synthetic construct	IFN-pseudo-omega 2	800	98
1608	Y57949	Homo sapiens	Human transmembrane protein HTPN-73.	1868	100
1609	AF151044	Homo sapiens	HSPC210	681	97
1610	X15218	Homo sapiens	ski protein (AA 1 - 728)	3765	100
1611	Y08200	Homo sapiens	rab geranylgeranyl transferase	2976	100
1612	AF220560	Homo sapiens	B/K protein	2486	99
1613	AC004481	Arabidopsis thaliana	nodulin-like protein	371	26
1614	Y09501	Homo sapiens	NADH-cytochrome-b5 reductase	1607	100
1615	Y15521	Homo sapiens	start position 1	3150	97
1616	AJ010750	Rattus norvegicus	Castration induced prostatic apoptosis related protein-1, (CIPAR-1)	890	62
1617	X58079	Homo sapiens	S100 alpha protein	481	100
1618	Y66678	Homo sapiens	Membrane-bound protein PRO1009.	967	100
1619	AJ242973	Homo sapiens	peptide methionine sulfoxide reductase	929	100
1620	AF150733	Homo sapiens	AD-014 protein	288	100
1621	AJ007509	Homo sapiens	ElB-55kDa-associated protein	4646	98
1622	X64177	Homo sapiens	metallothionein	380	100
1623	AE001045	Archaeoglobus fulgidus	A. fulgidus predicted coding region AF0859	240	36
1624	AL355013	Schizosaccharomyces pombe	mitochondrial carrier protein	403	34
1625	Y66746	Homo sapiens	Membrane-bound protein PRO1198.	1184	100
1626	D90053	Sus scrofa	destrin	863	100
1627	Y35954	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 203.	756	100
1628	AL031775	Homo sapiens	dJ30M3.2 (novel protein)	470	100
1629	AF132484	Mus musculus	unknown	286	68
1630	AF017096	Drosophila melanogaster	similar to C. elegans R10H10.6 and S. cerevisiae YD8419.03c	493	61
1631	X03077	Homo sapiens	lactate dehydrogenase-A	1704	100
1632	AF151084	Homo sapiens	HSPC250	763	100
1633	AJ001874	Homo sapiens	orf	255	97
1634	AC012187	Arabidopsis thaliana	Contains weak similarity to GATA-6 DNA-binding protein gb H36135, gb Z26200 come from this gene.	143	38

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	IDENTITY
1635	AF026246	Homo sapiens	HERV-E integrase	411	90
1636	Y50943	Homo sapiens	Human adult brain cDNA clone ve8_1 derived protein.	1126	95
1637	AF134593	Homo sapiens	L-pipecolic acid oxidase	2068	99
1638	AJ238247	Mus musculus	putative phosphatase subunit	1948	96
1639	Y94942	Homo sapiens	Human secreted protein clone yk251_1 protein sequence SEQ ID NO:90.	1320	100
1640	AF235030	Homo sapiens	BM88 antigen	766	99
1641	AF233288	Drosophila melanogaster	WDS	358	26
1642	M19351	Mus musculus	immunoglobulin heavy chain binding protein	145	34
1643	Y70452	Homo sapiens	Human membrane channel protein-2 (MECHP-2).	1352	100
1644	AF176520	Mus musculus	WD repeat-containing F-box protein FBW5	2676	88
1645	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1156	100
1646	X67155	Homo sapiens	mitotic kinase-like protein-1	4456	99
1647	M63180	Homo sapiens	threonyl-tRNA synthetase	1040	61
1648	Y87342	Homo sapiens	Human signal peptide containing protein HSPP-119 SEQ ID NO:119.	1566	93
1649	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	4137	100
1650	AC007136	Homo sapiens	Putative map kinase interacting kinase	856	99
1651	AB015346	Homo sapiens	Eps15R	4464	99
1652	AL161576	Arabidopsis thaliana	putative protein	1341	48
1653	AC005313	Arabidopsis thaliana	putative calmodulin	288	28
1654	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1655	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1656	AB017910	Dictyostellium discoideum	myoM	297	32
1657	Y28919	Homo sapiens	Human regulatory protein HRGP-5.	2251	99
1658	AF056191	Homo sapiens	TPA inducible protein	2744	98
1659	U76846	Arabidopsis thaliana	ubiquitin-specific protease	137	35
1660	AL078627	Schizosaccharomyces pombe	actin-like protein; (2 actin domains)	320	34
1662	X52022	Homo sapiens	collagen type VI, alpha 3 chain	16274	99
1663	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit 4	1811	100
1664	AF214736	Homo sapiens	EH domain containing protein 2	2774	100
1665	Z48613	Saccharomyces cerevisiae	unknown	138	26
1666	AF177385	Homo sapiens	cytochrome c oxidase assembly protein isoform 2	1395	99
1667	AC007842	Homo sapiens	BC331191_1	1581	47
1668	S67513	Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate, Peptide, 370	p40	397	43

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		aa			
1669	Z99753	Schizosaccharomyces pombe	putative NOL1-NOP2-sun family nucleolar protein	569	47
1670	G03130	Homo sapiens	Human secreted protein, SEQ ID NO: 7211.	427	97
1671	M96625	Gallus gallus	cardiac muscle tensin	1185	54
1672	AF174482	Homo sapiens	polycomb 3	2005	99
1673	Y51846	Homo sapiens	Human 18.1 homolog protein fragment.	233	29
1674	AF255334	Homo sapiens	EXP35	152	29
1675	Y94867	Homo sapiens	Human protein clone HP10563.	109	30
1676	Y25712	Homo sapiens	Human secreted protein encoded from gene 2.	3043	99
1677	Y25712	Homo sapiens	Human secreted protein encoded from gene 2.	1580	91
1678	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	170	17
1679	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	170	17
1680	AK024453	Homo sapiens	FLJ00045 protein	1349	100
1681	AF019236	Dictyostellium discoideum	TipD	613	34
1682	AJ243459	Leishmania major	proteophosphoglycan	153	26
1683	Z69369	Schizosaccharomyces pombe	putative GTP-binding protein	560	46
1684	X94910	Homo sapiens	ERp28	1334	100
1685	AF286475	Takifugu rubripes	retinitis pigmentosa GTPase regulator-like protein	196	19
1686	AF191298	Homo sapiens	vacuolar sorting protein 35	4087	100
1687	AJ275986	Homo sapiens	transcription factor	2958	100
1688	AJ275986	Homo sapiens	transcription factor	1886	88
1689	X07311	Drosophila melanogaster	heat shock protein	138	43
1690	AF240463	Rattus norvegicus	LIS1-interacting protein NUDE1	1383	83
1691	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	1256	68
1692	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	1336	60
1693	AF177942	Xenopus laevis	katanin p60	1664	66
1694	AF263539	Homo sapiens	arginine N-methyltransferase	1774	100
1695	AF222689	Homo sapiens	protein arginine N-methyltransferase 1-variant 2	1182	81
1696	AK000193	Homo sapiens	unnamed protein product	1060	100
1697	AB041035	Homo sapiens	kidney superoxide-producing NADPH oxidase	3122	100
1698	AB041035	Homo sapiens	kidney superoxide-producing NADPH oxidase	2181	100
1699	AF025772	Homo sapiens	C2H2 zinc finger protein	488	54
1700	Y44676	Homo sapiens	Human ARF-Related Protein-1 (HARP-1).	938	97
1701	AKC22407	Homo sapiens	unnamed protein product	315	98
1702	AB024574	Homo sapiens	GTP-binding like protein 2	1172	100
1703	AF055078	Homo sapiens	zinc finger protein 42	421	52
1704	AF198092	Mus musculus	RP42	1057	77
1705	AE003573	Drosophila melanogaster	CG12474 gene product	161	33
1706	AB036345	Drosophila melanogaster	aquaporin	164	24
1707	Y55927	Homo sapiens	Human STLK2 protein.	2146	100
1708	U27121	Danio rerio	G12	212	47
1709	AL391710	Arabidopsis	putative protein	505	50

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	% IDENTITY
		<i>thaliana</i>			
1710	B01311	<i>Homo sapiens</i>	Human PRO241 polypeptide.	1649	97
1711	U40750	<i>Mus musculus</i>	formin binding protein 30	4561	85
1712	AJ011118	<i>Mus musculus</i>	skeletal muscle and cardiac protein	1490	89
1713	AF255303	<i>Homo sapiens</i>	membrane-associated nucleic acid binding protein	4416	99
1714	AF255303	<i>Homo sapiens</i>	membrane-associated nucleic acid binding protein	2960	100
1715	U08227	<i>Rattus norvegicus</i>	Ras-related protein	511	51
1716	AF168795	<i>Rattus norvegicus</i>	schlafen-4	1129	44
1717	AF196304	<i>Homo sapiens</i>	SUMO-1-specific protease	5804	99
1718	AL355737	<i>Homo sapiens</i>	HMG20A	1782	100
1719	AB029333	<i>Halocynthia roretzi</i>	HrPET-1	1069	46
1720	AF071317	<i>Mus musculus</i>	COP9 complex subunit 7b	1297	97
1721	AJ272215	<i>Homo sapiens</i>	HEYL protein	1681	99
1722	G01982	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 6063.	718	100
1723	AL032643	<i>Caenorhabditis elegans</i>	similar to Uncharacterized protein family UPF0034.	825	41
1724	G01972	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 6053.	586	92
1725	Y94441	<i>Homo sapiens</i>	Human Adipose Specific Protein 1.	1231	100
1726	AF255443	<i>Homo sapiens</i>	CGI-201 protein	4397	99
1727	AF183426	<i>Homo sapiens</i>	HT004 protein	1810	99
1728	D10884	<i>Bos taurus</i>	neurocalcin	1002	99
1729	Z18529	<i>Gallus gallus</i>	tensin	1411	84
1730	Z73423	<i>Caenorhabditis elegans</i>	cDNA EST EMBL:Z14908 comes from this gene-cDNA EST this gene	233	41
1732	AF090891	<i>Homo sapiens</i>	PRO0105	470	30
1733	AJ277724	<i>Homo sapiens</i>	histone deacetylase 8	2015	100
1734	G04050	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 8131.	503	95
1735	D45913	<i>Mus musculus</i>	leucine-rich-repeat protein	3531	94
1736	AF096709	<i>Drosophila virilis</i>	failed axon connections protein	276	32
1737	AF195120	<i>Homo sapiens</i>	dynactin p62 subunit	2417	99
1738	L15314	<i>Caenorhabditis elegans</i>	contains similarity to Pfam family PF01772 N=1	206	37
1739	X54618	<i>Listeria monocytogenes</i>	phosphatidylinositol specific phospholipase C	134	27
1740	AL031658	<i>Homo sapiens</i>	dJ310013.4 (novel protein similar to predicted C. elegans an C. intestinalis proteins)	123	31
1741	Y35924	<i>Homo sapiens</i>	Extended human secreted protein sequence, SEQ ID NO. 173.	1013	99
1742	AC013354	<i>Arabidopsis thaliana</i>	F15H18.15	202	32
1743	W75771	<i>Homo sapiens</i>	Human GTP binding protein APD08.	1932	59
1744	W75771	<i>Homo sapiens</i>	Human GTP binding protein APD08.	1854	61
1745	AF221098	<i>Homo sapiens</i>	Ral guanine nucleotide exchange factor RalGPS1A	1224	70
1746	Y99372	<i>Homo sapiens</i>	Human PRO1430 (UNQ736) amino acid sequence SEQ ID NO:116.	1332	99
1747	Y94294	<i>Homo sapiens</i>	Human coenzyme A-utilising	842	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-WATERMAN SCORE	IDENTITY
			enzyme CoAEN-2.		
1748	AK024436	Homo sapiens	FLJ00026 protein	1619	100
1749	AE000877	Methanobacterium thermoautotrophicum	conserved protein	231	36
1750	AF101361	Drosophila melanogaster	Abnormal X segregation	193	33
1751	Y15067	Homo sapiens	ZNF232	889	100
1752	AF251038	Homo sapiens	GAP-like protein	822	100
1753	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059 (PID:g129308)	352	57
1754	X69089	Homo sapiens	165kD protein	5703	99
1755	AL049795	Homo sapiens	dJ622L5.3 (novel protein)	1039	100
1756	AL031393	Homo sapiens	dJ733D15.1 (Zinc-finger protein)	2765	100
1757	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-acetylgalactosaminyltransferase	2020	99
1758	AL022238	Homo sapiens	dJ1042K10.4 (novel protein)	776	43
1759	AF117653	Homo sapiens	double homeobox protein	375	54
1760	Y12065	Homo sapiens	hNop56	2959	99
1761	AL049712	Homo sapiens	dJ686C3.2 (nucleolar protein hNop56)	2595	99
1762	AC002394	Homo sapiens	Gene product with similarity to dynein beta subunit	1542	51
1763	AF169017	Homo sapiens	formiminotransferase cyclodeaminase	877	100
1764	U91541	Homo sapiens	human formiminotransferase cyclodeaminase (ftcd) protein, carboxy-terminal end	596	100
1765	AB013365	Bacillus halodurans	YlqF	350	34
1766	Y38421	Homo sapiens	Human secreted protein encoded by gene No. 36.	145	71
1767	AC009176	Arabidopsis thaliana	putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I	216	27
1768	AK000647	Homo sapiens	unnamed protein product	737	99
1769	AJ238982	Homo sapiens	VNN3 protein	2665	99
1770	U73522	Homo sapiens	AMSH	1214	56
1771	U89435	Mus musculus	unknown	829	86
1772	S70011	Rattus sp.	tricarboxylate carrier	1604	95
1773	AL035086	Homo sapiens	dJ44A20.2 (novel protein)	2036	100
1774	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	1057	99
1775	AF110330	Homo sapiens	glutaminase	3146	100
1776	AJ269529	Homo sapiens	glycerol 3-phosphate permease	2787	100
1777	Z81579	Caenorhabditis elegans	cDNA EST yk76f1.5 comes from this gene	232	31
1778	AY007239	Homo sapiens	monooxygenase X	1875	99
1779	AL109608	Schizosaccharomyces pombe	oxysterol-binding protein family	644	38
1780	AF254260	Homo sapiens	tuftelin 1	1729	100
1781	L07924	Mus musculus	guanine nucleotide dissociation stimulator	247	50
1782	AF295773	Homo sapiens	ral guanine nucleotide dissociation stimulator	142	49
1783	AK024475	Homo sapiens	FLJ00068 protein	4333	100
1784	AK024475	Homo sapiens	FLJ00068 protein	3996	93
1785	G03933	Homo sapiens	Human secreted protein, SEQ ID NO: 8014.	570	100
1786	S82637	Homo sapiens	Ig lambda-like gene/beta-	247	100

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	% IDENTITY
			glucuronidase exon 11 homolog		

TRADOC5:1416280.1(%CT4011.DOC)

TABLE 3

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
2	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 8.250e-12 157-181
3	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 8.085e-13 358-381
4	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.400e-10 1129-1146 BL00028 16.07 1.257e-09 820-837
5	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390
6	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390
7	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390
8	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e-33 413-450 BL00023 24.31 4.545e-27 353-390
9	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.119e-09 863-917
10	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464D 17.40 6.182e-12 294-312 PR00464G 12.41 4.231e-11 377-393
11	PR00734	GLYCOSYL HYDROLASE FAMILY 7 SIGNATURE	PR00734I 11.46 4.296e-09 502-520
12	PF00023	Ank repeat proteins.	PF00023B 14.20 6.500e-10 89-99 PF00023B 14.20 2.636e-09 56-66
14	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 3.848e-09 79-113
15	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 9.868e-10 517-535 PR00208A 12.59 2.233e-09 520-538
17	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-14 282-295 PD00066 13.92 9.400e-14 477-490 PD00066 13.92 6.500e-13 505-518 PD00066 13.92 9.500e-13 254-267 PD00066 13.92 1.429e-12 393-406 PD00066 13.92 6.571e-12 421-434
18	BL00845	CAP-Gly domain proteins.	BL00845 16.43 2.200e-25 55-80
20	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e-26 154-199 BL00487F 18.79 8.984e-22 235-276 BL00487G 26.82 4.082e-12 287-329
21	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e-26 154-199 BL00487F 18.79 8.984e-22 235-276 BL00487G 26.82 4.082e-12 348-390
22	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.250e-26 302-333

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
23	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 3.250e-26 302-333
25	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115T 8.45 7.273e-29 1208-1242 BL00115Q 18.08 2.776e-21 953-983 BL00115Y 11.86 8.000e-17 1604-1650 BL00115M 19.19 8.130e-16 731-774 BL00115H 14.34 9.392e-16 463-496 BL00115A 15.44 7.414e-15 43-82 BL00115R 6.50 6.128e-14 983-1010 BL00115J 16.71 9.289e-14 591-617 BL00115I 8.33 4.336e-13 535-590 BL00115L 12.25 5.939e-13 662-694 BL00115G 11.65 6.011e-13 435-463 BL00115K 15.03 3.417e-10 617-659 BL00115O 16.76 5.805e-10 863-913 BL00115P 11.54 7.538e-10 913-953 BL00115S 18.24 7.968e-10 1010-1052 BL00115U 10.34 4.475e-09 1242-1265
26	BL00420	Speract receptor repeat proteins domain proteins.	BL00420A 20.42 4.109e-11 81-110 BL00420A 20.42 8.820e-10 84-113
27	BL00050	Ribosomal protein L23 proteins.	BL00050A 23.71 9.250e-27 94-127 BL00050B 14.81 8.125e-12 133-147
28	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925B 3.73 3.089e-10 41-54
29	PF00756	Putative esterase.	PF00756C 14.12 1.108e-09 486-516
32	BL00557	FMN-dependent alpha-hydroxy acid dehydrogenases proteins.	BL00557D 17.76 5.065e-37 274-316 BL00557A 35.08 8.909e-29 24-73 BL00557C 15.59 1.000e-28 227-257 BL00557B 21.27 8.898e-22 130-169
34	PR00629	SHC PHOSPHOTYROSINE INTERACTION DOMAIN SIGNATURE	PR00629E 9.90 5.886e-35 299-328 PR00629F 10.95 8.364e-32 334-361 PR00629B 13.66 3.786e-27 224-247 PR00629A 13.45 8.364e-21 206-222 PR00629C 3.80 4.000e-12 249-261 PR00629D 12.45 3.739e-11 276-286
35	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 1.000e-40 39-79 PD01270B 22.18 2.875e-38 94-131 PD01270D 24.66 3.700e-34 171-207 PD01270C 19.54 3.455e-30 137-166
36	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 1.000e-40 39-79 PD01270B 22.18 2.875e-38 94-131

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PD01270D 24.66 3.700e-34 171-207 PD01270C 19.54 3.455e-30 137-166
37	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e-10 264-298
38	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e-10 264-298
39	BL00412	Neuromodulin (GAP-43) proteins.	BL00412C 10.28 9.241e-10 264-298
40	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380B 12.64 7.366e-14 342-360 PR00380C 13.18 6.927e-13 375-394 PR00380D 9.93 2.180e-12 429-451 PR00380A 14.18 5.154e-12 143-165
44	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-40 239-290 BL00345A 13.96 2.452e-14 204-223
45	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-40 215-266 BL00345A 13.96 2.452e-14 180-199
46	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551A 15.63 3.538e-26 172-202 DM01551C 14.62 3.571e-17 232-252 DM01551B 8.84 4.750e-11 214-226
47	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 9.328e-11 246-260
48	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.231e-33 6-45
50	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 7.750e-19 994-1019 BL00972A 11.93 7.120e-18 216-234 BL00972E 20.72 9.471e-14 1020-1042 BL00972C 16.48 7.000e-13 360-375 BL00972B 9.45 8.269e-10 302-312
51	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 7.750e-19 990-1015 BL00972A 11.93 7.120e-18 216-234 BL00972E 20.72 9.471e-14 1016-1038 BL00972C 16.48 7.000e-13 360-375 BL00972B 9.45 8.269e-10 302-312
52	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.063e-14 10-54
53	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 8.500e-17 20-38 PR00988F 12.23 7.828e-15 196-210 PR00988C 13.64 6.108e-14 104-120 PR00988E 8.27 3.872e-11 174-186 PR00988D 5.95 6.878e-10 160-171 PR00988B 11.60 2.915e-09 57-69
55	PR00762	CHLORIDE CHANNEL SIGNATURE	PR00762C 9.29 4.682e-21 294-314 PR00762D 11.29 4.103e-19 509-530 PR00762A 14.22 9.333e-18 199-217

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00762F 15.12 3.100e-16 563-583 PR00762B 12.12 6.063e-16 230-250 PR00762E 12.07 2.286e-15 545-562 PR00762G 14.13 6.276e-13 601-616
56	BL00216	Sugar transport proteins.	BL00216B 27.64 8.800e-10 153-203
58	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.049e-10 1080-1135
59	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.049e-10 1062-1117
61	PD01929	KINASE TYPE RESISTANCE ANTIBIOTIC TRANSFERASE AM.	PD01929E 10.76 9.018e-09 206-221
68	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-09 680-693
69	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-09 670-683
70	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 8.714e-10 51-64
72	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e-09 108-118
73	BL00239	Receptor tyrosine kinase class II proteins.	BL00239B 25.15 7.075e-12 118-166
74	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 6.116e-10 93-120
76	DM00471	0 PROKARYOTIC DNA TOPOISOMERASE I.	DM00471A 11.73 9.357e-13 53-66 DM00471B 8.45 4.857e-12 70-81
80	PD02876	DECARBOXYLASE PHOSPHATIDYLSERINE.	PD02876C 8.80 2.723e-13 223-236 PD02876D 12.13 2.588e-12 334-351
81	PD02876	DECARBOXYLASE PHOSPHATIDYLSERINE.	PD02876C 8.80 2.723e-13 282-295 PD02876D 12.13 2.588e-12 393-410
83	BL00708	Prolyl endopeptidase family serine proteins.	BL00708B 24.91 7.197e-12 570-601
84	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014C 15.44 8.043e-09 985-1004
86	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 1.379e-09 246-269
89	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 8.200e-09 264-279 PR00320B 12.19 8.650e-09 264-279
93	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 2.588e-14 316-332
95	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.000e-10 123-154
96	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.000e-10 212-243
97	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.318e-13 134-146 PR00081A 10.53 2.500e-12 54-72
98	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 5.500e-24 401-423 PR00380D 9.93 7.188e-20 613-635 PR00380B 12.64 7.517e-16 529-547 PR00380C 13.18 2.756e-13 560-579

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
102	PR00300	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT SIGNATURE	PR00300A 9.56 7.545e-14 289-308
104	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.786e-18 298-314 BL00479A 19.86 4.913e-16 155-178 BL00479A 19.86 4.300e-13 272-295 BL00479B 12.57 6.294e-12 181-197
106	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 8.013e-12 43-83
107	DM01970	0 kw 2K632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 5.000e-16 403-416
108	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191K 17.38 4.951e-27 238-282 BL00191J 11.37 6.447e-17 182-204
109	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.938e-37 8-47
110	BL01138	Scorpion short toxins proteins.	BL01138A 10.96 8.297e-10 38-50
113	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 5.800e-23 156-187 BL00107B 13.31 9.100e-14 225-241
117	BL00214	Cytosolic fatty-acid binding proteins.	BL00214B 26.51 1.000e-17 46-91 BL00214A 21.17 7.052e-11 5-31
118	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 8.560e-13 36-67
119	PR00529	GONADOTROPHIN RELEASING HORMONE RECEPTOR SIGNATURE	PR00529C 11.03 7.506e-10 158-177
120	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e-09 80-95
121	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e-09 80-95
127	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 7.158e-13 216-241
128	BL01032	Protein phosphatase 2C proteins.	BL01032C 6.14 3.195e-12 147-157 BL01032H 11.25 5.680e-11 318-331 BL01032G 8.33 8.932e-11 282-296 BL01032I 10.42 8.902e-09 379-389
129	BL01310	ATP1G1 / PLM / MAT8 family proteins.	BL01310 14.74 6.694e-26 28-64
130	PR00990	RIBOKINASE SIGNATURE	PR00990B 12.32 9.534e-15 47-67 PR00990A 16.23 5.500e-14 20-42 PR00990C 12.62 2.412e-09 119-133
133	BL00880	Acyl-CoA-binding protein.	BL00880 17.52 5.576e-26 72-122
134	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 9.308e-14 18-37
135	PR00215	NEUROMODULIN SIGNATURE	PR00215C 13.98 6.779e-10 475-496
136	BL01310	ATP1G1 / PLM / MAT8 family proteins.	BL01310 14.74 2.432e-29 71-107
140	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.882e-14 214-231 BL00028 16.07 9.471e-14 102-119 BL00028 16.07 2.800e-13 18-35

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			BL00028 16.07 5.500e-13 74-91 BL00028 16.07 9.100e-13 186-203 BL00028 16.07 8.043e-12 46-63 BL00028 16.07 8.435e-12 130-147 BL00028 16.07 9.217e-12 270-287 BL00028 16.07 6.192e-11 242-259 BL00028 16.07 4.000e-10 158-175
141	BL00501	Signal peptidases I serine proteins.	BL00501D 16.69 9.538e-14 113-133 BL00501C 9.61 8.688e-10 89-101
143	BL01020	SAR1 family proteins.	BL01020C 15.35 7.722e-20 79-130
146	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 6.400e-25 335-374
149	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126C 22.07 1.450e-25 509-550 BL00126E 35.22 3.951e-16 654-709 BL00126D 25.50 1.360e-15 565-604 BL00126B 15.20 8.200e-11 483-495 BL00126A 27.56 8.269e-11 442-479
151	BL00632	Ribosomal protein S4 proteins.	BL00632 23.79 5.271e-20 106-149
154	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559I 13.63 5.304e-19 29-58 BL00559K 13.17 2.957e-18 172-199 BL00559J 19.63 8.385e-13 99-151 BL00559L 13.60 5.814e-12 241-259
155	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.692e-13 13-35
157	BL00406	Actins proteins.	BL00406D 12.58 2.547e-18 275-330 BL00406A 9.95 5.776e-16 15-50 BL00406B 5.47 7.429e-12 69-124 BL00406C 6.75 9.682e-12 128-183
160	BL00132	Zinc carboxypeptidases, zinc-binding region 1 proteins.	BL00132A 26.07 7.000e-14 22-63 BL00132C 21.35 3.466e-12 104-145
165	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 9.043e-13 139-158
168	BL00362	Ribosomal protein S15 proteins.	BL00362 24.67 9.700e-15 129-172
169	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 1.000e-35 640-686 BL00039A 18.44 1.964e-13 212-251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e-12 465-489
175	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.721e-12 14-36
178	BL01310	ATP1G1 / PLM / MAT8 family proteins.	BL01310 14.74 2.432e-29 133-169
179	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 9.455e-36 6-45

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		BINDING NU.	
180	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 7.429e-20 160-180 PR00007A 19.33 4.938e-19 133-160 PR00007C 15.60 1.225e-15 206-228 PR00007D 9.64 6.885e-11 238-249
181	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e-24 280-323
182	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e-24 263-306
183	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e-24 280-323
184	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e-24 263-306
188	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929C 5.26 3.328e-09 460-471
189	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929C 5.26 3.328e-09 440-451
190	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383F 15.51 7.188e-17 666-682 BL00383A 13.34 8.714e-17 162-177 BL00383E 10.35 1.000e-14 333-344 BL00383E 10.35 7.300e-14 628-639 BL00383F 15.51 1.720e-13 371-387 BL00383C 10.10 3.000e-13 217-228 BL00383D 11.92 7.000e-13 295-308 BL00383B 7.61 1.692e-11 187-196 BL00383C 10.10 1.750e-09 509-520 BL00383D 11.92 4.000e-09 589-602 BL00383B 7.61 8.000e-09 479-488
191	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 7.911e-15 83-105 PR00450C 12.22 6.286e-13 47-69
193	PF00564	Octicosapeptide repeat proteins.	PF00564B 24.74 6.164e-16 227-278
194	PR00503	BROMODOMAIN SIGNATURE	PR00503D 20.81 9.156e-15 204-224 PR00503B 9.96 9.571e-13 170-187
195	BL00901	Cysteine synthase/cystathionine beta-synthase P-phosphate att.	BL00901C 20.63 3.429e-18 67-117
197	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 6.211e-17 40-57 BL00636B 15.11 2.000e-13 67-88
198	PR00690	ADHESIN FAMILY SIGNATURE	PR00690A 10.86 9.866e-09 463-482
199	BL01131	Ribosomal RNA adenine dimethylases proteins.	BL01131A 26.62 2.343e-12 84-130
201	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.352e-12 509-522
203	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.286e-10 39-72
206	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE	PR00261A 11.02 4.462e-19 65-87 PR00261C 11.37 9.308e-19 65-87 PR00261D 12.47 2.667e-18 65-87 PR00261B 14.12 4.000e-18 143-165 PR00261A 11.02

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			4.833e-18 143-165 PR00261D 12.47 7.500e-18 143-165 PR00261B 14.12 5.065e-16 65-87 PR00261C 11.37 8.967e-16 143-165 PR00261F 11.57 4.938e-13 143-165 PR00261E 11.08 7.188e-13 65-87 PR00261F 11.57 7.188e-13 65-87 PR00261E 11.08 1.643e-11 143-165
209	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 6.143e-13 118-173 PF00791C 20.98 7.680e-10 132-171
211	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007A 19.33 5.781e-19 131-158 PR00007B 14.16 4.115e-18 158-178 PR00007C 15.60 1.675e-15 201-223 PR00007D 9.64 7.231e-11 233-244
212	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.545e-30 43-91
213	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.545e-30 43-91
215	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 1.900e-29 568-614 BL00039A 18.44 1.871e-23 21-60 BL00039C 15.63 1.720e-11 364-388 BL00039B 19.19 4.064e-11 277-303
217	BL00100	Chloramphenicol acetyltransferase proteins.	BL00100D 17.22 8.484e-09 68-106
219	PR00213	MYELIN P0 PROTEIN SIGNATURE	PR00213C 15.94 3.969e-11 199-227
222	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.947e-09 144-155
224	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875A 5.83 1.000e-09 901-913
225	BL00636	Nt-dnaJ domain proteins.	BL00636B 15.11 8.200e-19 18-39
226	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 1.000e-21 21-38 BL00636B 15.11 8.200e-19 45-66
229	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE	PR00301F 13.98 7.563e-13 329-346 PR00301G 13.78 4.300e-12 361-382
230	BL00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 8.773e-20 35-70 BL00460B 9.73 7.429e-16 78-96 BL00460C 14.35 2.831e-12 111-134 BL00460D 16.89 8.773e-11 140-160
231	PR00647	SENR ORPHAN RECEPTOR SIGNATURE	PR00647B 10.19 8.522e-09 273-287
233	BL00292	Cyclins proteins.	BL00292B 20.31 7.429e-27 244-275 BL00292A 22.87 7.750e-27 201-235
234	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 6.308e-13 7-29 PR00449C

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			17.27 4.462e-11 47-70 PR00449D 10.79 7.120e-11 109-123
235	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e-10 251-265 PR00019B 11.36 5.320e-09 119-133 PR00019B 11.36 1.000e-08 229-243
236	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e-10 245-259 PR00019B 11.36 5.320e-09 113-127 PR00019B 11.36 1.000e-08 223-237
237	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESVNA.	PD00289 9.97 8.448e-09 67-81
240	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e-10 616-635
241	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e-10 616-635
244	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 8.941e-12 54-64
245	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 8.043e-09 124-134
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e-40 186-239 BL00246E 20.32 1.000e-40 305-351 BL00246B 13.69 4.176e-36 105-140 BL00246A 15.75 2.286e-24 70-90 BL00246C 15.56 4.857e-22 150-175
250	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 5.114e-10 253-275
254	BL00674	AAA-protein family proteins.	BL00674B 4.46 1.000e-09 223-245
255	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 6.045e-09 61-88
256	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 2.800e-10 421-435
258	PR00094	ADENYLATE KINASE SIGNATURE	PR00094C 12.94 2.200e-18 87-104 PR00094D 12.52 2.731e-14 161-177 PR00094A 10.31 5.500e-14 11-25 PR00094B 11.01 4.115e-13 39-54 PR00094E 11.25 7.333e-13 178-193
259	BL00892	HIT family proteins.	BL00892A 18.17 5.500e-13 60-91
262	BL00388	Proteasome A-type subunits proteins.	BL00388A 23.14 1.000e-40 8-54 BL00388B 31.38 3.864e-33 66-108 BL00388D 20.71 1.000e-21 153-184 BL00388C 18.79 8.147e-16 126-148
264	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 5.821e-09 91-101
267	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.529e-09 241-257
270	BL00226	Intermediate filaments proteins.	BL00226D 19.10 1.000e-37 362-409 BL00226B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			23.86 8.043e-35 196-244 BL00226C 13.23 7.000e-20 261-292 BL00226A 12.77 6.143e-15 96-111
271	PD02952	KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI.	PD02952C 15.76 9.731e-16 235-265 PD02952B 15.57 5.625e-09 215-229
272	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 1.000e-40 106-160 PD02929B 18.36 8.800e-17 179-199
274	BL01027	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e-09 213-250
275	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR00424D 14.32 6.451e-11 39-59
277	BL00052	Ribosomal protein S7 proteins.	BL00052A 27.85 6.000e-13 137-184 BL00052B 15.17 5.143e-12 208-235
279	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 5.659e-13 267-294
280	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e-23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e-21 51-68 PR00319B 11.47 8.200e-19 70-85
281	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e-23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e-21 38-55 PR00319B 11.47 8.200e-19 57-72
287	PF00929	Exonuclease.	PF00929D 16.17 7.366e-09 149-163
291	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e-09 93-127
292	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e-09 93-127
294	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.714e-12 203-216
295	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e-15 322-339 BL00028 16.07 9.471e-14 433-450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e-13 760-777 BL00028 16.07 9.550e-13 788-805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e-12 461-478 BL00028 16.07 8.435e-12 844-861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e-11 211-228 BL00028 16.07 5.154e-11 732-749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e-11 816-833 BL00028 16.07 7.231e-11 676-693 BL00028 16.07 9.654e-11 564-581

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			BL00028 16.07 4.086e-09 517-534 BL00028 16.07 7.429e-09 489-506
296	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 8.333e-16 111-136 BL00215A 15.82 2.723e-11 10-35 BL00215B 10.44 9.526e-11 152-165 BL00215B 10.44 7.375e-10 59-72 BL00215A 15.82 9.824e-10 205-230
302	PF00953	Glycosyl transferase.	PF00953C 19.70 8.773e-34 236-269 PF00953A 19.68 5.000e-25 102-129 PF00953B 6.17 1.000e-13 182-194
304	PF00152	tRNA synthetases class II.	PF00152D 21.30 8.364e-28 422-461 PF00152C 28.03 9.250e-21 220-257 PF00152B 15.67 2.658e-13 159-184 PF00152A 19.68 5.714e-11 44-67
305	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.250e-35 37-76
306	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 5.840e-09 92-135
307	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-09 1167-1186
308	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 5.091e-13 188-212 PR00237G 19.63 7.207e-13 268-295 PR00237A 11.48 4.375e-11 24-49 PR00237C 15.69 3.057e-10 101-124 PR00237D 8.94 4.750e-10 137-159 PR00237F 13.57 5.364e-10 230-255 PR00237B 13.50 9.438e-10 57-79
309	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 7.577e-24 315-339 BL00522F 14.90 1.310e-15 470-494 BL00522A 25.52 1.265e-14 179-226 BL00522E 19.63 8.615e-14 430-460 BL00522B 27.30 9.625e-12 267-313
310	BL00326	Tropomyosins proteins.	BL00326D 8.76 5.235e-10 856-897
312	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.706e-14 151-174 BL00290B 13.17 9.000e-12 211-229
313	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-40 34-85 BL00345A 13.96 9.217e-16 1-20
315	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 5.091e-15 63-76
317	BL01020	SARI family proteins.	BL01020C 15.35 3.198e-17 79-130
318	BL00216	Sugar transport proteins.	BL00216B 27.64 4.696e-11 164-214
320	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	PR00109B 12.27 4.814e-10 216-235

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	
321	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.688e-10 329-372
322	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 8.765e-12 558-577
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e-30 183-236 BL01241 35.81 3.222e-13 282-335
326	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e-12 515-566 BL00412D 16.54 5.705e-11 516-567 BL00412D 16.54 7.848e-10 518-569 BL00412D 16.54 1.827e-09 514-565 BL00412D 16.54 1.918e-09 513-564 BL00412D 16.54 2.102e-09 520-571
328	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e-20 151-199 BL00232B 32.79 2.246e-18 41-89 BL00232B 32.79 5.985e-18 370-418 BL00232B 32.79 5.500e-16 258-306 BL00232B 32.79 9.384e-15 475-523 BL00232C 10.65 2.537e-12 256-274 BL00232C 10.65 4.326e-11 368-386 BL00232C 10.65 7.261e-11 473-491 BL00232C 10.65 7.457e-11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-09 1167-1186
331	BL00598	Chromo domain proteins.	BL00598 14.45 8.393e-18 27-49
333	BL01016	Glycoprotease family proteins.	BL01016C 22.84 3.925e-32 70-115 BL01016E 14.88 5.286e-19 149-177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e-11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e-10 4-19 BL01016F 13.34 1.563e-09 200-212 BL01016B 8.93 8.855e-09 38-50
339	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.500e-11 17-61
340	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 1.231e-33 10-49
341	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.042e-09 55-109
342	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.400e-30 16-55
343	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-40 20-68
346	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.764e-11 135-154
347	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		CATALYTIC DOMAIN SIGNATURE	11 135-154
351	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 1.783e-13 100-116 BL01187B 12.04 8.435e-13 276-292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e-10 54-70 BL01187B 12.04 5.725e-09 231-247 BL01187A 9.98 7.000e-09 255-267
352	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e-10 366-379 PD00078B 13.14 4.522e-09 168-181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e-11 542-553
355	PF00628	PHD-finger.	PF00628 15.84 1.000e-11 116-131
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e-09 17-37
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e-15 261-274 PD00066 13.92 6.500e-13 233-246 PD00066 13.92 4.300e-09 289-302
361	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.604e-13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e-09 71-126 PF00791B 28.49 7.440e-09 184-239
362	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.273e-11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e-10 73-95 PR00450C 12.22 3.278e-09 109-131
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e-09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e-09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e-09 1038-1092
367	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e-09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e-09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 9.000e-15 30-49 PR00011A 14.06 9.830e-15 30-49 PR00011B 13.08 4.500e-14 30-49 PR00011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e-09 417-430
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e-12 410-425
373	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.757e-34 26-65
376	PR00170	SODIUM CHANNEL SIGNATURE	PR00170E 6.48 2.739e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			10 88-118
380	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 1.000e-23 276-307 BL00107B 13.31 1.692e-12 342-358
381	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 5.714e-12 50-66
382	PR00624	HISTONE H5 SIGNATURE	PR00624G 4.08 4.900e-09 524-544
384	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e-10 366-379 PD00078B 13.14 4.522e-09 168-181
385	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e-09 67-80
386	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 6.000e-10 97-130
388	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.000e-13 516-529
389	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.667e-09 151-174
390	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.200e-15 221-246 BL00215A 15.82 7.618e-14 20-45 BL00215A 15.82 8.851e-11 123-148 BL00215B 10.44 9.526e-11 69-82 BL00215B 10.44 7.300e-09 272-285 BL00215B 10.44 8.500e-09 165-178
394	BL00674	AAA-protein family proteins.	BL00674B 4.46 2.723e-16 299-321
397	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.579e-11 141-155
398	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761B 9.93 6.764e-09 55-74
399	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 7.907e-10 118-142
401	PF00676	Dehydrogenase E1 component.	PF00676B 24.71 8.071e-18 331-369 PF00676D 14.40 3.854e-15 486-506 PF00676C 16.88 9.182e-14 454-478
402	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 4.673e-28 4432-4469 BL00514G 15.98 6.092e-14 4555-4585 BL00514D 15.35 2.532e-12 4473-4486 BL00514F 11.65 4.288e-10 4519-4534 BL00514H 14.95 4.955e-10 4584-4609
403	PF00992	Troponin.	PF00992A 16.67 5.974e-09 105-140
404	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.450e-10 73-87 PR00019A 11.19 8.043e-10 76-90 PR00019B 11.36 1.000e-09 50-64 PR00019B 11.36 1.000e-09 96-110
405	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e-20 139-187 BL00232B 32.79 2.246e-18 29-77 BL00232B 32.79 5.985e-18 358-406 BL00232B 32.79 5.500e-16 246-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			294 BL00232B 32.79 9.384e-15 463-511 BL00232C 10.65 2.537e- 12 244-262 BL00232C 10.65 4.326e-11 356- 374 BL00232C 10.65 7.261e-11 461-479 BL00232C 10.65 7.457e- 11 27-45
407	PF00426	Outer Capsid protein VP4 (Hemagglutinin).	PF00426S 15.67 5.634e- 09 902-940
409	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.695e- 09 126-180
410	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 2.731e- 09 252-275
411	PF00646	F-box domain proteins.	PF00646A 14.37 6.344e- 09 86-100
412	BL00603	Thymidine kinase cellular-type proteins.	BL00603B 11.39 8.500e- 09 542-557
415	BL00866	Carbamoyl-phosphate synthase subdomain proteins.	BL00866B 36.29 3.571e- 31 245-291 BL00866C 23.26 9.000e-25 331- 366
418	PR00239	MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE	PR00239E 1.58 6.114e- 09 590-602
421	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.955e- 14 23-78 PF00791B 28.49 3.653e-12 273- 328 PF00791B 28.49 4.273e-11 156-211 PF00791B 28.49 7.818e- 11 89-144 PF00791B 28.49 1.524e-10 56-111 PF00791C 20.98 3.559e- 09 37-76 PF00791C 20.98 5.235e-09 170- 209 PF00791C 20.98 5.235e-09 381-420 PF00791B 28.49 6.202e- 09 189-244 PF00791B 28.49 7.028e-09 435- 490 PF00791B 28.49 8.679e-09 367-422
424	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 7.207e- 28 1645-1679
425	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 5.881e- 10 228-251
429	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.600e- 11 31-40
431	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 1.844e- 34 490-536 BL00039A 18.44 5.615e-19 205- 244 BL00039B 19.19 8.920e-16 251-277 BL00039C 15.63 5.781e- 15 333-357
432	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 7.652e- 12 169-185
433	PR00828	FORMIN SIGNATURE	PR00828B 5.23 8.218e- 10 382-405
436	BL00415	Synapsins proteins.	BL00415N 4.29 8.643e- 11 195-239 BL00415N 4.29 3.036e-09 809-853
443	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE	PR00834F 10.91 6.040e- 11 221-234
446	PF01140	Matrix protein (MA),	PF01140D 15.54 9.663e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		p15.	10 183-218 PF01140D 15.54 3.093e-09 246-281
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PR00568G 13.95 5.551e-09 39-53
451	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e-10 47-59
452	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e-09 618-649
456	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 1.000e-25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e-17 230-249 PR00380B 12.64 4.724e-16 194-212
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e-24 246-267 PR00253B 13.47 2.000e-23 272-294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e-21 452-473
467	PR00849	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	PR00849D 9.77 9.236e-09 910-937
471	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 8.200e-12 33-44
472	BL00226	Intermediate filaments proteins.	BL00226B 23.86 3.721e-09 282-330
473	BL00344	GATA-type zinc finger domain proteins.	BL00344 17.99 7.000e-12 814-852
474	BL00481	Thiol-activated cytolytic proteins.	BL00481E 13.07 8.909e-09 173-199
479	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 2.571e-09 393-408
480	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 1.900e-38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e-19 451-473 PR00405B 11.83 4.333e-18 430-448 PR00405A 17.71 4.971e-18 411-431
482	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.286e-10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e-09 937-952 PR00049D 0.00 8.322e-09 939-954
486	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 8.615e-23 653-673 PR00007A 19.33 6.192e-22 626-653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e-13 732-743
487	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e-09 200-214
488	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.569e-12 3-21
489	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.882e-27 30-69 PD01066 19.43 3.430e-10 71-110
490	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.864e-09 663-678
492	BL01128	Shikimate kinase proteins.	BL01128A 18.84 6.464e-17 58-92
497	PF00429	ENV polyprotein (coat	PF00429 31.08 7.171e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		polyprotein).	15 21-71
498	BL00120	Lipases, serine proteins.	BL00120B 11.37 7.923e-09 185-200
500	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.353e-11 299-318
501	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 8.579e-12 131-146
505	BL00021	Kringle domain proteins.	BL00021B 13.33 3.739e-17 492-510
508	PR00120	H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE	PR00120C 9.90 5.800e-19 705-722
509	DM01417	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417E 20.62 2.938e-16 362-395 DM01417D 11.08 3.800e-13 322-338
510	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-09 346-370
511	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-09 293-317
512	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-09 366-390
513	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e-40 110-160 PD01841B 14.35 1.000e-40 181-222 PD01841D 17.87 1.000e-40 243-295 PD01841F 13.36 1.000e-40 333-382 PD01841G 24.26 1.000e-40 386-440 PD01841L 18.42 1.000e-40 968-1010 PD01841I 23.00 4.545e-37 762-804 PD01841E 18.60 3.750e-36 295-333 PD01841J 14.94 6.023e-35 851-888 PD01841H 21.30 2.909e-33 490-527 PD01841K 14.81 7.088e-33 924-954 PD01841C 13.78 9.386e-23 222-243 PD01841M 10.82 8.594e-21 1054-1073 PD01841I 23.00 2.667e-13 549-591
514	PR00153	CYCLOPHILIN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE SIGNATURE	PR00153C 11.01 7.188e-13 95-111 PR00153E 9.10 4.150e-12 122-138
515	BL00740	MAM domain proteins.	BL00740A 13.87 7.188e-12 410-423
516	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e-12 1018-1052
517	BL00242	Integrins alpha chain proteins.	BL00242C 16.86 8.320e-09 12-42
523	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-39 20-68 DM00031B 15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 8.375e-10 61-95
526	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789B 19.70 3.308e-12 322-343 PF00789C 20.98 5.269e-09 367-392
528	BL01162	Quinone oxidoreductase / zeta-crystallin proteins.	BL01162C 22.80 1.500e-16 120-164

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
529	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 3.893e-09 60-73
532	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e-17 11-36 BL00215A 15.82 8.660e-11 123-148
533	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e-17 11-36 BL00215A 15.82 8.660e-11 97-122
534	BL00098	Thiolases acyl-enzyme intermediate proteins.	BL00098C 21.65 2.800e-38 181-227 BL00098B 32.59 5.345e-38 86-141 BL00098D 26.30 8.364e-35 245-288 BL00098E 22.12 1.000e-34 314-352 BL00098F 10.18 4.971e-22 365-386 BL00098A 10.60 6.455e-11 38-50
535	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	PR00370E 11.96 7.429e-22 321-340 PR00370D 16.33 6.143e-21 185-204 PR00370F 17.75 6.559e-21 376-396 PR00370B 10.91 9.591e-21 27-46 PR00370C 12.72 3.500e-20 140-157 PR00370A 3.35 6.442e-17 4-20
536	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.429e-16 285-302 BL00028 16.07 6.294e-14 341-358 BL00028 16.07 1.346e-11 369-386 BL00028 16.07 1.692e-11 397-414 BL00028 16.07 4.462e-11 453-470 BL00028 16.07 7.231e-11 425-442 BL00028 16.07 4.300e-10 313-330
537	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e-15 844-881
538	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e-15 819-856
539	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e-15 822-859
540	PR00985	LEUCYL-TRNA SYNTHETASE SIGNATURE	PR00985A 12.10 9.000e-10 357-375
541	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 1.000e-40 3-47 PD02102B 18.28 4.375e-34 57-100 PD02102D 21.69 1.923e-30 179-218 PD02102C 26.34 8.929e-26 100-146
543	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e-10 48-65 BL00028 16.07 6.400e-10 193-210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e-09 78-95
545	BL00250	TGF-beta family proteins.	BL00250A 21.24 8.000e-31 293-329 BL00250B 27.37 5.286e-24 354-390
547	PR00319	BETA G-PROTEIN	PR00319B 11.47 2.714e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		(TRANSDUCIN) SIGNATURE	09 186-201 PR00319A 15.27 7.344e-09 210-227
548	BL01204	NF-kappa-B/Rel/dorsal domain proteins.	BL01204A 17.74 1.000e-40 8-56 BL01204D 16.42 1.000e-40 177-221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e-22 141-160 BL01204B 15.41 4.333e-16 102-116
549	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.364e-15 255-276
551	PF00632	HECT-domain (ubiquitin-transferase).	PF00632C 20.66 3.302e-23 1569-1601 PF00632B 18.45 3.700e-21 1515-1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e-14 187-205 BL00290A 20.89 2.059e-14 130-153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e-09 846-879
559	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e-09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e-32 118-155
564	BL00141	Eukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e-10 472-488
566	PF00855	PWWP domain proteins.	PF00855 13.75 5.667e-15 272-289
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 4.977e-13 229-268
569	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 7.000e-19 118-149 BL00107B 13.31 5.500e-15 183-199
570	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 7.000e-19 118-149 BL00107B 13.31 5.500e-15 183-199
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e-34 454-483 PR00193C 12.60 2.636e-31 223-251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e-22 115-135 PR00193E 19.47 6.559e-19 508-537
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e-34 470-499 PR00193C 12.60 2.636e-31 239-267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e-22 115-135 PR00193E 19.47 6.559e-19 524-553
575	BL00752	XPA protein.	BL00752B 19.17 9.703e-10 885-929
576	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.000e-09 276-295
577	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	13 864-877 BL00116B 11.82 1.529e-12 952-965
578	BL00195	Glutaredoxin proteins.	BL00195B 15.31 7.158e-09 121-141
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 9.000e-11 217-231 PR00019B 11.36 1.360e-09 386-400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e-09 363-377
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 2.125e-25 275-296 PR00253B 13.47 7.923e-24 301-323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e-20 335-357
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e-11 1233-1252 PR00343C 16.85 5.500e-11 333-352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e-10 1491-1510 PR00343C 16.85 8.230e-10 1686-1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e-37 79-126 DM01537B 21.63 9.491e-30 916-963 DM01537A 15.14 3.186e-11 784-804
586	PF00013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.409e-13 262-296
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e-13 261-276 BL00478B 14.79 7.709e-09 321-336
590	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e-15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e-15 1062-1079
593	PF00628	PHD-finger.	PF00628 15.84 3.455e-12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e-16 558-576 PR00205A 14.73 9.308e-13 542-558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e-10 336-354
596	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.789e-18 307-338
598	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	PD01675C 19.89 2.330e-10 55-89
600	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e-27 985-1014 BL00242C 16.86 4.115e-26 286-316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e-12 189-199 BL00242D 13.57 3.455e-11 421-446 BL00242A 13.80

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			5.000e-11 61-73 BL00242D 13.57 4.986e-10 291-316
601	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 5.610e-09 198-213
602	PR00278	PANCREATIC HORMONE SIGNATURE	PR00278A 12.43 4.569e-10 331-348
603	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 3.250e-12 170-183
604	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e-09 424-452
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e-10 295-339
606	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 1.000e-13 335-358
608	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-15 265-282
609	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-15 211-228
612	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.411e-10 877-897 DM01206B 10.69 8.027e-10 861-881 DM01206B 10.69 9.137e-10 873-893 DM01206B 10.69 1.456e-09 859-879 DM01206B 10.69 1.797e-09 879-899 DM01206B 10.69 4.076e-09 865-885 DM01206B 10.69 7.038e-09 898-918 DM01206B 10.69 7.949e-09 871-891 DM01206B 10.69 8.291e-09 767-787
615	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699A 8.91 2.023e-28 129-158 PD02699C 24.84 1.000e-27 317-364 PD02699B 18.28 1.000e-17 158-182
616	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e-22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-16 410-428 PR00380C 13.18 2.976e-13 436-455
617	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e-22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-16 410-428 PR00380C 13.18 2.976e-13 436-455
618	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 5.143e-12 531-551 DM01206B 10.69 2.603e-10 535-555
621	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 3.160e-21 561-582
622	BL00239	Receptor tyrosine kinase class II proteins.	BL00239F 28.15 3.222e-10 647-692 BL00239C 18.75 8.304e-10 543-566
623	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407K 9.94 8.448e-09 326-339
624	BL00641	Respiratory-chain NADH dehydrogenase 75 Kd	BL00641C 21.10 1.000e-40 157-202 BL00641E

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		subunit proteins.	24.37 1.000e-40 255-308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e-37 48-80 BL00641B 12.62 5.846e-34 113-139 BL00641D 13.23 9.308e-29 216-240
627	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE	PR00103E 17.80 2.500e-18 367-380 PR00103B 13.39 2.080e-14 297-312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e-12 346-358 PR00103C 15.68 1.000e-11 334-344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e-10 160-175
630	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081A 10.53 6.211e-16 4-22
631	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 8.500e-14 37-50
632	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 2.233e-10 1324-1344 DM01206B 10.69 4.822e-10 1276-1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e-10 1280-1300 DM01206B 10.69 4.532e-09 1320-1340 DM01206B 10.69 7.266e-09 1326-1346
635	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 7.600e-23 145-176 BL00107B 13.31 2.636e-13 211-227
636	BL00657	Fork head domain proteins.	BL00657A 19.39 1.545e-30 101-143 BL00657B 22.27 7.750e-26 149-192
637	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.000e-10 607-623
643	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.913e-09 199-212
647	PF00628	PHD-finger.	PF00628 15.84 2.350e-13 385-400 PF00628 15.84 3.455e-12 464-479
648	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 4.000e-25 332-357 BL01129C 25.56 8.200e-23 236-279 BL01129B 12.51 6.118e-13 191-212
649	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 3.908e-10 455-480
650	BL00027	'Homeobox' domain proteins.	BL00027 26.43 6.684e-13 771-814
651	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 1.750e-12 1026-1045
653	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 4.000e-24 253-274 PR00253C 13.85 8.800e-24 313-335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			20 422-443
654	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 4.452e-11 969-997 PD01719A 12.89 3.961e-10 128-156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e-09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (Ahook).	BL00354C 6.61 8.397e-09 563-578
658	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (Ahook).	BL00354C 6.61 8.397e-09 580-595
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e-13 539-572 DM00215 19.43 4.750e-12 549-582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e-10 548-581 DM00215 19.43 4.054e-10 550-583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e-10 544-577
660	PR00688	XYLOSE ISOMERASE SIGNATURE	PR00688I 13.78 9.518e-09 224-236
661	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.950e-23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-10 596-610
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e-10 596-610
666	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 8.988e-10 704-720
667	BL50040	Elongation factor 1 gamma chain profile.	BL50040C 22.62 2.143e-16 135-178
668	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e-09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e-09 163-177
670	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT TRANSMEMBR.	PD00131B 34.97 1.000e-34 356-410 PD00131C 19.59 1.346e-26 504-542
673	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PR00667G 15.33 7.557e-10 106-123
674	PR00320	G-PROTEIN BETA WD-4C REPEAT SIGNATURE	PR00320A 16.74 4.857e-13 593-608 PR00320B 12.19 4.115e-12 635-650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e-10 635-650 PR00320C 13.01 6.400e-10 593-608 PR00320B 12.19 3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-4C REPEAT SIGNATURE	PR00320A 16.74 4.857e-13 572-587 PR00320B 12.19 4.115e-12 614-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			629 PR00320C 13.01 8.435e-11 696-711 PR00320C 13.01 2.800e- 10 614-629 PR00320C 13.01 6.400e-10 572- 587 PR00320B 12.19 3.250e-09 572-587
676	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.667e- 09 249-263
679	PF00642	Zinc finger C-x8-C-x5-C- x3-H type (and similar).	PF00642 11.59 3.700e- 16 225-236 PF00642 11.59 7.900e-12 187- 198
680	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.754e- 10 286-296
681	BL00019	Actinin-type actin- binding domain proteins.	BL00019D 15.33 4.200e- 19 227-257
682	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 4.000e- 09 99-118
687	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.500e- 10 538-553
689	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.	BL01024A 10.26 1.000e- 40 22-69 BL01024B 8.91 1.000e-40 86-127 BL01024C 7.80 1.000e- 40 146-185 BL01024D 13.22 1.000e-40 185- 222 BL01024E 11.96 1.000e-40 222-266 BL01024F 9.42 1.000e- 40 266-317 BL01024G 11.09 1.000e-40 317- 349 BL01024H 13.88 1.000e-40 389-442
691	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.071e- 31 152-195
692	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 45-57
693	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 45-57
694	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 58-70
696	BL00680	Methionine aminopeptidase subfamily 1 proteins.	BL00680 14.37 5.304e- 17 173-195
697	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 3.418e- 11 242-265
698	DM01930	2 kw FINGER SMCK SMCY YDR096W.	DM01930E 15.41 1.367e- 37 170-215 DM01930F 14.16 8.232e-28 267- 303 DM01930B 19.86 9.163e-10 37-71
700	PR00869	DNA-POLYMERASE FAMILY X SIGNATURE	PR00869A 12.80 1.281e- 16 245-263
701	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.174e- 10 77-91 PR00048A 10.52 6.870e-10 133- 147 PR00048A 10.52 8.826e-10 105-119 PR00048A 10.52 5.320e- 09 161-175
702	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e- 25 326-356 BL00523A 13.36 5.050e-16 38-55 BL00523B 8.64 5.909e- 15 86-98 BL00523C 12.64 5.500e-13 137-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			148 BL00523D 9.89 1.844e-11 290-302 BL00523G 9.46 5.500e-10 513-523 BL00523F 10.85 6.351e-09 413-424
703	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.412e-12 376-390 PR00048B 6.02 1.000e-10 334-344 PR00048B 6.02 1.474e-09 364-374
707	PD00787	SYNTHASE BIOSYNTHESIS TRANSFERASE.	PD00787A 14.84 8.941e-14 66-82
708	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 8.500e-10 822-841
712	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354Y 10.69 4.977e-38 425-465 DM01354X 13.86 7.300e-34 376-415 DM01354V 12.97 4.923e-17 311-358 DM01354W 12.64 5.596e-10 356-376
713	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 7.545e-27 450-496 BL00039A 18.44 2.537e-18 147-186 BL00039C 15.63 2.216e-14 280-304 BL00039B 19.19 1.947e-13 194-220
715	BL00383	Tyrosine specific protein phosphatases proteins.	BL00383E 10.35 4.981e-10 150-161
717	PF00777	Sialyltransferase family.	PF00777C 18.60 4.035e-21 106-161
718	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-39 20-68 DM00031B 15.41 2.688e-28 84-118 DM00031C 12.79 1.300e-12 131-142
719	BL00243	Integrins beta chain cysteine-rich domain proteins.	BL00243B 17.54 1.000e-40 131-172 BL00243C 16.42 1.000e-40 172-208 BL00243D 24.07 1.000e-40 222-274 BL00243F 22.63 1.000e-40 314-358 BL00243I 31.77 6.571e-39 607-650 BL00243E 16.70 3.077e-35 274-304 BL00243G 21.38 3.625e-34 358-400 BL00243H 17.53 5.235e-29 567-593 BL00243A 17.61 3.250e-21 63-84 BL00243H 17.53 7.167e-16 477-503 BL00243H 17.53 2.304e-11 524-550 BL00243H 17.53 5.304e-11 606-632 BL00243I 31.77 1.380e-09 610-653
720	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 8.022e-09 20-36
722	PR00704	CALPAIN CYSTEINE PROTEASE (C2) FAMILY SIGNATURE	PR00704D 11.05 5.909e-34 135-161 PR00704F 13.61 7.000e-26 190-218 PR00704E 12.55 8.071e-26 165-189

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00704B 17.94 2.241e-23 75-98 PR00704A 14.68 4.094e-19 30-54 PR00704C 11.88 1.871e-18 99-116
725	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-09 169-187
726	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-09 169-187
727	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.125e-13 277-292 PR00320A 16.74 1.310e-11 277-292 PR00320C 13.01 4.522e-11 323-338 PR00320A 16.74 6.586e-11 323-338 PR00320B 12.19 4.343e-10 323-338 PR00320B 12.19 6.914e-10 277-292
731	PR00195	DYNAMIN SIGNATURE	PR00195A 11.94 8.627e-16 288-307 PR00195E 9.82 3.912e-11 457-474
733	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.082e-10 787-798
738	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039A 18.44 2.565e-28 26-65 BL00039D 21.67 2.105e-20 338-384 BL00039C 15.63 9.100e-13 160-184 BL00039B 19.19 9.617e-11 73-99
739	BL01289	TSC-22 / dip / bun family proteins.	BL01289A 12.18 8.909e-31 326-353 BL01289B 10.45 9.571e-17 353-383
742	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 7.078e-12 41-81
743	BL00965	Phosphomannose isomerase type I proteins.	BL00965C 23.78 1.000e-40 256-305 BL00965B 17.77 1.600e-25 126-153 BL00965A 10.57 6.400e-19 94-113
747	BL00021	Kringle domain proteins.	BL00021D 24.56 4.563e-25 231-273 BL00021B 13.33 5.345e-21 60-78
748	BL00612	Osteonectin domain proteins.	BL00612B 11.35 2.034e-11 93-126
749	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 6.880e-10 135-157
752	BL00795	Involucrin proteins.	BL00795C 17.06 6.000e-11 384-429 BL00795C 17.06 9.444e-11 370-415
754	BL00051	Ribosomal protein L39e proteins.	BL00051 20.92 1.935e-16 4-50
755	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.723e-09 171-184
760	BL01020	SAR1 family proteins.	BL01020C 15.35 9.020e-12 99-150
762	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e-40 33-88
763	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 9.137e-10 206-240
764	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.800e-29 417-460
767	BL01208	VWFC domain proteins.	BL01208B 15.83 6.063e-10 309-324 BL01208B 15.83 8.031e-10 165-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			180 BL01208B 15.83 4.162e-09 85-100
770	BL00031	Nuclear hormones receptors DNA-binding region proteins.	BL00031A 19.55 9.571e-32 208-241 BL00031B 22.25 5.500e-27 242-274
772	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.450e-16 4-26 PR00449E 13.50 3.520e-14 142-165 PR00449C 17.27 3.032e-13 44-67 PR00449D 10.79 8.579e-13 107-121 PR00449B 14.34 3.455e-11 27-44
773	BL00523	Sulfatases proteins.	BL00523E 19.27 9.333e-23 299-329 BL00523A 13.36 2.200e-13 47-64 BL00523B 8.64 2.607e-13 91-103 BL00523D 9.89 7.923e-12 224-236 BL00523C 12.64 4.512e-10 141-152 BL00523F 10.85 5.821e-10 373-384
775	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 568-585
776	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 621-638
777	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 595-612
778	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 8.412e-11 322-341 BL00030A 14.39 7.000e-10 220-239
779	PR00079	GLUCOSE-6-PHOSPHATE DEHYDROGENASE SIGNATURE	PR00079B 12.98 2.929e-26 193-222 PR00079E 16.65 4.150e-23 348-375 PR00079C 8.68 6.351e-16 246-264 PR00079D 13.51 7.070e-16 264-281 PR00079A 16.12 6.769e-13 169-183
781	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 9.250e-17 10-35 BL00215A 15.82 6.000e-16 221-246 BL00215A 15.82 7.857e-12 108-133 BL00215B 10.44 9.526e-11 168-181
783	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESNA.	PD00289 9.97 6.276e-09 159-173
785	BL00690	DEAH-box subfamily ATP-dependent helicases proteins.	BL00690B 13.38 1.000e-12 147-165 BL00690A 6.87 5.320e-10 114-124 BL00690C 7.51 3.189e-09 218-228
786	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 8.500e-16 50-73 PR00449A 13.20 5.235e-14 8-30 PR00449E 13.50 2.853e-11 150-173 PR00449D 10.79 1.545e-09 111-125
788	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 8.767e-10 1-21
790	BL00915	Phosphatidylinositol 3- and 4-kinases proteins.	BL00915C 22.43 9.182e-39 725-764 BL00915B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			22.78 5.050e-33 633-671 BL00915D 27.02 1.529e-21 795-831 BL00915A 10.09 1.000e-13 395-407
791	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 6.294e-10 120-138 PR00208A 12.59 6.294e-10 121-139 PR00208A 12.59 6.294e-10 122-140 PR00208A 12.59 6.294e-10 123-141 PR00208A 12.59 6.294e-10 124-142 PR00208A 12.59 6.294e-10 125-143 PR00208A 12.59 6.294e-10 126-144 PR00208A 12.59 6.294e-10 127-145 PR00208A 12.59 6.294e-10 128-146 PR00208A 12.59 6.294e-10 129-147 PR00208A 12.59 7.411e-09 130-148 PR00208A 12.59 7.658e-09 131-149 PR00208A 12.59 7.904e-09 132-150 PR00208A 12.59 8.274e-09 118-136 PR00208A 12.59 8.274e-09 119-137
795	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.034e-16 302-320 PR00205A 14.73 1.257e-11 284-300 PR00205C 13.65 1.333e-11 337-352
796	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e-12 196-247 BL00412D 16.54 5.705e-11 197-248 BL00412D 16.54 7.848e-10 199-250 BL00412D 16.54 1.827e-09 195-246 BL00412D 16.54 1.918e-09 194-245 BL00412D 16.54 2.102e-09 201-252
797	BL00021	Kringle domain proteins.	BL00021B 13.33 6.339e-13 40-58
799	BL01052	Calponin family repeat proteins.	BL01052C 18.51 1.000e-40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e-25 52-78 BL01052D 10.26 5.737e-25 174-194
800	BL00348	p53 tumor antigen proteins.	BL00348F 23.19 3.714e-09 197-240
801	BL00309	Vertebrate galactoside-binding lectin proteins.	BL00309C 18.65 1.621e-09 62-87
802	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245D 10.47 5.224e-09 187-199
804	PF00774	Dihydropyridine sensitive L-type calcium channel (Beta subuni.	PF00774A 16.47 8.457e-10 110-156
808	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PR00667C 11.71 9.875e-09 12-28
810	PD02346	PHOTOSYSTEM II PROTEIN PRECURSOR	PD02346F 12.89 4.340e-09 317-354

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PHOTOSYNTHESIS.	
811	BL00685	CBF-A/NF-YB subunit proteins.	BL00685B 14.41 6.779e-14 54-95 BL00685A 11.22 4.798e-13 5-54
812	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE	PR00080A 9.32 9.419e-10 93-105
813	BL00357	Histone H2B proteins.	BL00357 7.74 1.988e-17 22-65
815	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.923e-15 158-171 PD00066 13.92 5.200e-14 46-59 PD00066 13.92 7.000e-14 18-31 PD00066 13.92 7.000e-13 130-143 PD00066 13.92 7.500e-13 214-227 PD00066 13.92 9.000e-13 102-115 PD00066 13.92 4.429e-12 186-199 PD00066 13.92 1.783e-11 74-87
816	BL01195	Peptidyl-tRNA hydrolase proteins.	BL01195C 20.12 3.348e-20 100-139
820	BL00520	Interleukin-10 family proteins.	BL00520A 6.21 6.471e-09 1-14
822	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972A 11.93 8.113e-09 224-242
825	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 2.268e-10 101-115
829	PD02855	FLAVOPROTEIN PROTEIN DNA/PANTOTHEN.	PD02855A 18.37 4.732e-28 88-124 PD02855B 8.36 6.478e-09 132-142
830	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 7.000e-21 44-62 PR00405C 19.41 1.000e-13 65-87 PR00405A 17.71 7.283e-13 25-45
831	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 1.000e-09 47-61 PR00019B 11.36 1.720e-09 136-150 PR00019B 11.36 3.880e-09 44-58
832	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 3.438e-16 164-183 PR00011D 14.03 6.850e-16 164-183 PR00011A 14.06 8.364e-14 164-183 PR00011C 24.25 5.415e-12 231-260 PR00011D 14.03 9.852e-11 212-231
834	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e-12 232-246
835	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 4.000e-10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e-12 216-230
837	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e-09 78-111
839	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 8.302e-09 73-116
840	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 5.091e-22 369-390 PR00700D 12.47 5.765e-21 491-510 PR00700C 13.17 4.750e-14 449-467 PR00700F 11.18 8.500e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			11 538-549 PR00700E 17.57 3.100e-10 522-538
841	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109E 12.27 5.404e-13 134-153
844	PD02785	PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP.	PD02785E 14.43 1.000e-40 58-112 PD02785A 15.23 1.915e-28 8-57
845	BL00826	MARCKS family proteins.	BL00826C 7.63 6.738e-09 203-230
846	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.429e-10 15-24
849	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e-08 340-349
850	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 6.506e-09 12-27
851	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 7.000e-16 246-280
852	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e-40 723-778 BL00420B 22.67 1.321e-38 933-988 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e-27 587-642 BL00420B 22.67 9.625e-27 270-325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e-23 55-110 BL00420B 22.67 6.464e-20 377-432 BL00420B 22.67 2.800e-15 830-885 BL00420C 11.90 1.900e-13 355-366 BL00420C 11.90 1.900e-12 808-819 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e-11 141-152 BL00420C 11.90 5.119e-11 1018-1029 BL00420C 11.90 7.955e-10 567-578
853	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e-40 756-811 BL00420B 22.67 1.321e-38 966-1021 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e-27 620-675 BL00420B 22.67 9.625e-27 270-325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e-23 55-110 BL00420B 22.67 6.464e-20 377-432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e-13 355-366 BL00420C 11.90 1.900e-12 841-852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e-11 141-152 BL00420C 11.90 5.119e-11 1051-1062 BL00420C 11.90

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			7.955e-10 567-578
857	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388A 10.45 2.778e-09 64-83
859	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 2.929e-13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e-10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.250e-17 23-41 PR00988C 13.64 8.714e-16 107-123 PR00988F 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e-12 176-188 PR00988D 5.95 8.250e-11 163-174 PR00988B 11.60 4.512e-10 60-72
863	BL00215	Mitochondrial energy transfer proteins.	BL00215B 10.44 8.071e-12 41-54
864	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775E 8.06 1.000e-24 198-221 PR00775B 3.52 1.837e-23 107-130 PR00775D 8.91 4.484e-17 171-189 PR00775A 9.90 8.342e-17 86-107 PR00775C 10.68 9.379e-17 153-171 PR00775G 10.64 6.850e-15 267-286 PR00775F 12.76 6.769e-14 249-267
866	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 9.460e-09 89-121
867	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.596e-29 14-53
868	BL01287	RNA 3'-terminal phosphate cyclase proteins.	BL01287A 17.95 2.688e-26 16-48
869	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e-10 304-337
872	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e-40 30-85
874	BL00188	Biotin-requiring enzymes attachment site proteins.	BL00188 30.29 9.036e-32 665-711
876	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e-09 298-315
877	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 4.176e-10 97-141
879	BL01189	Ribosomal protein S12e proteins.	BL01189A 14.27 1.000e-40 35-71 BL01189B 13.49 1.000e-40 71-125
882	BL00284	Serpins proteins.	BL00284C 28.56 6.400e-25 62-104 BL00284B 17.99 6.182e-12 35-56
889	BL00216	Sugar transport proteins.	BL00216B 27.64 4.375e-21 35-85
896	PR00391	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SIGNATURE	PR00391E 12.50 7.785e-15 211-231 PR00391B 8.39 1.000e-13 83-104 PR00391D 12.21 9.328e-13 191-207 PR00391A 7.83 5.390e-11 16-36
897	PR00327	ICE NUCLEATION PROTEIN	PR00327C 6.37 5.247e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	09 313-328
898	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 7.800e-26 386-432 BL00039A 18.44 6.674e-16 113-152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e-11 236-260
901	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e-16 254-267 PD00066 13.92 8.200e-16 282-295 PD00066 13.92 8.200e-16 310-323 PD00066 13.92 8.200e-16 366-379 PD00066 13.92 8.200e-16 394-407 PD00066 13.92 8.200e-14 338-351
902	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 9.321e-11 6-50
903	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.160e-09 97-111
904	PR00381	KINESIN LIGHT CHAIN SIGNATURE	PR00381E 8.75 6.586e-25 335-356 PR00381B 18.17 2.667e-24 204-224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e-24 226-245 PR00381D 13.94 1.084e-22 291-309 PR00381F 9.13 3.288e-22 370-392 PR00381F 9.13 7.181e-13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e-11 293-314 PR00381E 8.75 8.364e-10 377-398 PR00381D 13.94 5.230e-09 333-351 PR00381C 12.48 7.120e-09 310-329
906	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e-09 525-549
907	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e-09 513-537
908	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 9.308e-11 144-155
910	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.800e-30 48-87
912	BL01104	Ribosomal protein L13e proteins.	BL01104C 15.14 6.000e-09 364-392
922	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.842e-09 500-511
923	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.500e-09 323-338 PR00320C 13.01 5.500e-09 187-202
924	PD02181	PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT.	PD02181D 12.85 8.609e-09 36-64
926	BL00019	Actinin-type actin-binding domain proteins.	BL00019C 14.66 7.453e-25 108-144 BL00019B 13.34 6.510e-11 61-84 BL00019D 15.33 9.338e-11 205-235 BL00019A 12.56 2.373e-10 34-45
928	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 9.308e-11

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins proteins.	273-284 BL00678 9.67 1.600e-10 314-325 BL00678 9.67 7.600e-10 360-371 BL00678 9.67 8.579e-09 206-217
929	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.857e-10 137-146
930	BL01085	Ribulose-phosphate 3-epimerase family proteins.	BL01085D 16.55 4.600e-24 134-165 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e-20 172-202 BL01085C 21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3-epimerase family proteins.	BL01085D 16.55 4.600e-24 152-183 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e-20 190-220 BL01085C 21.81 2.038e-14 66-97
933	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 6.400e-09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e-12 336-362
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e-10 5-49
940	PR00862	PROLYL OLIGOPEPTIDASE SERINE PROTEASE (S9A) SIGNATURE	PR00862D 16.17 4.086e-09 63-84
945	BL01230	RNA methyltransferase trmA family proteins.	BL01230B 11.62 2.373e-09 407-420
948	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 7.429e-18 52-68 BL00479A 19.86 2.200e-13 26-49
949	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.474e-09 100-111
954	PD01311	PROTEIN OXIDOREDUCTASE NAD INTERGENIC RE.	PD01311A 30.23 5.909e-10 66-111
955	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.250e-12 47-60
956	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.250e-12 47-60
957	BL00379	CDP-alcohol phosphatidyltransferases proteins.	BL00379 24.64 1.610e-15 111-148
959	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 1.884e-10 31-75
960	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.438e-14 110-154
962	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 6.586e-13 198-236
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e-11 210-225
966	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 7.035e-09 55-70
967	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 1.286e-12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e-10 73-93 DM01206B 10.69 3.962e-09 108-128 DM01206B 10.69 5.671e-09 38-58
969	PF01008	Initiation factor 2 subunit.	PF01008B 25.59 4.724e-31 417-460 PF01008C 12.25 5.333e-18 506-526 PF01008A 20.14 5.875e-15 369-390

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
970	BL01277	Ribonuclease PH proteins.	BL01277C 10.18 7.648e-10 112-143 BL01277A 17.39 9.806e-10 40-78
975	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 3.605e-12 130-145 BL01159 13.85 4.122e-10 171-186
977	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791C 20.98 2.235e-09 55-94
978	BL01167	Ribosomal protein L17 proteins.	BL01167B 20.66 8.258e-19 88-127
979	BL00478	LIM domain proteins.	BL00478B 14.79 9.357e-13 33-48 BL00478B 14.79 7.250e-12 98-113
980	PR00312	CALSEQUESTRIN SIGNATURE	PR00312E 8.32 3.423e-36 169-199 PR00312I 15.78 5.286e-35 332-361 PR00312F 15.06 5.865e-35 199-229 PR00312H 13.31 8.313e-35 263-291 PR00312J 13.73 5.688e-34 363-392 PR00312D 9.43 2.636e-33 128-158 PR00312C 15.14 8.839e-33 92-122 PR00312B 15.08 8.941e-33 62-92 PR00312G 11.11 6.657e-32 230-258 PR00312A 11.70 6.914e-27 35-59
981	PF00992	Troponin.	PF00992A 16.67 8.816e-09 414-449
982	PR00299	ALPHA CRYSTALLIN SIGNATURE	PR00299F 13.20 2.367e-09 127-149
983	BL01150	Respiratory-chain NADH dehydrogenase 20 Kd subunit proteins.	BL01150B 17.16 1.000e-40 156-202 BL01150A 14.10 8.200e-39 100-138
986	BL00795	Involucrin proteins.	BL00795C 17.06 7.211e-14 4-49 BL00795C 17.06 1.778e-11 1-46 BL00795C 17.06 3.407e-10 14-59 BL00795C 17.06 7.802e-10 2-47 BL00795C 17.06 8.640e-10 19-64 BL00795C 17.06 7.400e-09 11-56 BL00795C 17.06 7.800e-09 3-48
987	BL00939	Ribosomal protein L1e proteins.	BL00939F 17.27 5.393e-09 810-840
988	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-11 525-541
989	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e-11 497-513
994	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.500e-25 146-189
997	BL01304	ubiH/COQ6 monooxygenase family proteins.	BL01304A 8.05 3.893e-11 65-79
998	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e-09 22-39
1000	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926C 16.07 1.750e-24 73-94 PR00926D 10.53 3.250e-23 126-145 PR00926F 17.75 6.211e-23 217-240 PR00926E 11.70 6.625e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			20 174-193 PR00926B 16.07 2.125e-18 24-39 PR00926A 10.41 1.000e- 15 11-25 PR00926F 17.75 5.565e-09 120- 143
1005	BL00406	Actins proteins.	BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406D 12.58 3.700e- 40 270-325 BL00406E 8.44 7.375e-38 327-377 BL00406A 9.95 3.348e- 29 11-46
1006	BL00406	Actins proteins.	BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406E 8.44 1.000e- 35 248-298 BL00406A 9.95 3.348e-29 11-46
1007	PR00304	TAILESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304D 11.04 8.714e- 22 384-407 PR00304C 8.69 4.667e-20 98-118 PR00304B 11.60 7.577e- 19 68-87 PR00304A 9.20 3.382e-16 46-63 PR00304E 7.79 6.870e- 13 418-431
1009	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.929e- 32 9-48
1011	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.929e- 32 68-107
1012	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.143e- 10 64-73
1016	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168H 12.08 1.000e- 11 174-194
1018	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 1.391e- 32 261-302 PD00930A 25.62 9.550e-22 157- 183
1022	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.	BL00175A 15.42 5.179e- 12 6-26 BL00175C 23.75 8.062e-10 79-111
1025	PR00305	14-3-3 PROTEIN ZETA SIGNATURE	PR00305D 16.34 1.439e- 10 158-185
1026	BL00353	HMG1/2 proteins.	BL00353B 11.47 2.436e- 18 238-288 BL00353C 14.83 8.844e-11 288- 335
1028	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.310e- 33 43-91
1033	PF00580	UvrD/REP helicase.	PF00580A 13.37 4.720e- 09 111-133
1034	PR00413	HALOACID DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE	PR00413E 15.78 3.429e- 09 154-171
1037	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.657e- 09 5-44
1038	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 4.259e- 11 55-82
1039	BL00299	Ubiquitin domain proteins.	BL00299 28.84 9.036e- 09 17-69
1040	PR00970	ARGININE ADP- RIBOSYLTRANSFERASE	PR00970A 17.73 6.143e- 20 56-78 PR00970D

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	9.96 2.154e-18 154-171 PR00970F 12.30 1.000e-16 224-241 PR00970G 9.97 9.229e-15 242-258 PR00970B 16.37 1.290e-13 86-105 PR00970C 11.05 1.643e-11 115-130 PR00970E 11.23 9.820e-11 202-218
1042	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 243-254
1043	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.786e-13 114-128 PR00048A 10.52 1.000e-09 172-186
1045	BL00615	C-type lectin domain proteins.	BL00615A 16.68 1.720e-11 218-236 BL00615B 12.25 1.857e-10 317-331
1046	BL01092	Adenylate cyclases class-I proteins.	BL01092N 13.54 8.924e-10 3-40
1047	BL01216	ATP-citrate lyase / succinyl-CoA ligases family proteins.	BL01216D 21.75 4.316e-28 314-344 BL01216A 13.91 1.000e-10 97-112
1049	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 7.618e-12 102-136
1050	BL01073	Ribosomal protein L24e proteins.	BL01073 24.30 1.000e-40 12-62
1054	BL00571	Amidases proteins.	BL00571 25.69 5.875e-31 160-212
1055	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 5.235e-11 98-117 BL00030B 7.03 4.316e-09 137-147
1058	BL00223	Annexins repeat proteins domain proteins.	BL00223C 24.79 8.754e-23 262-317 BL00223A 15.59 9.478e-14 46-80 BL00223A 15.59 5.557e-11 118-152
1060	BL00027	'Homeobox' domain proteins.	BL00027 26.43 3.455e-35 158-201
1064	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 6.211e-13 280-296
1065	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.000e-09 115-129 PR00019B 11.36 3.880e-09 87-101
1066	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 4.600e-16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e-14 172-191 PR00326D 19.09 1.257e-13 217-236
1071	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 8.518e-11 164-197
1072	PF00856	SET domain proteins.	PF00856A 26.14 5.976e-09 350-387
1075	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009D 14.19 4.300e-20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e-11 159-175
1077	PR00724	CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE	PR00724A 10.91 1.000e-08 366-379
1078	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 1.000e-12 170-195 BL00215A 15.82 7.529e-10 79-104
1079	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.316e-09

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins proteins.	298-309
1081	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e-10 23-57
1094	BL00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 3.204e-18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e-12 162-182 BL00460C 14.35 5.500e-09 133-156
1095	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e-22 67-105 PD02811B 17.07 2.263e-21 118-151 PD02811C 13.25 5.696e-13 154-167
1096	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e-22 60-98 PD02811B 17.07 2.263e-21 111-144 PD02811C 13.25 5.696e-13 147-160
1097	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.143e-09 200-216
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9.229e-13 111-147
1109	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.077e-10 15-37 PR00449E 13.50 1.857e-09 185-208 PR00449D 10.79 8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.737e-20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e-10 63-85
1116	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1117	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1120	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 4.857e-10 290-306
1123	PR00412	EPOXIDE HYDROLASE SIGNATURE	PR00412F 18.76 9.526e-12 301-324
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e-09 87-101
1129	BL00170	Cyclophilin-type peptidyl-prolyl cis-trans isomerase signatur.	BL00170C 18.49 3.077e-33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e-15 10-37
1131	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.304e-15 29-46 BL00636B 15.11 1.360e-14 59-80
1132	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1133	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1136	BL00990	Clathrin adaptor complexes medium chain proteins.	BL00990C 18.78 4.176e-38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e-27 157-187 BL00990D 16.13 5.320e-18 403-422
1137	PR00314	CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE	PR00314B 15.68 8.000e-34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			32 159-188 PR00314A 14.53 1.281e-22 13-34
1139	BL011115	GTP-binding nuclear protein ran proteins.	BL011115A 10.22 6.364e-13 13-57
1141	BL00107	Protein kinases ATP-binding region proteins.	BL00107A 18.39 4.000e-19 451-482 BL00107B 13.31 3.077e-12 519-535
1148	PR00685	TRANSCRIPTION INITIATION FACTOR IIB SIGNATURE	PR00685A 13.62 4.676e-09 21-42
1155	PD01652	RECEPTOR CELL NK GLYCOPROTEIN IMMUNOGLOB.	PD01652B 8.50 9.396e-10 522-574 PD01652B 8.50 9.463e-10 740-792
1157	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894A 21.96 7.873e-28 81-127 PD02894B 13.93 1.188e-27 178-211
1159	BL00623	GMC oxidoreductases proteins.	BL00623E 15.00 3.531e-20 391-414 BL00623C 10.86 4.240e-20 155-176
1161	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA-.	PD01937A 6.68 3.475e-09 330-341
1162	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA-.	PD01937A 6.68 3.475e-09 221-232
1163	PR00624	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e-10 214-239 PR00624D 11.94 1.961e-09 312-337
1167	BL00226	Intermediate filaments proteins.	BL00226B 23.86 7.384e-09 302-350
1177	BL01032	Protein phosphatase 2C proteins.	BL01032G 8.33 1.422e-10 34-48
1178	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 1.794e-10 205-220 PR00320C 13.01 7.840e-10 205-220 PR00320B 12.19 8.457e-10 35-50 PR00320A 16.74 7.146e-09 35-50 PR00320B 12.19 9.100e-09 79-94
1180	PR00454	ETS DOMAIN SIGNATURE	PR00454D 10.89 4.150e-19 765-784
1181	BL00291	Prion protein.	BL00291A 4.49 8.962e-11 152-187
1184	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 4.103e-18 1089-1113
1185	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.553e-13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e-11 104-129
1187	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 2.761e-10 77-93
1188	BL00878	Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment si.	BL00878B 10.95 6.000e-16 189-204 BL00878C 17.74 8.435e-15 225-245 BL00878F 19.67 3.625e-13 379-402 BL00878D 16.56 1.621e-09 270-289
1191	PD02939	PROTEIN GLUTATHIONE SYNTHETASE SY.	PD02939B 10.10 2.723e-12 203-220 PD02939C 20.01 1.000e-11 224-252
1193	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e-28 72-101 PR00345B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			8.54 7.652e-28 149-174 PR00345C 4.54 9.100e-28 101-125 PR00345D 10.97 1.964e-24 125-149 PR00345A 13.46 5.645e-16 43-62
1194	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e-28 108-137 PR00345E 8.54 7.652e-28 185-210 PR00345C 4.54 9.100e-28 137-161 PR00345D 10.97 1.964e-24 161-185 PR00345A 13.46 5.645e-16 79-98
1195	PF00995	Sec1 family.	PF00995B 17.37 1.120e-13 224-264
1196	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 6.738e-11 15-47
1197	BL01298	Dihydrodipicolinate reductase proteins.	BL01298A 13.90 5.959e-09 51-73
1203	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 1.000e-14 152-190
1204	PR00118	BETA-LACTAMASE CLASS A SIGNATURE	PR00118F 16.42 9.386e-09 213-229
1206	BL01183	ubiE/COQ5 methyltransferase family proteins.	BL01183B 21.31 1.429e-37 184-229 BL01183D 27.71 8.535e-27 264-307 BL01183A 13.25 3.250e-23 51-73 BL01183C 10.77 5.295e-09 246-258
1208	BL00979	G-protein coupled receptors family 3 proteins.	BL00979L 20.63 2.485e-09 105-146
1209	PF00023	Ank repeat proteins.	PF00023A 16.03 4.857e-11 49-65 PF00023B 14.20 1.818e-09 45-55
1212	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.750e-14 227-241 PR00048A 10.52 4.316e-11 199-213
1213	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 1.720e-10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e-09 44-64
1216	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.598e-10 179-230
1219	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 5.348e-11 249-264
1222	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.231e-15 295-308 PD00066 13.92 7.231e-15 406-419 PD00066 13.92 2.286e-12 378-391 PD00066 13.92 7.857e-12 434-447 PD00066 13.92 3.348e-11 350-363
1223	BL50058	G-protein gamma subunit profile.	BL50058 27.23 1.000e-40 13-61
1226	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 8.439e-09 279-330
1227	BL00437	Catalase proximal heme-ligand proteins.	BL00437A 18.82 1.000e-40 49-101 BL00437B 16.28 1.000e-40 114-168 BL00437C 21.86

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			1.000e-40 190-239 BL00437D 25.72 1.000e-40 248-301 BL00437E 23.95 1.000e-40 327-379
1230	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 8.297e-10 6-60
1231	PR00735	GLYCOSYL HYDROLASE FAMILY 8 SIGNATURE	PR00735A 11.19 6.857e-09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e-10 158-176
1233	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e-10 158-176
1235	BL00866	Carbamoyl-phosphate synthase subdomain proteins.	BL00866B 36.29 2.776e-09 75-121
1237	BL00027	'Homeobox' domain proteins.	BL00027 26.43 1.818e-21 36-79
1243	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 1.184e-11 10-25
1246	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168L 9.47 2.837e-10 31-46 PD01168L 9.47 4.490e-10 174-189 PD01168L 9.47 7.612e-10 183-198
1249	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.800e-10 183-196
1254	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 2.440e-36 96-144
1255	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e-11 8-52
1256	BL00373	Phosphoribosylglycinamide formyltransferase proteins.	BL00373C 10.35 3.348e-12 143-156
1258	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 3.217e-10 174-193
1259	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 8.286e-10 31-40
1261	PR00070	DIHYDROFOLATE REDUCTASE SIGNATURE	PR00070D 11.63 1.000e-15 112-127 PR00070C 13.09 9.500e-15 51-63 PR00070A 12.92 5.500e-12 16-27
1262	BL00462	Gamma-glutamyltranspeptidase proteins.	BL00462A 20.89 6.438e-24 140-183 BL00462B 17.88 5.500e-20 230-267 BL00462C 27.41 2.023e-11 292-347
1263	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038B 16.97 9.455e-11 62-83
1264	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e-12 17-61
1266	PR00837	ALLERGEN V5/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 2.714e-18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e-12 201-215
1269	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 9.308e-22 40-63 PR00449B 13.50 1.000e-16 137-160 PR00449D 10.79 3.520e-11 102-116
1270	BL00276	Channel forming collicins proteins.	BL00276A 8.87 1.500e-09 17-29
1275	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327C 15.47 9.769e-09 228-243
1276	PR00412	EPOXIDE HYDROLASE	PR00412B 12.59 7.894e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	12 119-135 PR00412C 11.30 1.857e-11 165- 179 PR00412A 13.23 3.400e-11 100-119
1277	PF00756	Putative esterase.	PF00756C 14.12 9.538e- 10 127-157
1279	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 9.325e- 13 128-145
1280	BL01220	Phosphatidylethanolamine -binding protein family proteins.	BL01220C 14.75 9.348e- 15 248-276
1285	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 2.286e- 10 33-42
1287	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.182e- 11 288-343
1292	PR00802	SERUM ALBUMIN FAMILY SIGNATURE	PR00802B 16.51 1.610e- 10 81-105
1297	PR00716	M-PHASE INDUCER PHOSPHATASE SIGNATURE	PR00716C 17.65 5.696e- 09 23-44
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e- 14 268-283
1301	BL00127	Pancreatic ribonuclease family proteins.	BL00127C 31.49 3.571e- 28 82-126 BL00127B 26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR SIGNATURE	PR00637E 11.27 4.250e- 09 290-306
1307	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.500e- 17 13-38 BL00215A 15.82 1.000e-16 226- 251 BL00215A 15.82 2.658e-13 107-132
1308	PR00898	VASOPRESSIN V2 RECEPTOR SIGNATURE	PR00898H 11.34 4.682e- 09 552-572
1309	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301B 5.49 2.731e- 09 390-401
1310	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 9.654e- 13 73-89 BL00983B 8.19 3.132e-09 12-22
1313	BL00194	Thioredoxin family proteins.	BL00194 12.16 1.900e- 11 15-28
1314	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 8.969e- 10 53-97
1316	BL00134	Serine proteases, trypsin family, histidine proteins.	BL00134A 11.96 9.325e- 13 128-145
1320	BL00783	Ribosomal protein L13 proteins.	BL00783C 22.43 6.559e- 24 87-117 BL00783A 14.55 1.600e-19 8-33 BL00783B 12.76 3.500e- 12 74-86
1327	PF00514	Armadillo/beta-catenin- like repeat proteins.	PF00514A 31.30 7.268e- 11 82-120
1329	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 6.294e- 11 129-148 BL00030B 7.03 4.789e-09 168-178
1331	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 7.239e- 09 25-43
1332	PR00161	NICKEL-DEPENDENT HYDROGENASE/B-TYPE CYTOCHROME SIGNATURE	PR00161C 9.51 4.930e- 09 317-337
1333	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 6.769e- 33 10-49
1336	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 2.200e- 09 262-281
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PHOSPHATASE SIGNATURE	09 211-230
1340	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860A 5.46 5.034e-13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e-16 46-71
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e-21 383-422
1344	DM00099	4 kw ASSR REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.313e-09 417-427
1345	BL00923	Aspartate and glutamate racemases proteins.	BL00923B 11.41 5.935e-10 135-146
1348	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 7.231e-13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 3.571e-32 416-445 PR00193C 12.60 6.318e-31 179-207 PR00193B 11.69 3.571e-24 133-159 PR00193E 19.47 9.069e-22 470-499 PR00193A 15.41 1.783e-20 77-97
1352	PR00447	NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN SIGNATURE	PR00447E 9.73 1.554e-15 299-319 PR00447D 13.54 3.408e-15 200-224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e-10 353-373
1353	BL00303	S-100/ICaBP type calcium binding protein.	BL00303A 21.77 6.667e-26 45-82 BL00303B 26.15 1.000e-24 93-130
1355	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 5.950e-29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e-18 225-249 BL00039B 19.19 3.182e-14 141-167
1357	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 2.216e-12 84-101 PF00615C 10.06 8.412e-12 162-176
1360	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.234e-29 10-49
1361	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925A 5.47 5.091e-18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e-12 53-64 PR00925D 6.56 1.857e-10 76-87
1362	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e-30 136-171 BL01272C 11.68 3.314e-25 249-274 BL01272A 6.49 1.231e-18 99-117
1363	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e-30 113-148 BL01272C 11.68 3.314e-25 226-251 BL01272A 6.49 1.231e-18 76-94
1364	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e-09 167-177
1368	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.592e-09 76-96
1370	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 1.794e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			10 1-19
1371	BL00242	Integrins alpha chain proteins.	BL00242B 8.13 8.615e-09 469-479
1372	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625B 13.48 7.353e-19 46-67 PR00625A 12.84 1.391e-16 14-34
1373	BL00434	HSF-type DNA-binding domain proteins.	BL00434C 23.85 3.778e-09 90-130
1374	PR00962	LETHAL(2) GIANT LARVAE PROTEIN SIGNATURE	PR00962C 8.00 6.337e-09 505-526
1375	PD02475	MUCIN EPITHELIAL TUMOR-ASSOCIATE.	PD02475A 23.18 8.552e-10 1111-1150
1376	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.571e-32 24-63
1380	BL00194	Thioredoxin family proteins.	BL00194 12.16 8.333e-12 48-61
1381	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 1.458e-15 1123-1136
1383	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10 243-254
1384	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10 271-282
1385	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 6.203e-10 95-132
1386	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.042e-09 1574-1628
1387	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e-11 52-61
1389	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.600e-30 10-49
1390	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 3.512e-31 32-71
1392	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 9.723e-10 127-137
1393	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.625e-25 88-110 PR00380D 9.93 2.406e-20 304-326 PR00380B 12.64 4.414e-16 208-226 PR00380C 13.18 6.538e-16 243-262
1394	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e-14 462-475 PD00066 13.92 8.800e-14 348-361 PD00066 13.92 9.571e-12 405-418 PD00066 13.92 6.087e-11 490-503 PD00066 13.92 8.043e-11 320-333
1398	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 6.786e-32 10-49
1400	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.038e-09 270-290
1406	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930A 25.62 7.324e-15 363-389
1407	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.500e-10 457-476
1408	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.550e-11 179-193 PR00019A 11.19 8.826e-10 228-242 PR00019B 11.36 1.360e-09 199-213 PR00019B 11.36 4.960e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			09 176-190
1409	PR00510	NEBULIN SIGNATURE	PR00510A 9.09 4.150e-12 182-202 PR00510B 12.96 8.767e-12 210-230 PR00510F 9.88 8.172e-10 58-75 PR00510D 9.21 2.367e-09 251-267
1410	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.696e-09 31-44
1412	BL00358	Ribosomal protein L5 proteins.	BL00358B 22.76 1.000e-40 57-103 BL00358C 13.75 6.087e-14 122-136 BL00358D 14.26 5.500e-13 143-158 BL00358A 13.06 1.931e-11 33-44
1414	BL00282	Kazal serine protease inhibitors family proteins.	BL00282 16.88 7.338e-10 511-534
1415	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 4.300e-29 40-77
1417	PR00681	RIBOSOMAL PROTEIN S1 SIGNATURE	PR00681G 12.54 2.149e-09 38-60
1418	DM00973	3 kw RESISTANCE BENOMYL YLLO28W CYCLOHEXIMIDE.	DM00973A 21.17 1.462e-09 171-208
1419	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 1.571e-09 428-443
1420	PD01941	TRANSMEMBRANE COTRANSPORTER SYMP.	PD01941A 14.81 1.000e-40 142-196 PD01941B 15.02 7.049e-30 400-447 PD01941E 15.92 2.475e-20 817-864 PD01941C 19.96 3.118e-19 488-543 PD01941D 27.18 9.614e-18 641-690 PD01941F 28.52 5.382e-15 1038-1093
1422	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 8.043e-12 199-217
1423	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	PR00209B 4.88 6.318e-11 1009-1028
1424	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 8.200e-14 367-386 BL50002A 14.19 9.250e-12 298-317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e-09 244-258
1425	PF00628	PHD-finger.	PF00628 15.84 3.045e-12 330-345
1426	PF00628	PHD-finger.	PF00628 15.84 3.045e-12 377-392
1427	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.114e-16 281-299 PR00405A 17.71 4.306e-14 262-282
1428	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 5.219e-34 147-193
1429	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 8.920e-10 577-592
1430	PR00378	INOSITOL PHOSPHATASE SIGNATURE	PR00378D 16.86 7.563e-12 295-314 PR00378B 13.80 8.650e-10 166-186
1431	PR00928	GRAVES DISEASE CARRIER	PR00928B 13.53 3.769e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		PROTEIN SIGNATURE	10 103-124
1433	BL01113	Clq domain proteins.	BL01113B 18.26 7.049e-15 14-50 BL01113C 13.18 7.000e-12 82-102
1434	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 7.983e-10 135-150
1436	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 1.000e-12 84-103
1438	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.500e-09 250-268 BL00290A 20.89 4.000e-09 188-211
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-09 38-52
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-09 88-102
1444	BL00422	Granins proteins.	BL00422D 19.48 1.000e-08 114-138
1445	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e-40 73-123 PD01841B 14.35 1.000e-40 144-185 PD01841D 17.87 1.000e-40 206-258 PD01841F 13.36 1.000e-40 296-345 PD01841G 24.26 1.000e-40 349-403 PD01841I 23.00 1.000e-40 494-536 PD01841J 14.94 1.000e-40 895-932 PD01841L 18.42 1.000e-40 1083-1125 PD01841E 18.60 9.719e-38 258-296 PD01841K 14.81 1.000e-35 1041-1071 PD01841H 21.30 3.189e-31 435-472 PD01841C 13.78 1.000e-25 185-206 PD01841M 10.82 1.250e-20 1175-1194
1446	PF00816	H-NS histone family.	PF00816B 13.84 8.875e-09 190-220
1447	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 2.080e-09 402-416
1448	DM00315	072 RIBONUCLEASE INHIBITOR.	DM00315D 18.40 7.393e-09 23-67
1451	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 2.800e-10 94-104
1454	DM01688	2 POLY-IG RECEPTOR.	DM01688D 13.44 7.146e-09 382-405
1455	PF00777	Sialyltransferase family.	PF00777C 18.60 2.929e-22 4-59
1457	BL00927	Trehalase proteins.	BL00927C 10.83 8.085e-09 42-53
1460	BL00545	Aldose 1-epimerase proteins.	BL00545C 11.28 7.353e-17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e-09 140-153
1466	PR00097	ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE	PR00097C 9.42 9.069e-09 233-245
1472	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 5.250e-22 170-195 BL01129C 25.56 9.526e-18 63-106
1473	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e-09 2114-2145
1475	PF00686	Starch binding domain proteins.	PF00686A 13.45 9.100e-09 267-277

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1477	PF00566	Probable rabGAP domain proteins.	PF00566A 12.64 7.333e-10 466-476
1478	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 9.400e-10 43-53
1479	DM00406	GLIADIN.	DM00406 7.73 8.541e-10 292-305
1480	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.385e-15 69-87 BL00290A 20.89 5.091e-11 12-35
1481	PR00150	PHOSPHOENOLPYRUVATE CARBOXYLASE SIGNATURE	PR00150F 10.45 9.039e-09 21-51
1482	PF00780	Domain found in NIK1-like kinases, mouse citron and yeast ROM.	PF00780I 14.69 4.825e-09 107-137
1483	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.153e-09 108-162
1485	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 5.909e-25 17-56
1486	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.529e-09 34-50
1488	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 9.586e-10 116-162
1490	BL00166	Enoyl-CoA hydratase/isomerase proteins.	BL00166D 22.87 2.607e-24 190-226 BL00166C 18.93 5.500e-14 140-167 BL00166B 16.92 9.357e-11 93-115
1491	BL00452	Guanylate cyclases proteins.	BL00452D 28.59 3.700e-31 63-106 BL00452E 11.92 3.045e-13 115-131
1492	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 3.667e-09 532-546
1497	BL00107	Protein kinases ATP-binding region proteins.	BL00107B 13.31 1.000e-11 384-400 BL00107A 18.39 5.345e-11 322-353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e-10 107-117
1502	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e-24 112-155
1503	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e-24 112-155
1505	BL01177	Anaphylatoxin domain proteins.	BL01177E 20.64 5.800e-24 448-475 BL01177C 17.39 5.333e-19 402-421 BL01177B 13.61 7.840e-16 155-171 BL01177D 17.50 1.900e-15 427-445
1506	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 5.500e-14 311-336 BL00972A 11.93 7.429e-14 48-66 BL00972E 20.72 8.759e-10 341-363
1512	BL00523	Sulfatases proteins.	BL00523E 19.27 4.536e-22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e-09 159-170 BL00523G 9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 7.045e-14 168-218
1518	BL00600	Aminotransferases class-III pyridoxal-phosphate attachment si.	BL00600A 17.98 6.143e-19 98-122 BL00600E 16.43 1.771e-17 302-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			331 BL00600G 12.43 9.625e-17 377-396 BL00600B 19.60 5.091e- 15 160-186 BL00600C 16.18 6.040e-12 190- 206 BL00600F 8.77 1.000e-11 343-356 BL00600D 8.71 1.000e- 10 281-295
1523	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 9.600e- 18 41-82
1528	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 4.774e- 11 192-207 PR00320B 12.19 8.839e-11 272- 287 PR00320B 12.19 9.743e-10 106-121 PR00320A 16.74 1.878e- 09 192-207 PR00320A 16.74 2.317e-09 106- 121 PR00320A 16.74 8.683e-09 272-287 PR00320C 13.01 8.800e- 09 106-121
1538	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 4.508e- 15 171-184
1539	PF00781	Diacylglycerol kinase catalytic domain proteins (presumed).	PF00781D 11.11 7.593e- 10 103-127
1540	PR00965	OCULAR ALBINISM TYPE 1 PROTEIN SIGNATURE	PR00965H 10.73 1.231e- 29 312-334 PR00965E 12.93 5.846e-29 172- 195 PR00965F 5.98 1.123e-28 209-231 PR00965C 15.04 1.000e- 27 131-151 PR00965D 5.84 1.000e-27 150-170 PR00965G 8.52 2.440e- 27 258-279 PR00965B 4.80 8.650e-26 88-109 PR00965A 12.52 1.000e- 25 35-55 PR00965I 3.91 6.442e-25 385-406
1541	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 9.719e- 17 163-207
1543	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699C 24.84 1.000e- 40 599-646 PD02699A 8.91 2.286e-34 219-248 PD02699B 18.28 6.143e- 21 485-509
1544	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.857e- 10 182-197 PR00049D 0.00 7.102e-09 67-82
1547	BL00951	ER lumen protein retaining receptor proteins.	BL00951C 19.35 1.000e- 40 93-142 BL00951D 13.94 8.714e-40 142- 177 BL00951A 15.10 1.000e-38 2-38 BL00951B 14.23 6.250e- 33 38-69
1548	BL00536	Ubiquitin-activating enzyme proteins.	BL00536F 13.65 8.920e- 30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536E 16.94 4.696e- 18 248-279
1549	PR00139	ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE	PR00139C 11.72 9.679e- 09 550-569
1553	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 5.119e- 09 58-73

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1556	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 6.276e-13 67-105
1557	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e-12 107-132
1558	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e-12 107-132
1559	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e-12 107-132
1562	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 6.600e-18 412-436 BL00522B 27.30 1.738e-16 364-410 BL00522A 25.52 6.000e-16 279-326 BL00522E 19.63 6.123e-14 502-532 BL00522F 14.90 2.385e-13 551-575
1563	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 1.947e-11 46-59
1564	BL00299	Ubiquitin domain proteins.	BL00299 28.84 2.823e-10 324-376
1566	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 8.594e-17 184-228 BL01013C 9.97 4.906e-12 14-24
1567	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.400e-10 378-389 BL00678 9.67 5.800e-10 418-429 BL00678 9.67 8.800e-10 295-306
1570	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 5.235e-17 297-313 BL00479A 19.86 6.625e-15 271-294 BL00479A 19.86 2.667e-14 147-170 BL00479B 12.57 6.294e-12 173-189
1576	PR00665	OXYTOCIN RECEPTOR SIGNATURE	PR00665G 12.36 4.673e-24 364-384 PR00665D 9.93 1.200e-22 138-155 PR00665F 11.73 4.000e-22 337-354 PR00665C 5.89 1.000e-20 65-80 PR00665B 5.29 4.337e-19 24-39 PR00665E 5.60 2.929e-15 246-260 PR00665A 5.99 5.622e-15 11-25
1577	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 9.308e-10 127-137
1579	BL00524	Somatomedin B domain proteins.	BL00524A 9.65 6.776e-14 52-73
1580	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894B 13.93 6.959e-16 182-215 PD02894A 21.96 2.125e-10 57-103
1581	BL00411	Kinesin motor domain proteins.	BL00411C 15.04 5.292e-12 32-54 BL00411H 15.66 4.441e-11 245-276
1582	PR00604	CLASS IA AND IB CYTOCHROME C SIGNATURE	PR00604A 11.13 2.440e-09 79-87
1584	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 1.000e-10 225-238
1585	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551C 14.62 9.455e-11 125-145
1586	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354S 11.61 7.750e-09 474-495

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1587	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955e-33 180-210 PR00072A 12.75 6.040e-25 120-145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e-22 276-295 PR00072E 10.54 1.360e-19 301-318 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e-15 332-349
1589	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191H 15.64 1.537e-22 61-113 BL00191K 17.38 9.027e-12 398-442
1590	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.716e-13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUP1 CHROMOSOME.	DM00517B 10.96 6.625e-16 1175-1193 DM00517A 8.21 1.000e-11 1015-1026
1592	BL00037	Myb DNA-binding domain proteins repeat proteins proteins.	BL00037B 15.92 3.250e-27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e-12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e-10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e-09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e-11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 5.500e-09 980-995
1600	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e-10 30-39
1602	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.402e-10 136-187
1605	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.571e-10 44-57
1607	BL00252	Interferon alpha, beta and delta family proteins.	BL00252A 18.49 6.657e-23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e-08 61-94
1611	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904C 8.98 7.353e-10 91-125 BL00904D 1.47 6.018e-09 127-168
1612	PF00168	C2 domain proteins.	PF00168C 27.49 3.250e-09 365-391
1613	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.051e-09 932-983 BL00412D 16.54 7.153e-09 933-984
1614	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559I 13.63 3.531e-25 54-83 BL00559K 13.17 2.957e-18 197-224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e-16 266-284
1615	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 3.025e-22 500-541 PD01427A 19.94 8.773e-18 439-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			472
1616	BL00115	Eukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115Z 3.12 7.485e-09 152-201 BL00115Z 3.12 9.603e-09 145-194
1617	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 7.750e-32 51-88 BL00303A 21.77 1.947e-31 4-41
1618	BL01254	Fetuin family proteins.	BL01254F 10.02 8.754e-09 137-147
1619	PD01888	PEPTIDE REDUCTASE PROTEIN METHI.	PD01888B 25.10 1.000e-40 47-97 PD01888C 21.56 7.000e-30 125-155 PD01888A 12.84 8.800e-15 7-23
1621	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239E 1.58 3.455e-09 692-704 PR00239E 1.58 4.580e-09 697-709 PR00239E 1.58 4.580e-09 702-714 PR00239E 1.58 5.193e-09 703-715
1622	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860B 7.04 1.900e-18 27-41 PR00860C 9.61 1.474e-14 41-51 PR00860A 5.46 1.720e-14 5-18
1624	PR00784	MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN SIGNATURE	PR00784D 15.86 8.027e-11 77-95
1626	BL00325	Actin-depolymerizing proteins.	BL00325B 21.66 1.000e-40 93-139 BL00325A 24.83 6.786e-23 61-93
1631	BL00064	L-lactate dehydrogenase proteins.	BL00064B 23.57 1.000e-40 82-130 BL00064C 17.28 1.000e-40 137-182 BL00064E 27.20 1.000e-40 223-275 BL00064F 25.14 7.882e-36 286-331 BL00064A 21.16 1.000e-33 22-60 BL00064D 14.19 6.500e-31 182-212
1632	PR00063	RIBOSOMAL PROTEIN L27 SIGNATURE	PR00063B 15.24 9.700e-11 59-84 PR00063A 11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C-TERMINAL TAIL SIGNATURE	PR00239D 0.00 1.105e-11 36-49 PR00239C 3.51 2.538e-09 37-45
1636	BL01210	Caveolins proteins.	BL01210B 13.92 9.531e-10 133-183
1637	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 5.388e-11 11-43
1639	BL01183	ubiE/COQ5 methyltransferase family proteins.	BL01183B 21.31 8.144e-12 132-177
1640	PR00015	GRAM-POSITIVE COCCUS SURFACE PROTEIN ANCHOR SIGNATURE	PR00015B 9.84 8.468e-10 128-149
1641	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 5.935e-11 364-379 PR00320A 16.74 7.828e-11 364-379 PR00320C 13.01 2.800e-10 279-294 PR00320C 13.01 2.800e-10 364-379 PR00320B 12.19 5.114e-10 279-294 PR00320A 16.74 1.659e-09 279-294

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00320A 16.74 2.098e-09 229-244
1642	PF00023	Ank repeat proteins.	PF00023A 16.03 6.464e-09 114-130
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.806e-11 74-94
1644	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e-17 56-89
1646	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.270e-21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e-16 332-351 PR00380B 12.64 6.657e-15 292-310
1647	DM01242	3 THREONINE--TRNA LIGASE.	DM01242C 17.15 9.791e-37 340-381 DM01242E 23.00 5.071e-31 463-505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e-18 265-314 DM01242F 10.61 7.618e-14 526-540
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e-10 13-34
1651	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.720e-11 431-485
1652	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933A 17.50 4.673e-12 11-35 BL00933E 13.80 9.217e-09 456-472
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e-10 70-115
1654	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e-17 302-334
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e-17 282-314
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e-16 607-630
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.938e-11 114-136
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e-10 442-455
1659	BL00972	Ubiquitin carboxyl-terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e-12 376-401 BL00972E 20.72 5.629e-09 446-468
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e-15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00105A 10.36 4.900e-13 1140-1157 PR00105B 12.32 2.800e-12 1259-1274 PR00105C 10.86 1.000e-10 1305-1319
1662	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e-33 3119-3163
1663	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e-23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e-19 51-68 PR00319B 11.47 8.200e-19 70-85

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1664	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.050e-10 489-502
1667	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 8.500e-38 7-46
1669	BL01153	NOL1/NOP2/sun family proteins.	BL01153D 19.69 1.188e-17 115-141 BL01153C 13.67 8.977e-15 66-80 BL01153B 20.52 1.885e-10 13-37
1671	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 3.100e-10 1146-1169
1672	BL00598	Chromo domain proteins.	BL00598 14.45 8.500e-20 27-49
1673	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.329e-09 686-707
1674	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.580e-11 343-358 PR00049D 0.00 1.286e-10 342-357
1676	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747H 12.76 8.636e-19 427-448 PR00747G 14.50 2.286e-18 368-393 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747D 15.23 8.759e-17 163-183 PR00747E 15.13 8.244e-15 254-272 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 311-328
1677	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747H 12.76 8.636e-19 309-330 PR00747G 14.50 2.286e-18 250-275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 193-210
1680	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331
1681	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 329-340 BL00678 9.67 6.684e-09 243-254
1683	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 1.346e-13 389-410
1685	PR00646	RDC1 ORPHAN RECEPTOR SIGNATURE	PR00646H 6.32 4.188e-09 755-771
1690	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e-09 75-129
1691	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 7.281e-10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e-10 420-435
1692	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 7.281e-10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e-10 489-504
1693	BL00674	AAA-protein family proteins.	BL00674C 22.60 8.043e-24 274-317 BL00674B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			4.46 4.000e-23 241-263 BL00674D 23.41 8.560e-18 338-385 BL00674E 15.24 1.720e-15 414-434
1697	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 4.388e-10 427-447
1698	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PR00466C 10.17 3.443e-13 187-208 PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e-09 498-517
1699	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e-12 283-300 BL00028 16.07 3.769e-11 255-272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e-11 227-244 BL00028 16.07 1.600e-10 199-216
1700	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 3.348e-15 62-102 BL01019B 19.49 4.000e-15 107-162
1703	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 2.484e-12 200-239
1707	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.558e-14 134-153
1710	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.565e-10 116-130 PR00019B 11.36 4.600e-09 113-127 PR00019B 11.36 7.120e-09 204-218
1711	BL01159	WW/resp5/WWP domain proteins.	BL01159 13.85 6.523e-11 232-247 BL01159 13.85 5.408e-10 613-628
1712	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e-10 187-203
1713	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e-11 230-241
1714	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e-11 230-241
1715	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 7.129e-09 7-51
1718	BL00353	HMG1/2 proteins.	BL00353C 14.83 6.018e-10 136-183 BL00353B 11.47 8.866e-09 86-136
1719	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.408e-09 432-483
1721	BL00038	Myc-type, 'helix-loop-helix' dimerization domain proteins.	BL00038B 16.97 8.448e-12 79-100 BL00038A 13.61 4.000e-11 52-68
1723	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567C 9.17 8.500e-09 418-428
1724	BL01279	Protein-L-isoaspartate (D-aspartate) O-methyltransferase signa.	BL01279A 24.27 5.663e-12 233-281
1728	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.059e-11 73-86 BL00018 7.41 4.176e-11 157-170
1730	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 1.089e-09 17-61

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1731	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e-10 296-350
1732	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e-10 316-370
1733	PF00850	Histone deacetylase family.	PF00850F 15.70 4.349e-22 246-279 PF00850D 14.76 6.850e-20 177-201 PF00850E 8.88 8.691e-18 209-235 PF00850G 22.75 4.098e-14 281-323
1734	BL00354	HMG-I and HMG-Y DNA-binding domain proteins (Ahook).	BL00354C 6.61 5.932e-09 292-307
1735	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.263e-10 492-502
1743	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e-11 5-27 PR00449D 10.79 2.241e-10 109-123 PR00449E 13.50 9.289e-10 144-167
1744	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e-11 5-27 PR00449D 10.79 2.241e-10 109-123 PR00449E 13.50 9.289e-10 144-167
1745	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 8.297e-15 136-160
1746	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.727e-11 45-57 PR00081E 17.54 3.935e-10 150-168
1747	BL00439	Acyltransferases ChoActase / COT / CPT family proteins.	BL00439H 18.24 8.435e-14 65-91 BL00439G 13.40 2.895e-12 3-14
1749	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 7.158e-11 4-20
1751	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e-14 33-46 PD00066 13.92 1.000e-13 89-102 PD00066 13.92 7.000e-13 61-74 PD00066 13.92 6.571e-12 117-130
1753	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 6.516e-18 33-77
1754	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.393e-09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e-09 287-318
1756	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU.	PD01066 19.43 9.750e-35 10-49
1758	DM00406	GLIADIN.	DM00406 7.73 7.600e-09 653-666
1762	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 4.529e-09 224-278
1765	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 5.950e-11 146-167
1775	PF00023	Ank repeat proteins.	PF00023A 16.03 3.077e-14 523-539
1776	BL00942	glpT family of transporters proteins.	BL00942F 15.07 4.343e-10 371-389 BL00942B 20.36 8.040e-09 94-137
1777	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.373e-09 279-312

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e-20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e-11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e-18 611-655 BL01013A 25.14 2.881e-15 344-380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e-12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e-13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e-13 492-515

* results include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence.

TRADOC5:1416223.1(%CRJ01!.DOC)

TABLE 4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
2	ig	Immunoglobulin domain	2.1e-32	109.5
3	pkinase	Eukaryotic protein kinase domain	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
5	fn3	Fibronectin type III domain	0	1097.1
6	fn3	Fibronectin type III domain	0	1035.0
7	fn3	Fibronectin type III domain	0	1090.4
8	fn3	Fibronectin type III domain	0	1097.1
9	TBC	TBC domain	4e-40	146.7
10	p450	Cytochrome P450	9.5e-17	62.0
12	ank	Ank repeat	6e-20	79.7
14	ig	Immunoglobulin domain	1.7e-05	22.7
15	zf-MYND	MYND finger	1.3e-06	35.4
16	zf-MYND	MYND finger	1.3e-06	35.4
17	zf-C2H2	Zinc finger, C2H2 type	1.7e-99	343.9
18	CAP_GLY	CAP-Gly domain	1.2e-25	98.7
20	IMPDH_C	IMP dehydrogenase / GMP reductase C terminus	1.6e-119	410.5
21	IMPDH_C	IMP dehydrogenase / GMP reductase C terminus	4.3e-102	352.6
22	pkinase	Eukaryotic protein kinase domain	2.4e-79	277.0
23	pkinase	Eukaryotic protein kinase domain	8.4e-74	258.6
25	RNA_pol_A	RNA polymerase alpha subunit	0	1077.7
26	Clq	Clq domain	1.9e-10	44.4
27	Ribosomal_L23	Ribosomal protein L23	7.8e-32	111.2
28	Ribosomal_L23	Ribosomal protein L23	1e-29	104.2
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction domain (PTB/PID)	3.8e-59	209.9
35	ig	Immunoglobulin domain	1.4e-13	48.8
36	ig	Immunoglobulin domain	1.4e-13	48.8
40	Kinesin	Kinesin motor domain	6.7e-76	265.6
44	Ets	Ets-domain	1.4e-56	182.1
45	Ets	Ets-domain	1.4e-56	182.1
46	LRR	Leucine Rich Repeat	1.7e-13	58.3
48	zf-C2H2	Zinc finger, C2H2 type	2.3e-162	552.8
49	ITAM	Immunoreceptor tyrosine-based activation mot	1.4e-05	31.9
50	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
51	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
52	ras	Ras family	8.5e-45	162.3
53	PRK	Phosphoribulokinase	2.1e-65	230.7
54	myb_DNA-binding	Myb-like DNA-binding domain	0.096	15.2
55	voltage_CLC	Voltage gated chloride channels	3.3e-186	631.9
56	sugar_tr	Sugar (and other) transporter	0.00015	-64.3
57	TBC	TBC domain	2.2e-37	137.6
58	ank	Ank repeat	5.9e-25	96.3
59	ank	Ank repeat	5.9e-25	96.3
67	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	7.9e-49	175.6
68	C2	C2 domain	7.9e-54	192.2
69	C2	C2 domain	2.3e-54	194.0
70	Kelch	Kelch motif	9.4e-99	341.5
72	ig	Immunoglobulin domain	8.2e-28	94.7
73	pkinase	Eukaryotic protein kinase	8e-69	242.1

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
		domain		
74	pkinase	Eukaryotic protein kinase domain	2.8e-38	140.6
76	zf-C4 Topoisom	Topoisomerase DNA binding C4 zinc fing	5.4e-54	192.8
83	Peptidase_S9	Prolyl oligopeptidase family	4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoglobulin domain	0.0091	14.0
89	WD40	WD domain, G-beta repeat	2.1e-21	84.6
92	laminin G	Laminin G domain	6.1e-27	98.5
93	AMP-binding	AMP-binding enzyme	2.4e-13	-37.2
95	pkinase	Eukaryotic protein kinase domain	1.4e-59	211.4
96	pkinase	Eukaryotic protein kinase domain	2.6e-51	183.9
97	adh_short	short chain dehydrogenase	2e-61	217.5
98	kinesin	Kinesin motor domain	2.2e-86	300.4
101	IRS	PTB domain (IRS-1 type)	5.4e-36	133.0
102	AAA	ATPases associated with various cellular act	6.8e-05	-5.2
104	pkinase	Eukaryotic protein kinase domain	2.7e-73	256.9
106	ras	Ras family	8.3e-24	92.5
107	FYVE	FYVE zinc finger	5.4e-27	100.7
108	Cyt_reductase	FAD/NAD-binding Cytochrome reductase	7.7e-61	215.5
109	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
113	pkinase	Eukaryotic protein kinase domain	4e-88	306.2
116	PH	PH domain	3.1e-11	45.2
117	lipocalin	Lipocalin / cytosolic fatty-acid binding pr	2.4e-14	53.5
118	pkinase	Eukaryotic protein kinase domain	4.5e-20	76.3
120	WD40	WD domain, G-beta repeat	2.4e-14	61.1
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IF5_eIF4_eIF2	eIF4-gamma/eIF5/eIF2-epsilon	1e-32	122.2
124	ig	Immunoglobulin domain	6.5e-08	30.6
127	mito_carr	Mitochondrial carrier proteins	3e-16	58.6
128	PP2C	Protein phosphatase 2C	2.2e-71	250.6
129	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	3.1e-20	80.6
130	pfkB	pfkB family carbohydrate kinase	4.5e-42	137.1
133	ACBP	Acyl CoA binding protein	4.6e-22	86.7
134	rrm	RNA recognition motif.	1.2e-31	118.5
135	IQ	IQ calmodulin-binding motif	2.6e-08	41.0
136	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	9.3e-22	85.7
139	WH2	Wiskott Aldrich syndrome homology region 2	0.0067	23.1
140	zf-C2H2	Zinc finger, C2H2 type	1.7e-82	287.5
141	Peptidase_S26	Signal peptidase I	5.7e-10	35.7
143	arf	ADP-ribosylation factor family	1.2e-39	145.2
146	KRAB	KRAB box	7.3e-30	112.6
148	DUF6	Integral membrane protein DUF6	0.096	8.0
149	PDEase	3'-5'-cyclic nucleotide phosphodiesterase	3.8e-80	231.1
151	S4	S4 domain	1.1e-08	42.3
153	tRNA-synt_1d	tRNA synthetases class I (R)	3.8e-103	356.1
154	Cyt_reductase	FAD/NAD-binding Cytochrome reductase	7.8e-60	212.2
155	ras	Ras family	3.6e-28	107.0
157	actin	Actin	3.8e-26	87.1

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
158	Jacalin	Jacalin-like lectin domain	0.09	-24.9
160	Zn_carbopept	Zinc carboxypeptidase	5e-138	471.9
165	pkinaase	Eukaryotic protein kinase domain	5.1e-67	236.1
167	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-07	27.0
168	Ribosomal_S15	Ribosomal protein S15	1.1e-06	29.0
169	DEAD	DEAD/DEAH box helicase	1e-48	157.0
171	DUF59	Domain of unknown function DUF59	0.07	-17.4
172	pkinaase	Eukaryotic protein kinase domain	3.7e-15	58.6
173	globin	Globin	4.6e-18	67.4
174	WW	WW domain	7.3e-06	32.9
175	ras	Ras family	1e-31	118.8
178	ATP1G1_PLM_MAT8	ATP1G1/PLM/MAT8 family	2.5e-17	71.0
179	zf-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	Clq	Clq domain	8.8e-72	251.9
190	Y_phosphatase	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinaase	Eukaryotic protein kinase domain	6.5e-82	285.6
194	bromodomain	Bromodomain	5.8e-31	111.4
195	PALP	Pyridoxal-phosphate dependent enzyme	2.5e-64	227.1
197	DnaJ	DnaJ domain	1.6e-38	141.4
199	RrnaAD	Ribosomal RNA adenine dimethylases	0.00018	16.9
200	acid_phosphat	Histidine acid phosphatase	2.5e-10	37.2
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	vATP-synt_AC39	ATP synthase (C/AC39) subunit	1.3e-159	543.7
205	vATP-synt_AC39	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	ldl_recept_a	Low-density lipoprotein receptor domain	2.4e-25	97.6
209	ank	Ank repeat	1.4e-19	78.4
210	Rhomboid	Rhomboid family	0.0035	1.2
211	Clq	Clq domain	1.6e-70	247.7
212	UQ_con	Ubiquitin-conjugating enzyme	7.4e-74	258.8
213	UQ_con	Ubiquitin-conjugating enzyme	1e-53	191.9
215	DEAD	DEAD/DEAH box helicase	1.8e-43	140.4
216	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	4.5e-21	83.4
218	Glycos_transf_2	Glycosyl transferases	4e-21	83.6
219	lg	Immunoglobulin domain	0.092	10.7
222	WD40	WD domain, G-beta repeat	7.4e-23	89.4
224	TPR	TPR Domain	1.2e-08	42.1
225	DnaJ_CXXCXGXG	DnaJ central domain (4 repeats)	1.5e-38	141.5
226	DnaJ_CXXCXGXG	DnaJ central domain (4 repeats)	1.5e-38	141.5
229	HSP70	Hsp70 protein	2.4e-54	194.0
230	GSHPx	Glutathione peroxidases	3.4e-47	170.2
231	tsp_1	Thrombospondin type 1 domain	0.0075	17.1
233	cyclin	Cyclin	4.6e-144	492.0
234	ras	Ras family	4.8e-50	179.7
235	LRR	Leucine Rich Repeat	1.2e-30	115.3
236	LRR	Leucine Rich Repeat	6.7e-29	109.4
237	PDZ	PDZ domain (Also known as DHR or GLGF).	1.7e-09	45.0

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
244	dCMP_cyt_dea m	Cytidine and deoxycytidylate deaminase	2.5e-05	31.1
245	ig	Immunoglobulin domain	6.7e-08	30.5
248	wnt	wnt family of developmental signaling protei	9.1e-270	742.6
250	mito_carr	Mitochondrial carrier proteins	1.3e-55	193.6
254	adenylatekin ase	Adenylate kinase	1.8e-14	55.7
255	Cation_efflu x	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid transporter protein	2.6e-52	187.2
258	adenylatekin ase	Adenylate kinase	2.1e-110	380.2
259	HIT	HIT family	8.2e-07	25.3
260	Bacterial_PQ Q	PQQ enzyme repeat	1.6e-15	65.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kina se	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal_S7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Eukaryotic protein kinase domain	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
292	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
297	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
302	Glycos_trans f_4	Glycosyl transferase	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-84	294.8
305	KRAB	KRAB box	2e-44	161.0
306	rrm	RNA recognition motif.	2.7e-44	160.6
308	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-39	126.1
309	DNA_polymera seX	DNA polymerase X family	2.4e-64	227.2
311	F-box	F-box domain.	9.5e-08	39.2
312	ig	Immunoglobulin domain	6.8e-19	65.9
313	Ets	Ets-domain	8.1e-60	192.3
315	Kelch	Kelch motif	1.3e-106	367.6
317	arf	ADP-ribosylation factor family	3.2e-35	130.4
318	sugar_tr	Sugar (and other) transporter	0.0003	-73.1
320	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Eukaryotic protein kinase domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	331.5
326	ARID	ARID DNA binding domain	5.1e-37	136.4
327	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
328	cadherin	Cadherin domain	8.1e-81	281.9
331	chromo	'chromo' (CHRromatin Organization Modifier)	4e-18	66.7
333	Peptidase_M2 2	Glycoprotease family	1.2e-136	467.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
335	vwa	von Willebrand factor type A domain	2.3e-07	37.9
339	ras	Ras family	7.8e-07	-59.1
340	zf-C2H2	Zinc finger, C2H2 type	8.2e-64	225.4
342	zf-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
343	ig	Immunoglobulin domain	0.0005	18.0
346	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
347	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
351	EGF	EGF-like domain	8.5e-20	79.2
352	ank	Ank repeat	2.5e-101	350.0
354	TBC	TBC domain	5.1e-15	63.3
355	PHD	PHD-finger	3.2e-07	37.4
358	DUF6	Integral membrane protein DUF6	0.033	15.8
359	zf-C2H2	Zinc finger, C2H2 type	7.4e-20	79.4
361	ank	Ank repeat	6.6e-34	126.1
362	ArfGap	Putative GTP-ase activating protein for Arf	4.7e-53	189.7
363	efhand	EF hand	5.4e-10	46.6
367	LRR	Leucine Rich Repeat	8.8e-44	158.9
368	laminin_G	Laminin G domain	1.5e-33	121.7
369	PP2C	Protein phosphatase 2C	5.3e-20	73.9
372	LIM	LIM domain containing proteins	9.9e-15	57.1
373	KRAB	KRAB box	4.8e-23	90.0
376	ion_trans	Ion transport protein	2.9e-09	-4.2
377	Beach	Beige/BEACH domain	4.9e-208	704.5
380	pkinase	Eukaryotic protein kinase domain	1.6e-94	327.5
381	AMP-binding	AMP-binding enzyme	1.4e-07	-140.3
382	HECT	HECT-domain (ubiquitin-transferase).	1.3e-07	-13.5
384	ank	Ank repeat	2.5e-101	350.0
386	ig	Immunoglobulin domain	9.5e-06	23.6
388	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	154.6
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito_carr	Mitochondrial carrier proteins	3.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
393	SH3	SH3 domain	3.5e-09	43.9
394	AAA	ATPases associated with various cellular act	4.1e-21	83.6
396	spectrin	Spectrin repeat	2.1e-67	237.3
397	zf-C2H2	Zinc finger, C2H2 type	0.0066	23.1
399	fn3	Fibronectin type III domain	4.1e-102	352.6
400	WD40	WD domain, G-beta repeat	0.00049	26.8
401	E1_dehydrog	Dehydrogenase E1 component	3e-119	409.6
402	fn3	Fibronectin type III domain	0	1719.6
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
405	cadherin	Cadherin domain	8.1e-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
410	RhoGEF	RhoGEF domain	1.1e-23	92.1
411	F-box	F-box domain.	4.2e-06	33.7
412	SNF2_N	SNF2 and others N-terminal domain	5.8e-16	61.6
415	CPSase_L_cha in	Carbamoyl-phosphate synthase (CPSase)	1.5e-172	586.6
418	LRR	Leucine Rich Repeat	3.8e-24	93.6
419	DENN	DENN (AEX-3) domain	2e-58	207.5
420	RasGEF	RasGEF domain	8.1e-43	155.7
421	ank	Ank repeat	1.4e-153	523.7
424	G-patch	G-patch domain	1e-19	78.9
425	pkinase	Eukaryotic protein kinase domain	2.2e-31	117.1
426	Plexin_repea t	Plexin repeat	0.0023	24.6
427	Plexin_repea	Plexin repeat	0.0023	24.6

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
	t			
429	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	8.6e-11	39.2
431	DEAD	DEAD/DEAH box helicase	1e-66	214.0
432	SH3	SH3 domain	3.4e-16	67.2
433	GTP_CDC	Cell division protein	2.1e-114	393.5
436	Collagen	Collagen triple helix repeat (20 copies)	4.6e-194	658.1
438	Ricin_B_lectin	Similarity to lectin domain of ricin b	0.0085	10.5
441	Alpha_adaptin_C	Alpha adaptin carboxyl-terminal domain	1.2e-256	866.0
442	Alpha_adaptin_C	Alpha adaptin carboxyl-terminal domain	1.8e-235	795.7
443	PDZ	PDZ domain (Also known as DHR or GLGF).	1.9e-65	230.9
445	LON	ATP-dependent protease La (LON) domain	0.00012	-17.1
446	ig	Immunoglobulin domain	0.00011	20.1
451	sushi	Sushi domain (SCR repeat)	1.4e-18	75.2
452	fn3	Fibronectin type III domain	1.5e-06	35.2
454	pyridoxal_dependent	Pyridoxal-dependent decarboxylase conse	8.3e-14	50.3
456	kinesin	Kinesin motor domain	4.9e-217	734.4
457	neur_chan	Neurotransmitter-gated ion-channel	1e-175	597.1
458	Josephin	Josephin	0.0002	18.7
468	bZIP	bZIP transcription factor	1.7e-07	31.8
470	NTP_transferase	Nucleotidyl transferase	6.3e-06	-26.3
471	WD40	WD domain, G-beta repeat	2e-28	107.9
473	LIM	LIM domain containing proteins	0.00021	20.7
477	zf-RanBP	Zn-finger in Ran binding protein and others.	0.028	21.0
479	WD40	WD domain, G-beta repeat	6.5e-18	73.0
480	KRAB	KRAB box	1e-31	118.8
481	ArfGap	Putative GTP-ase activating protein for Arf	8.4e-66	232.0
485	SH2	Src homology domain 2	0.011	11.4
486	Clg	Clg domain	4.3e-74	259.6
487	dserm	Double-stranded RNA binding motif	1.1e-47	171.9
489	zf-C2H2	Zinc finger, C2H2 type	4.8e-153	521.9
490	Alpha_adaptin_C	Alpha adaptin carboxyl-terminal domain	3.4e-222	751.6
492	SKI	Shikimate kinase	1.2e-10	48.8
497	ENV_polyprotein	ENV polyprotein (coat polyprotein)	2.6e-22	77.6
498	abhydrolase_2	Phospholipase/Carboxylesterase	0.041	-48.1
500	rrm	RNA recognition motif.	5.4e-34	126.4
501	WW	WW domain	4.6e-18	73.4
502	ig	Immunoglobulin domain	1.1e-10	39.5
504	abhydrolase	alpha/beta hydrolase fold	0.045	-3.6
505	vwa	von Willebrand factor type A domain	7.1e-62	219.0
508	Na_K_ATPase_C	Na+/K+ ATPase C-terminus	2.3e-145	496.3
509	Exonuclease	Exonuclease	1.3e-56	201.5
510	Glycosyl_transferase_1	Glycosyl transferases group 1	2.9e-06	27.0
511	Glycosyl_transferase_1	Glycosyl transferases group 1	2.9e-06	27.0
512	Glycosyl_transferase_1	Glycosyl transferases group 1	1.9e-09	38.5
514	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	1.8e-63	221.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
515	EGF	EGF-like domain	1.9e-18	74.7
516	Surp	Surp module	4.3e-38	140.0
523	lg	Immunoglobulin domain	3.3e-06	25.0
526	UBX	UBX domain	1.1e-34	128.6
528	adh_zinc	Zinc-binding dehydrogenases	2.7e-34	127.4
530	SAM	SAM domain (Sterile alpha motif)	0.046	10.0
531	adh_short	short chain dehydrogenase	0.0025	-34.1
532	mito_carr	Mitochondrial carrier proteins	2.5e-81	281.7
533	mito_carr	Mitochondrial carrier proteins	2e-61	213.5
534	thiolase	Thiolase	3.5e-183	622.0
535	FMO-like	Flavin-binding monooxygenase-like	0	1153.7
536	SCAN	SCAN domain	4e-55	196.6
537	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
538	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
539	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	1.9e-117	403.6
540	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
541	vATP-synt_E	ATP synthase (E/31 kDa) subunit	5.9e-85	295.7
543	zf-C2H2	Zinc finger, C2H2 type	5.5e-69	242.6
544	DUF101	Protein of unknown function DUF101	8.5e-38	139.0
545	TGFb_propept ide	TGF-beta propeptide	1.1e-67	238.2
547	WD40	WD domain, G-beta repeat	2.6e-32	120.8
548	RHD	Rel homology domain (RHD).	1.6e-238	686.2
549	MMR_HSR1	GTPase of unknown function	5.4e-67	236.0
551	HECT	HECT-domain (ubiquitin-transferase).	4.3e-127	435.6
554	MHC_II_alpha	Class II histocompatibility antigen, alp	3.5e-74	259.8
555	zf-UBR1	Putative zinc finger in N-recogin	3.3e-16	67.3
556	Kelch	Kelch motif	5.5e-29	109.7
561	AMP-binding	AMP-binding enzyme	2.8e-06	-163.7
562	PABP	Poly-adenylate binding protein, unique domai	4.9e-38	139.8
564	Gag_p30	Gag P30 core shell protein	1.2e-67	238.2
566	PWWP	PWWP domain	8.1e-16	66.0
567	SCAN	SCAN domain	7.3e-68	238.9
569	pkinase	Eukaryotic protein kinase domain	1.5e-84	294.3
570	pkinase	Eukaryotic protein kinase domain	1.5e-84	294.3
571	CN_hydrolase	Carbon-nitrogen hydrolase	0.00081	-79.7
572	myosin_head	Myosin head (motor domain)	0	1495.2
573	myosin_head	Myosin head (motor domain)	0	1490.4
575	Surp	Surp module	1.7e-23	91.5
576	Surp	Surp module	1.7e-23	91.5
577	DNA_pol_B	DNA polymerase family B	0	1138.6
578	PDZ	PDZ domain (Also known as DHR or GLGF).	8.3e-09	42.7
579	LRR	Leucine Rich Repeat	4.9e-21	83.3
580	neur_chan	Neurotransmitter-gated ion-channel	5.9e-177	601.3
583	sushi	Sushi domain (SCR repeat)	0	1673.0
584	DEAD	DEAD/DEAH box helicase	7.3e-36	116.3
586	KH-domain	KH domain	2.9e-13	57.5
587	G-patch	G-patch domain	2.3e-14	61.2
589	LIM	LIM domain containing proteins	2.3e-36	133.4
590	bromodomain	Bromodomain	6.6e-32	114.7
591	bromodomain	Bromodomain	6.6e-32	114.7

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
592	hormone_rec	Ligand-binding domain of nuclear hormone	3.5e-22	87.1
593	PHD	PHD-finger	3.8e-12	53.8
594	cadherin	Cadherin domain	4.2e-99	342.7
596	pkinase	Eukaryotic protein kinase domain	5e-92	319.2
597	WD40	WD domain, G-beta repeat	0.00054	26.7
600	FG-GAP	FG-GAP repeat	4.3e-75	262.9
602	G_Adapt_CT	Gamma-adaptin, C-terminus	1.1e-53	191.8
603	pkinase	Eukaryotic protein kinase domain	2.3e-86	300.4
605	Collagen	Collagen triple helix repeat (20 copies)	8e-42	152.4
606	mito_carr	Mitochondrial carrier proteins	6.3e-67	232.3
608	PWWP	PWWP domain	2.6e-28	107.5
609	PWWP	PWWP domain	2.6e-28	107.5
613	CAP_GLY	CAP-Gly domain	0.0046	20.1
615	RFX_DNA_bind ing	RFX DNA-binding domain	5.2e-54	192.9
616	kinesin	Kinesin motor domain	1.1e-81	284.8
617	kinesin	Kinesin motor domain	8.4e-80	278.5
618	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0098	13.1
620	MATH	MATH domain	7.8e-05	22.2
621	Y_phosphatas e	Protein-tyrosine phosphatase	1.4e-32	121.6
622	pkinase	Eukaryotic protein kinase domain	4.4e-40	146.6
623	BNR	BNR repeat	2.1e-11	51.3
624	molybdopteri n	Prokaryotic molybdopterin oxidoreductas	1.4e-12	42.2
625	TPR	TPR Domain	1.1e-17	72.2
627	cNMP_binding	Cyclic nucleotide-binding domain	3.7e-58	206.6
630	adh_short	short chain dehydrogenase	5e-17	70.0
631	zf-C2H2	Zinc finger, C2H2 type	2.1e-88	307.1
632	rrm	RNA recognition motif.	4e-05	30.5
635	pkinase	Eukaryotic protein kinase domain	1.6e-104	360.7
636	Fork_head	Fork head domain	5.9e-27	103.0
637	pkinase	Eukaryotic protein kinase domain	3.8e-70	246.5
642	TPR	TPR Domain	4.8e-08	40.1
643	efhand	EF hand	1.9e-27	104.6
647	SNF2_N	SNF2 and others N-terminal domain	1.2e-101	351.1
648	PseudoU_synt h_2	RNA pseudouridylate synthase	1.9e-55	197.6
650	zf-C2H2	Zinc finger, C2H2 type	0.0087	22.7
651	ank	Ank repeat	1.3e-17	71.9
652	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
653	neur_chan	Neurotransmitter-gated ion-channel	4.1e-171	581.8
654	tsp_1	Thrombospondin type 1 domain	4.1e-47	169.9
659	FH2	Formin Homology 2 Domain	1e-107	371.2
661	pou	Pou domain - N-terminal to homeobox domain	5.3e-45	162.9
662	C2	C2 domain	6.7e-19	76.2
663	C2	C2 domain	6.7e-19	76.2
664	C2	C2 domain	6.7e-19	76.2
667	GST	Glutathione S-transferases.	9.3e-34	114.4
668	LRR	Leucine Rich Repeat	9.3e-31	115.6
670	spectrin	Spectrin repeat	4e-57	203.2
671	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
672	ABC_tran	ABC transporter	5.3e-60	212.8
674	WD40	WD domain, G-beta repeat	4.8e-24	93.3

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
675	WD40	WD domain, G-beta repeat	4.8e-24	93.3
676	LRR	Leucine Rich Repeat	0.0015	25.2
679	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-29	107.7
680	zf-C2H2	Zinc finger, C2H2 type	5.2e-05	30.1
681	CH	Calponin homology (CH) domain	2.4e-17	71.1
682	DSPc	Dual specificity phosphatase, catalytic doma	4.3e-43	156.6
683	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.051	10.8
687	Synapsin	Synapsin	0	1890.8
689	PR55	Protein phosphatase 2A regulatory subunit PR	0	1038.8
691	homeobox	Homeobox domain	8.5e-30	112.4
696	Peptidase_M24	metallopeptidase family M24	2.6e-59	210.5
697	RhoGEF	RhoGEF domain	9.5e-35	128.9
698	PHD	PHD-finger	0.008	9.3
701	zf-C2H2	Zinc finger, C2H2 type	5.5e-123	422.0
702	Sulfatase	Sulfatase	3e-231	781.6
703	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	79.8
707	Acyl_transf	Acyl transferase domain	1.1e-22	88.8
708	WD40	WD domain, G-beta repeat	4.8e-19	76.7
710	Ran_BP1	RanBP1 domain.	8.4e-06	-7.3
713	DEAD	DEAD/DEAH box helicase	9.9e-42	134.9
714	PH	PH domain	1.6e-09	39.0
715	DSPc	Dual specificity phosphatase, catalytic doma	1.5e-37	138.2
717	Sialyltransf	Sialyltransferase family	7.5e-31	115.9
718	ig	Immunoglobulin domain	1e-29	100.8
719	integrin_B	Integrins, beta chain	0	1125.4
720	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-08	32.4
722	Peptidase_C2	Calpain family cysteine protease	3e-145	495.9
723	ig	Immunoglobulin domain	2.2e-05	22.4
724	F-box	F-box domain.	0.007	23.0
725	Nop	Putative snRNA binding domain	8.1e-58	205.5
726	Nop	Putative snRNA binding domain	8.1e-58	205.5
727	WD40	WD domain, G-beta repeat	7.5e-26	99.3
730	dsrm	Double-stranded RNA binding motif	0.027	12.1
731	dynamin	Dynamins family	4.2e-16	66.9
733	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.8e-10	41.7
735	CDP-OH_P_transf	CDP-alcohol phosphatidyltransferase	4.2e-26	100.1
738	DEAD	DEAD/DEAH box helicase	8.6e-57	182.5
739	TSC22	TSC-22/dip/bun family	6.5e-32	119.5
742	ras	Ras family	2.2e-100	346.9
743	PMI_typeI	Phosphomannose isomerase type I	1.2e-243	822.9
747	trypsin	Trypsin	6.4e-88	279.4
748	kazal	Kazal-type serine protease inhibitor domain	2.2e-52	187.4
749	efhand	EF hand	6.3e-06	33.1
751	PHD	PHD-finger	4.9e-16	66.7
752	zf-C2H2	Zinc finger, C2H2 type	3.2e-21	83.9
753	Hydrolase	haloacid dehalogenase-like hydrolase	6.1e-11	49.8
754	Ribosomal_L39	Ribosomal L39 protein	0.00018	26.7
755	PH	PH domain	3.6e-14	55.7
758	SCAN	SCAN domain	1.4e-53	191.5
759	PA	PA domain	0.0065	23.1
760	arf	ADP-ribosylation factor family	2.2e-19	77.8
761	CIDE-N	CIDE-N domain	2.2e-40	147.6

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
762	histone	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
763	zf-MYND	MYND finger	4.1e-14	60.3
764	pou	Pou domain - N-terminal to homeobox domain	1e-52	188.6
767	vwc	von Willebrand factor type C domain	2.9e-34	127.3
769	efhand	EF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two domains)	2.4e-53	181.6
772	ras	Ras family	7e-90	312.0
773	Sulfatase	Sulfatase	1e-142	487.5
775	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
778	rrm	RNA recognition motif.	2.1e-32	121.1
779	G6PD	Glucose-6-phosphate dehydrogenase	1.5e-76	236.6
780	spectrin	Spectrin repeat	3.7e-29	110.3
781	mito_carr	Mitochondrial carrier proteins	4.6e-57	198.5
782	SCAN	SCAN domain	1.3e-24	95.2
783	PDZ	PDZ domain (Also known as DHR or GLGF).	4.1e-07	37.1
785	DEAD	DEAD/DEAH box helicase	6e-06	21.7
786	ras	Ras family	5.3e-39	143.0
787	RNase_HII	Ribonuclease HII	2.5e-67	237.1
790	PI3_PI4_kinase	Phosphatidylinositol 3- and 4-kinases	5.4e-108	372.2
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797	trypsin	Trypsin	9.9e-20	64.8
799	CH	Calponin homology (CH) domain	3.7e-15	63.8
801	Gal-bind_lectin	Vertebrate galactoside-binding lectin	4.1e-25	88.7
803	WD40	WD domain, G-beta repeat	0.00082	26.1
806	TBC	TBC domain	1.8e-26	101.4
807	TBC	TBC domain	1.8e-26	101.4
808	CN_hydrolase	Carbon-nitrogen hydrolase	8.8e-80	278.5
811	CBFD_NFYB_HMF	Histone-like transcription factor	6e-14	59.8
812	adh_short	short chain dehydrogenase	8.1e-20	79.3
814	IMP4	Domain of unknown function	3.3e-71	250.0
815	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
816	Pept_tRNA_hydro	Peptidyl-tRNA hydrolase	1.6e-37	138.0
817	ARID	ARID DNA binding domain	2.5e-18	74.3
826	IF5_eIF4_eIF2	eIF4-gamma/eIF5/eIF2-epsilon	1.6e-32	121.5
830	ArfGap	Putative GTP-ase activating protein for Arf	1.5e-53	191.3
831	LRR	Leucine Rich Repeat	2.1e-26	101.1
832	laminin_EGF	Laminin EGF-like (Domains III and V)	2e-57	204.2
839	rrm	RNA recognition motif.	1.3e-22	88.5
840	Y_phosphatase	Protein-tyrosine phosphatase	2.6e-119	409.8
841	pkinase	Eukaryotic protein kinase domain	3.4e-100	346.3
844	Ribosomal_L22e	Ribosomal L22e protein family	1e-64	228.4
846	IBR	IBR domain	9e-15	62.5
849	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.4e-07	26.5
850	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00016	18.9
851	SET	SET domain	5e-30	113.2
852	SRCR	Scavenger receptor cysteine-	0	1025.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
		rich domain		
853	SRCR	Scavenger receptor cysteine-rich domain	0	1025.4
857	lactamase_B	Metallo-beta-lactamase superfamily	0.012	-6.0
858	COX6A	Cytochrome c oxidase subunit VIa	3.4e-58	206.7
859	rrm	RNA recognition motif.	5.4e-45	162.9
861	PRK	Phosphoribulokinase	5.1e-62	219.4
863	mito_carr	Mitochondrial carrier proteins	2.9e-53	185.5
864	HSP90	Hsp90 protein	4.7e-158	538.5
866	ig	Immunoglobulin domain	4e-12	44.1
867	zf-C2H2	Zinc finger, C2H2 type	7e-135	461.5
872	histone	Core histone H2A/H2B/H3/H4	4.9e-41	149.8
874	CPSase_L_cha in	Carbamoyl-phosphate synthase (CPSase)	2.1e-218	739.0
879	Ribosomal_S12e	Ribosomal protein S12e	2.1e-98	340.3
882	serpin	Serpins (serine protease inhibitors)	2.5e-42	145.7
883	Patatin	Patatin	1.2e-51	182.0
884	RA	Ras association (RalGDS/AF-6) domain	0.044	8.0
887	DUF92	Integral membrane protein DUF92	2.7e-12	54.3
889	sugar_tr	Sugar (and other) transporter	8.2e-63	222.1
893	DUF28	Domain of unknown function DUF28	1.3e-43	158.3
896	IP_trans	Phosphatidylinositol transfer protein	6.5e-98	338.7
898	DEAD	DEAD/DEAH box helicase	1.5e-48	156.5
899	KE2	KE2 family protein	7e-61	215.7
900	KE2	KE2 family protein	4.3e-51	183.2
901	zf-C2H2	Zinc finger, C2H2 type	2.7e-57	203.8
902	ras	Ras family	2.3e-75	263.8
904	TPR	TPR Domain	3.2e-22	87.2
906	GBP	Guanylate-binding protein	8.9e-253	853.1
907	GBP	Guanylate-binding protein	1.1e-239	809.6
908	WD40	WD domain, G-beta repeat	2.6e-26	100.8
909	PH	PH domain	1.3e-09	39.4
910	zf-C2H2	Zinc finger, C2H2 type	2.5e-39	144.1
913	Epimerase	NAD dependent epimerase/dehydratase family	5e-07	-88.5
921	TBC	TBC domain	1.5e-09	30.7
922	WD40	WD domain, G-beta repeat	1.6e-25	98.2
923	WD40	WD domain, G-beta repeat	8.2e-07	36.1
924	Hydrolase	haloacid dehalogenase-like hydrolase	2.9e-05	29.1
925	UQ_con	Ubiquitin-conjugating enzyme	0.00033	-27.6
926	CH	Calponin homology (CH) domain	3.3e-53	190.2
928	WD40	WD domain, G-beta repeat	5.9e-48	172.7
929	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1e-10	37.4
930	Ribul_P_3_ep im	Ribulose-phosphate 3 epimerase family	7.2e-105	361.8
931	Ribul_P_3_ep im	Ribulose-phosphate 3 epimerase family	1.2e-96	334.4
936	C2	C2 domain	2.2e-62	220.7
937	NAP_family	Nucleosome assembly protein (NAP)	1.1e-22	84.6
940	abhydrolase	alpha/beta hydrolase fold	0.011	3.1
944	Tropomyosin	Tropomyosins	3.2e-07	25.1
948	pkinase	Eukaryotic protein kinase domain	3.4e-75	263.2
949	WD40	WD domain, G-beta repeat	1.8e-27	104.7
950	Acyltransferase	Acyltransferase	1.6e-07	38.4

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
951	SAM	SAM domain (Sterile alpha motif)	0.014	14.5
954	GFO_IDH_MocA	Oxidoreductase family	1.3e-11	52.0
955	BTB	BTB/POZ domain	7e-22	86.1
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-OH_P_transf	CDP-alcohol phosphatidyltransferase	0.053	-22.2
959	ras	Ras family	2.4e-97	336.8
960	ras	Ras family	8.4e-43	155.6
961	Acetyltransf	Acetyltransferase (GNAT) family	1.2e-08	42.2
962	adh_short	short chain dehydrogenase	2.4e-31	117.6
963	mutT	Bacterial mutT protein	5.6e-06	26.2
969	IF-2B	Initiation factor 2 subunit family	8.4e-193	653.9
970	RNase_PH	3' exoribonuclease family	9e-24	92.4
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR or GLGF).	3.6e-21	83.7
978	Ribosomal_L17	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LIM domain containing proteins	5.8e-42	152.8
980	Calsequestrin	Calsequestrin	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
983	oxidored_q6	NADH ubiquinone oxidoreductase, 20 Kd sub	4.8e-63	222.9
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
993	tRNA_int_endo	tRNA intron endonuclease	0.0017	-34.2
994	homeobox	Homeobox domain	4e-18	73.6
997	pyr_redox	Pyridine nucleotide-disulphide oxidoreductase	0.012	11.6
1000	mito_carr	Mitochondrial carrier proteins	9.7e-123	421.2
1001	RA	Ras association (RalGDS/AF-6) domain	1.2e-15	65.4
1004	DUF81	Domain of unknown function DUF81	0.099	10.2
1005	actin	Actin	1.3e-174	574.3
1006	actin	Actin	3.1e-130	428.6
1007	cpn60_TCP1	TCP-1/cpn60 chaperonin family	3.7e-195	661.8
1008	TPR	TPR Domain	8.1e-44	159.0
1009	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.7e-15	53.1
1016	tRNA-synt_2c	tRNA synthetases class II (A)	2.3e-15	55.2
1018	RhoGAP	RhoGAP domain	1.6e-78	274.3
1022	PGAM	Phosphoglycerate mutase family	3.8e-18	69.7
1026	HMG_box	HMG (high mobility group) box	8.4e-20	79.2
1027	TBC	TBC domain	7.3e-45	162.5
1028	UQ_con	Ubiquitin-conjugating enzyme	1.4e-49	178.1
1032	PDZ	PDZ domain (Also known as DHR or GLGF).	0.028	16.3
1034	Hydrolase	haloacid dehalogenase-like hydrolase	2e-21	84.6
1037	KRAB	KRAB box	4.8e-06	32.4
1038	Cation_efflux	Cation efflux family	7.1e-42	152.5
1040	ART	NAD:arginine ADP-ribosyltransferase	4.7e-47	169.1
1042	WD40	WD domain, G-beta repeat	1.9e-18	74.7
1043	zf-C2H2	Zinc finger, C2H2 type	3.7e-24	93.7
1045	lectin_c	Lectin C-type domain	1.9e-28	108.0
1046	Glucosamine_iso	Glucosamine-6-phosphate isomerase	0.00013	-25.1

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1049	ig	Immunoglobulin domain	1.7e-09	35.6
1050	Ribosomal_L24e	Ribosomal protein L24e	2e-33	124.5
1054	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin	Annexin	6.9e-44	159.2
1059	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	0.023	-23.6
1060	homeobox	Homeobox domain	3.2e-31	117.2
1062	Acyltransferase	Acyltransferase	0.00065	10.5
1064	AMP-binding	AMP-binding enzyme	6.6e-100	345.3
1065	LRR	Leucine Rich Repeat	3.3e-14	60.6
1066	GTP1_OBG	GTP1/OBG family	4.8e-41	141.8
1071	ig	Immunoglobulin domain	8.4e-48	159.1
1072	PHD	PHD-finger	6.8e-07	36.3
1074	DENN	DENN (AEX-3) domain	8.3e-33	121.5
1075	SCP	SCP-like extracellular protein	4.7e-41	149.8
1077	OLF	Olfactomedin-like domain	2.2e-66	234.0
1078	mito_carr	Mitochondrial carrier proteins	1e-42	149.3
1079	WD40	WD domain, G-beta repeat	6.2e-45	162.7
1087	START	START domain	1.5e-48	174.7
1093	DSFp	Dual specificity phosphatase, catalytic doma	3.3e-63	223.4
1094	GSHPx	Glutathione peroxidases	9.6e-41	148.8
1095	DUF25	Domain of unknown function DUF25	2e-75	264.0
1096	DUF25	Domain of unknown function DUF25	6e-75	262.4
1105	Nitroreductase	Nitroreductase family	1.3e-13	58.6
1106	PTE	Phosphotriesterase family	1.3e-179	610.1
1107	DAGKc	Diacylglycerol kinase catalytic domain	0.00049	19.6
1109	ras	Ras family	1.3e-15	40.7
1115	ArfGap	Putative GTP-ase activating protein for Arf	9.7e-47	168.7
1116	HMG14_17	HMG14 and HMG17	4.4e-21	83.5
1117	HMG14_17	HMG14 and HMG17	9.9e-12	52.4
1119	FAA_hydrolase	Fumarylacetoacetate (FAA) hydrolase fam	2e-83	290.6
1120	pkinase	Eukaryotic protein kinase domain	1.4e-94	327.6
1123	abhydrolase	alpha/beta hydrolase fold	9.2e-23	89.0
1129	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-tr	2.2e-56	197.1
1131	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	17.8
1136	Adap_comp_sub	Adaptor complexes medium subunit family	1.2e-256	866.0
1137	Adap_comp_sub	Adaptor complexes medium subunit family	2.5e-209	708.8
1139	ras	Ras family	1.5e-86	301.0
1141	pkinase	Eukaryotic protein kinase domain	9.4e-74	258.4
1152	Acyltransferase	Acyltransferase	1.2e-05	29.9
1153	IRS	PTB domain (IRS-1 type)	5.4e-55	196.1
1155	ig	Immunoglobulin domain	1.3e-31	106.9
1157	Asparaginase_2	Asparaginase	6.4e-72	252.3
1159	GMC_oxred	GMC oxidoreductases	4.7e-142	485.3
1160	zf-AN1	AN1-like Zinc finger	0.00021	27.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1163	linker_histo ne	linker histone H1 and H5 family	3.8e-14	60.4
1164	DED	Death effector domain	3.9e-05	30.5
1165	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1166	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1168	SAM	SAM domain (Sterile alpha motif)	0.04	10.5
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9e-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	WD domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple helix repeat (20 copies)	0.00016	24.7
1182	TCL1_MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGEF	RasGEF domain	1.7e-88	307.4
1185	mito_carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR_LY6	u-PAR/Ly-6 domain	0.0042	15.6
1188	Orn_DAP_Arg_ deC	Pyridoxal-dependent decarboxylase	6.2e-128	430.6
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Sec1	Sec1 family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.8
1197	Glyco_transf _8	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation domain	0.022	-16.8
1203	adh_short	short chain dehydrogenase	8.3e-45	162.3
1206	UbiE_methylt ran	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm_3	7 transmembrane receptor	7.2e-09	29.0
1209	ank	Ank repeat	3.9e-15	63.7
1210	vATP- synt_AC39	ATP synthase (C/AC39) subunit	2.5e-128	439.7
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	EF hand	3.2e-07	37.4
1219	rrm	RNA recognition motif.	2.1e-40	147.7
1220	DUF6	Integral membrane protein DUF6	0.015	21.5
1222	SCAN	SCAN domain	1.5e-71	251.1
1223	G-gamma	GGL domain	3.6e-36	129.5
1227	catalase	Catalase	0	1158.9
1232	PX	PX domain	2.2e-15	64.5
1233	PX	PX domain	2.2e-15	64.5
1236	FCH	Fes/CIP4 homology domain	3.3e-09	44.0
1241	Peptidase_M2 0	Peptidase family M20/M25/M40	2e-63	224.1
1243	WW	WW domain	0.044	17.9
1247	UPF0006	Metalloenzyme of unknown function UPF0006	6.3e-61	215.8
1248	Glycos_trans f_2	Glycosyl transferases	4.5e-10	46.9
1249	efhand	EF hand	4e-11	50.4
1254	UQ_con	Ubiquitin-conjugating enzyme	2.1e-73	257.3
1255	ras	Ras family	2.2e-62	220.7
1256	formyl_trans f	Formyl transferase	4.9e-30	108.3
1259	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-13	46.4
1261	Dihfolate_re d	Dihydrofolate reductase	2.1e-69	241.7
1262	G_glu_transp ept	Gamma-glutamyltranspeptidase	1.8e-110	380.4
1263	PAS	PAS domain	1.3e-08	36.9
1265	LRR	Leucine Rich Repeat	4.2e-22	86.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1266	SCP	SCP-like extracellular protein	6e-29	108.0
1267	K_tetra	K ⁺ channel tetramerisation domain	2.8e-27	104.0
1269	ras	Ras family	1.3e-85	297.9
1275	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.2e-10	37.0
1276	abhydrolase	alpha/beta hydrolase fold	5.4e-23	89.8
1277	abhydrolase	alpha/beta hydrolase fold	5.6e-21	83.1
1279	trypsin	Trypsin	4.4e-41	132.0
1280	PBP	Phosphatidylethanolamine-binding protein	1.3e-13	58.7
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-14	49.6
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0.026	20.9
1295	GBP	Guanylate-binding protein	0.00026	-70.0
1296	PMP22_Claudin	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1297	Rhodanese	Rhodanese-like domain	3.2e-14	60.7
1298	LIM	LIM domain containing proteins	5.8e-21	79.1
1301	rnaseA	Pancreatic ribonucleases	4.9e-43	145.2
1307	mito_carr	Mitochondrial carrier proteins	2.1e-53	186.0
1308	WD40	WD domain, G-beta repeat	1.6e-17	71.6
1310	UPAR_LY6	u-PAR/Ly-6 domain	7.1e-20	75.5
1313	thioredo	Thioredoxin	3.6e-05	21.6
1314	Aa_trans	Transmembrane amino acid transporter protein	1.5e-67	237.9
1316	trypsin	Trypsin	4.4e-41	132.0
1320	Ribosomal_L13	Ribosomal protein L13	3.9e-62	219.8
1327	Armadillo_se	Armadillo/beta-catenin-like repeats	0.0054	23.4
1328	KRAB	KRAB box	0.052	-5.6
1329	rrm	RNA recognition motif.	2.1e-40	147.7
1330	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	0.014	-1.6
1331	PX	PX domain	2.1e-10	48.0
1333	KRAB	KRAB box	1.8e-36	134.6
1334	UPP_synthetase	Putative undecaprenyl diphosphate synt	2.3e-89	310.3
1335	UPP_synthetase	Putative undecaprenyl diphosphate synt	1.8e-59	211.0
1336	DSPc	Dual specificity phosphatase, catalytic doma	1.2e-31	118.6
1337	DSPc	Dual specificity phosphatase, catalytic doma	2.3e-12	54.5
1338	TPR	TPR Domain	0.00021	28.1
1340	metalthio	Metallothionein	0.013	20.3
1341	mutT	Bacterial mutT protein	5.8e-09	36.5
1343	Band_41	FERM domain (Band 4.1 family)	1.3e-38	122.5
1344	Kelch	Kelch motif	1.4e-44	161.5
1345	Antifreeze	Antifreeze protein	1.2e-10	48.8
1347	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomera	0.086	-177.2
1348	BTB	BTB/POZ domain	5.3e-28	106.5
1349	DUF6	Integral membrane protein DUF6	0.033	15.8
1350	myosin_head	Myosin head (motor domain)	0	1088.7
1352	Nramp	Natural resistance-associated macrophage pro	1.2e-202	686.6
1353	S_100	S-100/ICaBP type calcium binding domain	5.3e-23	89.9
1355	DEAD	DRAD/DEAH box helicase	3.6e-65	209.0
1356	C2	C2 domain	2.4e-15	64.4
1357	RBD	Raf-like Ras-binding domain	4.2e-57	203.1
1360	zf-C2H2	Zinc finger, C2H2 type	7.4e-141	481.4
1361	HMG14_17	HMG14 and HMG17	7.9e-40	145.7

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1362	SIS	SIS domain	3.8e-30	113.6
1363	SIS	SIS domain	1.3e-28	108.5
1364	ig	Immunoglobulin domain	0.00026	19.0
1368	K_tetra	K ⁺ channel tetramerisation domain	1.1e-16	68.9
1371	Collagen	Collagen triple helix repeat (20 copies)	2.2e-113	390.1
1372	DnaJ	DnaJ domain	6.6e-36	132.7
1376	KRAB	KRAB box	2.1e-38	141.0
1378	ELM2	ELM2 domain	2e-23	91.3
1380	thioredo	Thioredoxin	1.2e-23	82.8
1381	ank	Ank repeat	2.3e-83	290.4
1382	BTB	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1384	WD40	WD domain, G-beta repeat	6.3e-24	92.9
1387	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-09	35.6
1389	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1390	zf-C2H2	Zinc finger, C2H2 type	2.5e-85	296.9
1393	kinesin	Kinesin motor domain	7.8e-188	637.4
1394	zf-C2H2	Zinc finger, C2H2 type	1.2e-49	178.4
1398	KRAB	KRAB box	5.1e-22	86.6
1402	bZIP	bZIP transcription factor	0.035	13.1
1405	sugar_tr	Sugar (and other) transporter	0.003	-101.5
1406	RhoGAP	RhoGAP domain	8.9e-47	168.8
1407	rrm	RNA recognition motif.	1e-35	132.1
1408	LRR	Leucine Rich Repeat	2.1e-13	58.0
1409	Nebulin_repe at	Nebulin repeat	6e-54	192.6
1410	ank	Ank repeat	1.6e-17	71.6
1412	Ribosomal_L5 _C	ribosomal L5P family C-terminus	8.2e-58	205.5
1415	trypsin	Trypsin	4.7e-85	270.4
1416	aminotran_1	Aminotransferases class-I	4.4e-05	-91.2
1417	S1	S1 RNA binding domain	1.6e-07	33.1
1419	WD40	WD domain, G-beta repeat	2.2e-09	44.6
1422	cadherin	Cadherin domain	8.3e-42	152.3
1424	SH3	SH3 domain	2.5e-80	280.3
1425	PHD	PHD-finger	3.2e-17	70.6
1426	PHD	PHD-finger	3.2e-17	70.6
1427	ArfGap	Putative GTP-ase activating protein for Arf	1e-37	138.8
1428	helicase_C	Helicases conserved C-terminal domain	1e-26	102.2
1429	WD40	WD domain, G-beta repeat	3.9e-07	37.2
1430	inositol_P	Inositol monophosphatase family	2.5e-10	40.2
1431	mito_carr	Mitochondrial carrier proteins	4.3e-83	287.7
1433	Clq	Clq domain	2.9e-16	66.2
1434	WD40	WD domain, G-beta repeat	1.6e-13	58.3
1435	Inos-1- P_synth	Myo-inositol-1-phosphate synthase	7e-228	770.4
1436	rrm	RNA recognition motif.	1.4e-34	128.3
1438	ig	Immunoglobulin domain	1.3e-12	45.6
1440	G_Adapt_CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1441	G_Adapt_CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1443	Kelch	Kelch motif	0.00013	28.7
1446	ARID	ARID DNA binding domain	1.8e-21	84.7
1447	zf-C2H2	Zinc finger, C2H2 type	9.4e-28	105.6
1448	AMP-binding	AMP-binding enzyme	2.6e-07	-145.1
1451	rrm	RNA recognition motif.	6.5e-21	82.9
1454	ig	Immunoglobulin domain	5.6e-44	146.7
1455	Sialyltransf	Sialyltransferase family	5.4e-21	83.2
1460	Aldose_epim	Aldose 1-epimerase	1.9e-35	131.2
1461	C2	C2 domain	4e-18	73.6
1470	TIG	IPT/TIG domain	3.1e-19	77.3
1472	PseudoU_synt	RNA pseudouridylation synthase	4.3e-16	66.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
	h_2			
1474	DENN	DENN (AEX-3) domain	1.3e-44	161.6
1475	Cation_efflux	Cation efflux family	4.6e-49	176.4
1477	TBC	TBC domain	8e-47	169.0
1478	rrm	RNA recognition motif.	2e-21	84.6
1480	ig	Immunoglobulin domain	5.5e-06	24.3
1484	Telo_bind_alpha	Telomere-binding protein alpha subunit	0.028	-225.9
1485	zf-C2H2	Zinc finger, C2H2 type	1.8e-68	240.9
1486	pkinase	Eukaryotic protein kinase domain	9.5e-13	49.9
1488	helicase_C	Helicases conserved C-terminal domain	1.4e-15	65.2
1489	DUF89	Protein of unknown function DUF89	0.079	-132.4
1490	ECH	Enoyl-CoA hydratase/isomerase family	5.2e-41	149.7
1491	guanylate_cyclase	Adenylate and Guanylate cyclase catalytic	5.9e-46	166.1
1492	LRR	Leucine Rich Repeat	3.4e-19	77.2
1495	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.1e-10	36.3
1497	pkinase	Eukaryotic protein kinase domain	1e-22	85.8
1500	SH3	SH3 domain	9.3e-05	27.2
1502	homeobox	Homeobox domain	0.084	13.8
1503	homeobox	Homeobox domain	0.084	13.8
1505	EGF	EGF-like domain	2.7e-23	90.8
1506	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.7e-21	84.2
1508	Peptidase_M20	Peptidase family M20/M25/M40	2.8e-28	101.8
1511	PX	PX domain	1.9e-11	51.5
1512	Sulfatase	Sulfatase	2.8e-35	130.7
1516	Syntaxin	Syntaxin	0.011	-62.3
1518	aminotran_3	Aminotransferases class-III pyridoxal-pho	9.7e-106	305.6
1520	ig	Immunoglobulin domain	0.075	11.0
1521	RA	Ras association (RalGDS/AF-6) domain	0.013	13.3
1523	RhoGAP	RhoGAP domain	2.5e-05	18.7
1528	WD40	WD domain, G-beta repeat	5.4e-24	93.1
1535	impB/mucB/samB	impB/mucB/samB family	7.8e-95	328.5
1538	FYVE	FYVE zinc finger	3.2e-27	101.5
1539	DAGKc	Diacylglycerol kinase catalytic domain	6e-07	36.5
1540	Ocular_alb	Ocular albinism type 1 protein	0	1184.7
1653	SAP	SAP domain	6e-06	33.2
1654	Amino_oxidase	Flavin containing amine oxidase	3.2e-43	157.0
1655	Amino_oxidase	Flavin containing amine oxidase	3.2e-43	157.0
1656	RhoGEF	RhoGEF domain	1.4e-24	95.1
1657	MMR_HSR1	GTPase of unknown function	0.0011	-45.5
1659	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.5e-11	51.1
1660	actin	Actin	6.6e-21	69.9
1661	BAH	BAH domain	1.7e-82	287.5
1662	vwa	von Willebrand factor type A domain	0	1909.4
1663	WD40	WD domain, G-beta repeat	1.4e-67	237.9
1667	zf-C2H2	Zinc finger, C2H2 type	1.3e-93	324.4
1669	Nol1_Nop2_sun	NOL1/NOP2/sun family	1.3e-23	84.3
1671	SH2	Src homology domain 2	5.4e-15	46.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1672	chromo	'chromo' (CHRromatin Organization Modifier)	2.1e-18	67.7
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	0.0025	17.6
1676	Glyco_hydro_47	Glycosyl hydrolase family 47	1.8e-187	636.2
1677	Glyco_hydro_47	Glycosyl hydrolase family 47	4.5e-74	259.5
1680	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1681	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1683	MMR_HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric_reduc t	Ferric reductase like transmembrane com	8.4e-82	285.2
1698	Ferric_reduc t	Ferric reductase like transmembrane com	3.5e-53	190.1
1699	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf	ADP-ribosylation factor family	9e-19	75.8
1702	GTP_EFTU	Elongation factor Tu family	0.014	11.4
1703	SCAN	SCAN domain	1.8e-54	194.4
1707	pkinase	Eukaryotic protein kinase domain	1.2e-88	307.9
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1715	ras	Ras family	4.4e-41	149.9
1718	HMG_box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	HLH	Helix-loop-helix DNA-binding domain	9.2e-10	45.9
1723	dsrm	Double-stranded RNA binding motif	2.9e-05	30.9
1724	RrnaAD	Ribosomal RNA adenine dimethylases	0.045	9.2
1725	CIDE-N	CIDE-N domain	5.9e-40	146.2
1726	HAT	HAT (Half-A-TPR) repeats	2.9e-44	160.5
1728	efhand	EF hand	5.1e-20	79.9
1733	Hist_deacety l	Histone deacetylase family	1.7e-104	360.6
1735	LRR	Leucine Rich Repeat	4.6e-34	126.6
1739	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.0023	16.1
1743	ras	Ras family	3.7e-10	-21.3
1744	ras	Ras family	3.7e-10	-21.3
1745	RasGEF	RasGEF domain	3.2e-49	176.9
1746	adh_short	short chain dehydrogenase	7.1e-08	34.6
1751	zf-C2H2	Zinc finger, C2H2 type	9e-39	142.2
1754	fn3	Fibronectin type III domain	5.5e-101	348.9
1756	zf-C2H2	Zinc finger, C2H2 type	6.3e-93	322.1
1758	rrm	RNA recognition motif.	0.017	21.2
1760	Nop	Putative snRNA binding domain	6.1e-95	328.8
1761	Nop	Putative snRNA binding domain	6.1e-95	328.8
1765	MMR_HSR1	GTPase of unknown function	6.4e-41	149.4
1769	CN_hydrolase	Carbon-nitrogen hydrolase	3e-06	-43.9
1775	ank	Ank repeat	4.1e-07	37.1
1779	Oxysterol_BP	Oxysterol-binding protein	4.7e-56	199.6
1783	RhoGEF	RhoGEF domain	1.6e-23	91.6
1784	RhoGEF	RhoGEF domain	1.6e-23	91.6

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1785	rrm	RNA recognition motif.	6.4e-14	59.7

TRADOCs:1416227.1(%CRN01!.DOC)

TABLE 5

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1	1-21	0.991	0.955
2	1-31	0.995	0.944
3	1-33	0.949	0.736
4	1-19	0.970	0.951
5	1-26	0.971	0.863
6	1-26	0.971	0.863
7	1-26	0.971	0.863
8	1-26	0.971	0.863
9	1-46	0.982	0.901
10	1-21	0.991	0.955
11	1-23	0.989	0.899
12	1-25	0.955	0.803
13	1-18	0.932	0.625
14	1-18	0.938	0.876
15	1-25	0.941	0.811
16	1-17	0.972	0.939
17	1-27	0.964	0.777
18	1-16	0.914	0.657
19	1-19	0.953	0.840
20	1-20	0.935	0.701
21	1-22	0.974	0.850
22	1-33	0.961	0.895
23	1-19	0.991	0.959
24	1-31	0.995	0.944
25	1-22	0.976	0.935
26	1-27	0.996	0.928
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	0.893
31	1-19	0.993	0.976
32	1-22	0.998	0.909
35	1-33	0.949	0.736
36	1-33	0.949	0.736
46	1-19	0.970	0.951
67	1-25	0.968	0.848
71	1-18	0.949	0.845
72	1-30	0.991	0.919
75	1-29	0.958	0.854
88	1-20	0.986	0.945
94	1-33	0.994	0.943
97	1-46	0.964	0.595
103	1-49	0.983	0.570
108	1-26	0.978	0.885
111	1-23	0.989	0.899
126	1-25	0.955	0.803
129	1-19	0.963	0.918
138	1-29	0.971	0.844
143	1-18	0.914	0.628
148	1-20	0.969	0.904
156	1-25	0.941	0.811
158	1-22	0.979	0.927
160	1-17	0.972	0.939
161	1-48	0.903	0.571
162	1-25	0.937	0.729
168	1-16	0.939	0.826
171	1-27	0.964	0.777
178	1-21	0.945	0.825
180	1-27	0.981	0.941
187	1-28	0.982	0.936
190	1-19	0.953	0.840
196	1-22	0.975	0.916
197	1-22	0.963	0.936

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
199	1-20	0.935	0.701
200	1-23	0.977	0.773
206	1-30	0.984	0.890
207	1-19	0.990	0.924
208	1-22	0.974	0.850
210	1-40	0.940	0.670
211	1-28	0.971	0.849
216	1-24	0.986	0.956
218	1-33	0.961	0.895
219	1-19	0.970	0.871
221	1-19	0.904	0.553
222	1-21	0.917	0.555
230	1-19	0.991	0.959
231	1-26	0.953	0.800
232	1-25	0.988	0.826
239	1-23	0.969	0.828
240	1-17	0.982	0.955
241	1-17	0.982	0.955
245	1-30	0.970	0.722
248	1-22	0.976	0.935
249	1-23	0.968	0.940
252	1-18	0.971	0.923
261	1-24	0.883	0.587
265	1-18	0.939	0.868
272	1-24	0.953	0.739
283	1-21	0.906	0.688
284	1-29	0.997	0.854
290	1-31	0.986	0.841
302	1-28	0.980	0.893
304	1-16	0.907	0.635
312	1-19	0.993	0.976
313	1-17	0.930	0.753
323	1-22	0.998	0.909
324	1-17	0.982	0.954
328	1-19	0.971	0.865
329	1-22	0.963	0.924
330	1-33	0.978	0.841
331	1-24	0.920	0.712
332	1-24	0.975	0.881
333	1-19	0.984	0.941
334	1-20	0.899	0.567
335	1-27	0.942	0.813
336	1-20	0.952	0.850
337	1-38	0.942	0.653
338	1-27	0.973	0.772
339	1-36	0.979	0.804
340	1-27	0.888	0.597
343	1-19	0.971	0.865
344	1-22	0.994	0.928
345	1-17	0.966	0.687
346	1-19	0.936	0.822
347	1-22	0.963	0.924
349	1-24	0.982	0.966
351	1-21	0.918	0.815
352	1-31	0.988	0.912
354	1-31	0.974	0.839
355	1-29	0.932	0.632
356	1-15	0.994	0.969
357	1-33	0.935	0.726
360	1-27	0.938	0.827
361	1-25	0.954	0.674
362	1-22	0.929	0.788
363	1-21	0.881	0.715
364	1-33	0.978	0.841
365	1-33	0.978	0.841

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
366	1-21	0.916	0.820
367	1-19	0.936	0.822
368	1-29	0.972	0.874
370	1-24	0.920	0.712
371	1-24	0.961	0.773
372	1-27	0.919	0.768
373	1-19	0.986	0.945
375	1-32	0.994	0.932
376	1-34	0.987	0.810
377	1-17	0.995	0.950
378	1-49	0.971	0.749
380	1-20	0.968	0.874
381	1-20	0.928	0.782
382	1-19	0.986	0.934
383	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	1-16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
409	1-33	0.897	0.570
410	1-25	0.990	0.962
411	1-38	0.977	0.827
412	1-20	0.944	0.768
413	1-20	0.988	0.965
414	1-46	0.993	0.638
415	1-23	0.981	0.940
417	1-29	0.941	0.672
418	1-20	0.952	0.850
419	1-19	0.986	0.967
420	1-29	0.965	0.861
421	1-22	0.889	0.785
422	1-48	0.982	0.862
424	1-19	0.979	0.933
428	1-38	0.942	0.653
430	1-18	0.947	0.595
432	1-33	0.957	0.789
433	1-26	0.979	0.904
434	1-27	0.962	0.777
435	1-24	0.998	0.977
436	1-27	0.973	0.772
443	1-15	0.966	0.940
448	1-36	0.979	0.804
453	1-41	0.958	0.609
455	1-33	0.943	0.606
457	1-27	0.888	0.597
462	1-16	0.925	0.681
486	1-27	0.972	0.845
495	1-24	0.917	0.636
498	1-26	0.993	0.890
505	1-20	0.976	0.926
507	1-17	0.966	0.687
510	1-23	0.930	0.593

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
511	1-23	0.930	0.593
512	1-23	0.930	0.593
515	1-18	0.978	0.956
523	1-19	0.936	0.822
529	1-22	0.963	0.924
545	1-24	0.982	0.966
550	1-30	0.933	0.713
552	1-21	0.973	0.912
554	1-23	0.969	0.784
571	1-21	0.918	0.815
574	1-31	0.988	0.912
580	1-39	0.925	0.556
594	1-31	0.974	0.839
608	1-29	0.932	0.632
609	1-29	0.932	0.632
610	1-21	0.990	0.948
621	1-15	0.994	0.969
623	1-33	0.935	0.726
653	1-27	0.938	0.827
668	1-22	0.929	0.788
677	1-16	0.948	0.807
685	1-21	0.881	0.715
699	1-22	0.975	0.816
702	1-31	0.968	0.898
707	1-16	0.880	0.562
713	1-25	0.966	0.743
718	1-19	0.936	0.822
719	1-20	0.961	0.824
729	1-29	0.972	0.874
735	1-46	0.903	0.598
746	1-14	0.916	0.730
747	1-22	0.965	0.876
748	1-29	0.968	0.785
759	1-24	0.961	0.773
767	1-27	0.919	0.768
768	1-33	0.900	0.585
773	1-42	0.959	0.702
779	1-19	0.986	0.945
797	1-19	0.944	0.759
798	1-19	0.900	0.568
820	1-17	0.995	0.950
827	1-49	0.971	0.749
848	1-20	0.968	0.874
864	1-20	0.928	0.782
866	1-19	0.986	0.934
873	1-23	0.948	0.886
881	1-28	0.965	0.829
887	1-39	0.970	0.551
927	1-30	0.989	0.868
934	1-48	0.988	0.777
939	1-39	0.994	0.889
944	1-26	0.971	0.782
950	1-29	0.957	0.845
963	1-20	0.981	0.900
964	1-20	0.886	0.558
973	1-16	0.968	0.890
980	1-34	0.961	0.749
981	1-20	0.953	0.822
984	1-12	0.938	0.780
1015	1-22	0.985	0.854
1040	1-46	0.977	0.698
1052	1-18	0.969	0.842
1059	1-20	0.927	0.867
1065	1-33	0.983	0.918
1069	1-22	0.993	0.935

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1075	1-27	0.992	0.934
1080	1-19	0.931	0.829
1092	1-19	0.991	0.973
1094	1-46	0.992	0.653
1095	1-30	0.974	0.929
1105	1-23	0.994	0.921
1123	1-35	0.987	0.658
1138	1-32	0.954	0.613
1140	1-38	0.989	0.789
1142	1-33	0.897	0.570
1152	1-25	0.990	0.962
1170	1-38	0.977	0.827
1176	1-20	0.944	0.768
1187	1-20	0.988	0.965
1189	1-35	0.967	0.839
1192	1-46	0.993	0.638
1193	1-16	0.925	0.710
1197	1-29	0.985	0.853
1208	1-23	0.981	0.940
1225	1-29	0.941	0.672
1245	1-19	0.986	0.967
1258	1-29	0.965	0.861
1265	1-22	0.889	0.785
1266	1-20	0.944	0.809
1276	1-48	0.982	0.862
1292	1-19	0.979	0.933
1296	1-21	0.984	0.944
1297	1-19	0.984	0.953
1332	1-38	0.942	0.653
1358	1-18	0.947	0.595
1371	1-33	0.957	0.789
1380	1-26	0.979	0.904
1397	1-27	0.962	0.777
1399	1-23	0.997	0.960
1404	1-24	0.998	0.977
1410	1-15	0.946	0.845
1414	1-24	0.913	0.588
1415	1-19	0.982	0.929
1416	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0.588
1428	1-25	0.967	0.899
1430	1-34	0.977	0.819
1431	1-28	0.979	0.923
1432	1-36	0.957	0.613
1433	1-32	0.921	0.753
1434	1-39	0.983	0.621
1435	1-25	0.910	0.631
1436	1-42	0.988	0.868
1437	1-22	0.998	0.980
1442	1-20	0.918	0.753
1448	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.881	0.561
1518	1-17	0.968	0.863
1525	1-21	0.885	0.591
1547	1-28	0.974	0.891
1561	1-25	0.967	0.899
1580	1-17	0.923	0.824
1593	1-28	0.979	0.923

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1596	1-16	0.929	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TRADOCS:1416234.1(%CR%01!.DOC)

TABLE 6

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1	1787	3573	5359	784CIP2_1	1103
2	1788	3574	5360	784CIP2_2	2673
3	1789	3575	5361	784CIP2_3	4117
4	1790	3576	5362	784CIP2_4	5556
5	1791	3577	5363	784CIP2_5	5562
6	1792	3578	5364	784CIP2_6	5562
7	1793	3579	5365	784CIP2_7	5562
8	1794	3580	5366	784CIP2_8	5562
9	1795	3581	5367	784CIP2_9	5563
10	1796	3582	5368	784CIP2_10	5564
11	1797	3583	5369	784CIP2_11	5565
12	1798	3584	5370	784CIP2_12	5689
13	1799	3585	5371	784CIP2_13	5729
14	1800	3586	5372	784CIP2_14	5745
15	1801	3587	5373	784CIP2_15	5777
16	1802	3588	5374	784CIP2_16	5777
17	1803	3589	5375	784CIP2_17	5789
18	1804	3590	5376	784CIP2_18	5792
19	1805	3591	5377	784CIP2_19	5804
20	1806	3592	5378	784CIP2_20	5805
21	1807	3593	5379	784CIP2_21	5805
22	1808	3594	5380	784CIP2_22	5844
23	1809	3595	5381	784CIP2_23	5844
24	1810	3596	5382	784CIP2_24	5850
25	1811	3597	5383	784CIP2_25	5867
26	1812	3598	5384	784CIP2_26	5973
27	1813	3599	5385	784CIP2_27	5995
28	1814	3600	5386	784CIP2_28	5995
29	1815	3601	5387	784CIP2_29	6005
30	1816	3602	5388	784CIP2_30	6007
31	1817	3603	5389	784CIP2_31	6007
32	1818	3604	5390	784CIP2_32	6009
33	1819	3605	5391	784CIP2_33	6012
34	1820	3606	5392	784CIP2_34	6015
35	1821	3607	5393	784CIP2_35	6016
36	1822	3608	5394	784CIP2_36	6016
37	1823	3609	5395	784CIP2_37	6018
38	1824	3610	5396	784CIP2_38	6018
39	1825	3611	5397	784CIP2_39	6018
40	1826	3612	5398	784CIP2_40	6023
41	1827	3613	5399	784CIP2_41	6070
42	1828	3614	5400	784CIP2_42	6081
43	1829	3615	5401	784CIP2_43	6089
44	1830	3616	5402	784CIP2_44	6118
45	1831	3617	5403	784CIP2_45	6118
46	1832	3618	5404	784CIP2_46	6130
47	1833	3619	5405	784CIP2_47	6177
48	1834	3620	5406	784CIP2_48	6189
49	1835	3621	5407	784CIP2_49	6191
50	1836	3622	5408	784CIP2_50	6204
51	1837	3623	5409	784CIP2_51	6204
52	1838	3624	5410	784CIP2_52	6284
53	1839	3625	5411	784CIP2_53	6367
54	1840	3626	5412	784CIP2_54	6436
55	1841	3627	5413	784CIP2_55	6442
56	1842	3628	5414	784CIP2_56	6445
57	1843	3629	5415	784CIP2_57	6457
58	1844	3630	5416	784CIP2_58	6458
59	1845	3631	5417	784CIP2_59	6458

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
60	1846	3632	5418	784CIP2_60	6462
61	1847	3633	5419	784CIP2_61	6472
62	1848	3634	5420	784CIP2_62	6499
63	1849	3635	5421	784CIP2_63	6499
64	1850	3636	5422	784CIP2_64	6505
65	1851	3637	5423	784CIP2_65	6534
66	1852	3638	5424	784CIP2_66	6534
67	1853	3639	5425	784CIP2_67	6540
68	1854	3640	5426	784CIP2_68	6550
69	1855	3641	5427	784CIP2_69	6550
70	1856	3642	5428	784CIP2_70	6592
71	1857	3643	5429	784CIP2_71	6645
72	1858	3644	5430	784CIP2_72	6671
73	1859	3645	5431	784CIP2_73	6763
74	1860	3646	5432	784CIP2_74	6763
75	1861	3647	5433	784CIP2_75	6786
76	1862	3648	5434	784CIP2_76	6824
77	1863	3649	5435	784CIP2_77	6830
78	1864	3650	5436	784CIP2_78	6831
79	1865	3651	5437	784CIP2_79	6832
80	1866	3652	5438	784CIP2_80	6834
81	1867	3653	5439	784CIP2_81	6834
82	1868	3654	5440	784CIP2_82	6835
83	1869	3655	5441	784CIP2_83	6837
84	1870	3656	5442	784CIP2_84	6843
85	1871	3657	5443	784CIP2_85	6859
86	1872	3658	5444	784CIP2_86	6915
87	1873	3659	5445	784CIP2_87	6932
88	1874	3660	5446	784CIP2_88	6957
89	1875	3661	5447	784CIP2_89	6961
90	1876	3662	5448	784CIP2_90	6973
91	1877	3663	5449	784CIP2_91	6973
92	1878	3664	5450	784CIP2_93	7007
93	1879	3665	5451	784CIP2_94	7018
94	1880	3666	5452	784CIP2_95	7019
95	1881	3667	5453	784CIP2_96	7020
96	1882	3668	5454	784CIP2_97	7020
97	1883	3669	5455	784CIP2_98	7021
98	1884	3670	5456	784CIP2_99	7023
99	1885	3671	5457	784CIP2_100	7027
100	1886	3672	5458	784CIP2_101	7028
101	1887	3673	5459	784CIP2_102	7029
102	1888	3674	5460	784CIP2_103	7031
103	1889	3675	5461	784CIP2_104	7032
104	1890	3676	5462	784CIP2_105	7033
105	1891	3677	5463	784CIP2_106	7035
106	1892	3678	5464	784CIP2_107	7036
107	1893	3679	5465	784CIP2_108	7039
108	1894	3680	5466	784CIP2_109	7043
109	1895	3681	5467	784CIP2_110	7044
110	1896	3682	5468	784CIP2_111	7046
111	1897	3683	5469	784CIP2_112	7054
112	1898	3684	5470	784CIP2_113	7061
113	1899	3685	5471	784CIP2_114	7077
114	1900	3686	5472	784CIP2_115	7092
115	1901	3687	5473	784CIP2_116	7094
116	1902	3688	5474	784CIP2_117	7106
117	1903	3689	5475	784CIP2_118	7107
118	1904	3690	5476	784CIP2_119	7111
119	1905	3691	5477	784CIP2_120	7123
120	1906	3692	5478	784CIP2_121	7142
121	1907	3693	5479	784CIP2_122	7142

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
122	1908	3694	5480	784CIP2_123	7154
123	1909	3695	5481	784CIP2_124	7160
124	1910	3696	5482	784CIP2_125	7169
125	1911	3697	5483	784CIP2_126	7185
126	1912	3698	5484	784CIP2_127	7197
127	1913	3699	5485	784CIP2_128	7219
128	1914	3700	5486	784CIP2_129	7226
129	1915	3701	5487	784CIP2_130	7229
130	1916	3702	5488	784CIP2_131	7234
131	1917	3703	5489	784CIP2_132	7235
132	1918	3704	5490	784CIP2_133	7235
133	1919	3705	5491	784CIP2_134	7238
134	1920	3706	5492	784CIP2_135	7247
135	1921	3707	5493	784CIP2_136	7261
136	1922	3708	5494	784CIP2_137	7262
137	1923	3709	5495	784CIP2_138	7267
138	1924	3710	5496	784CIP2_139	7272
139	1925	3711	5497	784CIP2_140	7273
140	1926	3712	5498	784CIP2_141	7282
141	1927	3713	5499	784CIP2_142	7288
142	1928	3714	5500	784CIP2_143	7291
143	1929	3715	5501	784CIP2_144	7293
144	1930	3716	5502	784CIP2_145	7294
145	1931	3717	5503	784CIP2_146	7299
146	1932	3718	5504	784CIP2_147	7300
147	1933	3719	5505	784CIP2_148	7312
148	1934	3720	5506	784CIP2_149	7313
149	1935	3721	5507	784CIP2_150	7315
150	1936	3722	5508	784CIP2_151	7318
151	1937	3723	5509	784CIP2_152	7321
152	1938	3724	5510	784CIP2_153	7330
153	1939	3725	5511	784CIP2_154	7331
154	1940	3726	5512	784CIP2_155	7333
155	1941	3727	5513	784CIP2_156	7350
156	1942	3728	5514	784CIP2_157	7352
157	1943	3729	5515	784CIP2_158	7384
158	1944	3730	5516	784CIP2_159	7403
159	1945	3731	5517	784CIP2_160	7431
160	1946	3732	5518	784CIP2_161	7441
161	1947	3733	5519	784CIP2_162	7453
162	1948	3734	5520	784CIP2_163	7467
163	1949	3735	5521	784CIP2_164	7471
164	1950	3736	5522	784CIP2_165	7493
165	1951	3737	5523	784CIP2_166	7502
166	1952	3738	5524	784CIP2_167	7511
167	1953	3739	5525	784CIP2_168	7514
168	1954	3740	5526	784CIP2_169	7520
169	1955	3741	5527	784CIP2_170	7541
170	1956	3742	5528	784CIP2_171	7570
171	1957	3743	5529	784CIP2_172	7578
172	1958	3744	5530	784CIP2_173	7583
173	1959	3745	5531	784CIP2_174	7592
174	1960	3746	5532	784CIP2_175	7601
175	1961	3747	5533	784CIP2_176	7602
176	1962	3748	5534	784CIP2_177	7608
177	1963	3749	5535	784CIP2_178	7615
178	1964	3750	5536	784CIP2_179	7617
179	1965	3751	5537	784CIP2_181	7624
180	1966	3752	5538	784CIP2_182	7626
181	1967	3753	5539	784CIP2_183	7640
182	1968	3754	5540	784CIP2_184	7641
183	1969	3755	5541	784CIP2_185	7641

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
184	1970	3756	5542	784CIP2_186	7641
185	1971	3757	5543	784CIP2_187	7642
186	1972	3758	5544	784CIP2_188	7649
187	1973	3759	5545	784CIP2_189	7656
188	1974	3760	5546	784CIP2_190	7657
189	1975	3761	5547	784CIP2_191	7657
190	1976	3762	5548	784CIP2_192	7662
191	1977	3763	5549	784CIP2_193	7668
192	1978	3764	5550	784CIP2_194	7673
193	1979	3765	5551	784CIP2_195	7690
194	1980	3766	5552	784CIP2_196	7700
195	1981	3767	5553	784CIP2_197	7709
196	1982	3768	5554	784CIP2_198	7736
197	1983	3769	5555	784CIP2_199	7737
198	1984	3770	5556	784CIP2_200	7744
199	1985	3771	5557	784CIP2_201	7771
200	1986	3772	5558	784CIP2_202	7786
201	1987	3773	5559	784CIP2_203	7791
202	1988	3774	5560	784CIP2_204	7797
203	1989	3775	5561	784CIP2_205	7806
204	1990	3776	5562	784CIP2_206	7812
205	1991	3777	5563	784CIP2_207	7812
206	1992	3778	5564	784CIP2_208	7818
207	1993	3779	5565	784CIP2_209	7822
208	1994	3780	5566	784CIP2_210	7827
209	1995	3781	5567	784CIP2_211	7830
210	1996	3782	5568	784CIP2_212	7835
211	1997	3783	5569	784CIP2_214	7840
212	1998	3784	5570	784CIP2_215	7858
213	1999	3785	5571	784CIP2_216	7858
214	2000	3786	5572	784CIP2_217	7861
215	2001	3787	5573	784CIP2_218	7866
216	2002	3788	5574	784CIP2_219	7868
217	2003	3789	5575	784CIP2_220	7896
218	2004	3790	5576	784CIP2_221	7898
219	2005	3791	5577	784CIP2_222	7900
220	2006	3792	5578	784CIP2_223	7906
221	2007	3793	5579	784CIP2_224	7908
222	2008	3794	5580	784CIP2_225	7909
223	2009	3795	5581	784CIP2_226	7917
224	2010	3796	5582	784CIP2_227	7932
225	2011	3797	5583	784CIP2_228	7940
226	2012	3798	5584	784CIP2_229	7940
227	2013	3799	5585	784CIP2_230	7984
228	2014	3800	5586	784CIP2_231	7984
229	2015	3801	5587	784CIP2_232	8001
230	2016	3802	5588	784CIP2_233	8021
231	2017	3803	5589	784CIP2_234	8029
232	2018	3804	5590	784CIP2_235	8033
233	2019	3805	5591	784CIP2_236	8040
234	2020	3806	5592	784CIP2_237	8052
235	2021	3807	5593	784CIP2_238	8096
236	2022	3808	5594	784CIP2_239	8096
237	2023	3809	5595	784CIP2_240	8113
238	2024	3810	5596	784CIP2_241	8126
239	2025	3811	5597	784CIP2_242	8132
240	2026	3812	5598	784CIP2_243	8137
241	2027	3813	5599	784CIP2_244	8137
242	2028	3814	5600	784CIP2_245	8159
243	2029	3815	5601	784CIP2_246	8159
244	2030	3816	5602	784CIP2_247	8161
245	2031	3817	5603	784CIP2_248	8176

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number, corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
246	2032	3818	5604	784CIP2_249	8196
247	2033	3819	5605	784CIP2_250	8200
248	2034	3820	5606	784CIP2_251	8212
249	2035	3821	5607	784CIP2_252	8220
250	2036	3822	5608	784CIP2_253	8238
251	2037	3823	5609	784CIP2_254	8254
252	2038	3824	5610	784CIP2_255	8255
253	2039	3825	5611	784CIP2_256	8288
254	2040	3826	5612	784CIP2_257	8296
255	2041	3827	5613	784CIP2_258	8329
256	2042	3828	5614	784CIP2_259	8362
257	2043	3829	5615	784CIP2_260	8429
258	2044	3830	5616	784CIP2_261	8436
259	2045	3831	5617	784CIP2_262	8448
260	2046	3832	5618	784CIP2_263	8472
261	2047	3833	5619	784CIP2_264	8502
262	2048	3834	5620	784CIP2_265	8504
263	2049	3835	5621	784CIP2_266	8507
264	2050	3836	5622	784CIP2_268	8509
265	2051	3837	5623	784CIP2_269	8515
266	2052	3838	5624	784CIP2_270	8519
267	2053	3839	5625	784CIP2_271	8530
268	2054	3840	5626	784CIP2_272	8532
269	2055	3841	5627	784CIP2_273	8532
270	2056	3842	5628	784CIP2_274	8539
271	2057	3843	5629	784CIP2_275	8541
272	2058	3844	5630	784CIP2_276	8543
273	2059	3845	5631	784CIP2_277	8593
274	2060	3846	5632	784CIP2_278	8595
275	2061	3847	5633	784CIP2_279	8615
276	2062	3848	5634	784CIP2_280	8620
277	2063	3849	5635	784CIP2_281	8621
278	2064	3850	5636	784CIP2_282	8623
279	2065	3851	5637	784CIP2_283	8625
280	2066	3852	5638	784CIP2_284	8628
281	2067	3853	5639	784CIP2_285	8628
282	2068	3854	5640	784CIP2_286	8629
283	2069	3855	5641	784CIP2_287	8630
284	2070	3856	5642	784CIP2_288	8631
285	2071	3857	5643	784CIP2_289	8633
286	2072	3858	5644	784CIP2_290	8634
287	2073	3859	5645	784CIP2_291	8635
288	2074	3860	5646	784CIP2_292	8636
289	2075	3861	5647	784CIP2_293	8659
290	2076	3862	5648	784CIP2_294	8660
291	2077	3863	5649	784CIP2_295	8667
292	2078	3864	5650	784CIP2_296	8667
293	2079	3865	5651	784CIP2_297	8685
294	2080	3866	5652	784CIP2_298	8805
295	2081	3867	5653	784CIP2_299	8896
296	2082	3868	5654	784CIP2_300	8978
297	2083	3869	5655	784CIP2_301	9046
298	2084	3870	5656	784CIP2_302	9048
299	2085	3871	5657	784CIP2_303	9116
300	2086	3872	5658	784CIP2_304	9195
301	2087	3873	5659	784CIP2_305	9201
302	2088	3874	5660	784CIP2_306	9307
303	2089	3875	5661	784CIP2_307	9321
304	2090	3876	5662	784CIP2_308	9397
305	2091	3877	5663	784CIP2_309	9405
306	2092	3878	5664	784CIP2_310	9406
307	2093	3879	5665	784CIP2_311	9422

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
308	2094	3880	5666	784CIP2_312	9494
309	2095	3881	5667	784CIP2_313	9512
310	2096	3882	5668	784CIP2_314	9632
311	2097	3883	5669	784CIP2_315	9661
312	2098	3884	5670	784CIP2_316	9664
313	2099	3885	5671	784CIP2_317	9691
314	2100	3886	5672	784CIP2_318	9700
315	2101	3887	5673	784CIP2_319	9716
316	2102	3888	5674	784CIP2_320	9721
317	2103	3889	5675	784CIP2_321	9870
318	2104	3890	5676	784CIP2_322	9887
319	2105	3891	5677	784CIP2_323	9923
320	2106	3892	5678	784CIP2_324	9938
321	2107	3893	5679	784CIP2_325	9964
322	2108	3894	5680	784CIP2_326	10007
323	2109	3895	5681	784CIP2_327	10009
324	2110	3896	5682	784CIP2_328	10046
325	2111	3897	5683	784CIP2_329	10156
326	2112	3898	5684	784CIP2_330	10276
327	2113	3899	5685	784CIP2_331	10283
328	2114	3900	5686	784CIP2B_1	152
329	2115	3901	5687	784CIP2B_2	167
330	2116	3902	5688	784CIP2B_3	205
331	2117	3903	5689	784CIP2B_4	210
332	2118	3904	5690	784CIP2B_5	225
333	2119	3905	5691	784CIP2B_6	226
334	2120	3906	5692	784CIP2B_7	264
335	2121	3907	5693	784CIP2B_8	268
336	2122	3908	5694	784CIP2B_9	293
337	2123	3909	5695	784CIP2B_10	293
338	2124	3910	5696	784CIP2B_11	293
339	2125	3911	5697	784CIP2B_12	302
340	2126	3912	5698	784CIP2B_13	311
341	2127	3913	5699	784CIP2B_14	352
342	2128	3914	5700	784CIP2B_15	358
343	2129	3915	5701	784CIP2B_16	368
344	2130	3916	5702	784CIP2B_17	393
345	2131	3917	5703	784CIP2B_18	477
346	2132	3918	5704	784CIP2B_19	508
347	2133	3919	5705	784CIP2B_20	508
348	2134	3920	5706	784CIP2B_21	515
349	2135	3921	5707	784CIP2B_22	578
350	2136	3922	5708	784CIP2B_23	588
351	2137	3923	5709	784CIP2B_24	591
352	2138	3924	5710	784CIP2B_25	593
353	2139	3925	5711	784CIP2B_26	594
354	2140	3926	5712	784CIP2B_27	619
355	2141	3927	5713	784CIP2B_28	620
356	2142	3928	5714	784CIP2B_29	654
357	2143	3929	5715	784CIP2B_30	692
358	2144	3930	5716	784CIP2B_31	753
359	2145	3931	5717	784CIP2B_32	758
360	2146	3932	5718	784CIP2B_33	787
361	2147	3933	5719	784CIP2B_34	833
362	2148	3934	5720	784CIP2B_35	838
363	2149	3935	5721	784CIP2B_36	870
364	2150	3936	5722	784CIP2B_37	891
365	2151	3937	5723	784CIP2B_38	891
366	2152	3938	5724	784CIP2B_39	921
367	2153	3939	5725	784CIP2B_40	924
368	2154	3940	5726	784CIP2B_41	932
369	2155	3941	5727	784CIP2B_42	942

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
370	2156	3942	5728	784CIP2B_43	958
371	2157	3943	5729	784CIP2B_44	968
372	2158	3944	5730	784CIP2B_45	992
373	2159	3945	5731	784CIP2B_46	1025
374	2160	3946	5732	784CIP2B_47	1074
375	2161	3947	5733	784CIP2B_48	1104
376	2162	3948	5734	784CIP2B_49	1114
377	2163	3949	5735	784CIP2B_50	1144
378	2164	3950	5736	784CIP2B_51	1262
379	2165	3951	5737	784CIP2B_52	1318
380	2166	3952	5738	784CIP2B_53	1319
381	2167	3953	5739	784CIP2B_54	1328
382	2168	3954	5740	784CIP2B_55	1436
383	2169	3955	5741	784CIP2B_56	1464
384	2170	3956	5742	784CIP2B_57	1584
385	2171	3957	5743	784CIP2B_58	1617
386	2172	3958	5744	784CIP2B_59	1724
387	2173	3959	5745	784CIP2B_60	1728
388	2174	3960	5746	784CIP2B_61	1772
389	2175	3961	5747	784CIP2B_62	1809
390	2176	3962	5748	784CIP2B_63	1868
391	2177	3963	5749	784CIP2B_64	1898
392	2178	3964	5750	784CIP2B_65	1926
393	2179	3965	5751	784CIP2B_66	1965
394	2180	3966	5752	784CIP2B_67	1967
395	2181	3967	5753	784CIP2B_68	1995
396	2182	3968	5754	784CIP2B_69	2005
397	2183	3969	5755	784CIP2B_70	2027
398	2184	3970	5756	784CIP2B_71	2055
399	2185	3971	5757	784CIP2B_72	2103
400	2186	3972	5758	784CIP2B_73	2106
401	2187	3973	5759	784CIP2B_74	2166
402	2188	3974	5760	784CIP2B_75	2175
403	2189	3975	5761	784CIP2B_76	2176
404	2190	3976	5762	784CIP2B_78	2236
405	2191	3977	5763	784CIP2B_79	2250
406	2192	3978	5764	784CIP2B_80	2300
407	2193	3979	5765	784CIP2B_81	2323
408	2194	3980	5766	784CIP2B_82	2340
409	2195	3981	5767	784CIP2B_83	2371
410	2196	3982	5768	784CIP2B_84	2399
411	2197	3983	5769	784CIP2B_85	2411
412	2198	3984	5770	784CIP2B_86	2428
413	2199	3985	5771	784CIP2B_87	2430
414	2200	3986	5772	784CIP2B_88	2439
415	2201	3987	5773	784CIP2B_89	2447
416	2202	3988	5774	784CIP2B_90	2461
417	2203	3989	5775	784CIP2B_91	2487
418	2204	3990	5776	784CIP2B_92	2492
419	2205	3991	5777	784CIP2B_93	2512
420	2206	3992	5778	784CIP2B_94	2564
421	2207	3993	5779	784CIP2B_95	2678
422	2208	3994	5780	784CIP2B_96	2816
423	2209	3995	5781	784CIP2B_97	2818
424	2210	3996	5782	784CIP2B_98	2819
425	2211	3997	5783	784CIP2B_99	2943
426	2212	3998	5784	784CIP2B_100	3137
427	2213	3999	5785	784CIP2B_101	3137
428	2214	4000	5786	784CIP2B_102	3160
429	2215	4001	5787	784CIP2B_103	3323
430	2216	4002	5788	784CIP2B_104	3360
431	2217	4003	5789	784CIP2B_105	3362

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
432	2218	4004	5790	784CIP2B_106	3417
433	2219	4005	5791	784CIP2B_107	3418
434	2220	4006	5792	784CIP2B_108	3442
435	2221	4007	5793	784CIP2B_109	3442
436	2222	4008	5794	784CIP2B_110	3444
437	2223	4009	5795	784CIP2B_111	3855
438	2224	4010	5796	784CIP2B_112	3863
439	2225	4011	5797	784CIP2B_113	4090
440	2226	4012	5798	784CIP2B_114	4105
441	2227	4013	5799	784CIP2B_115	4142
442	2228	4014	5800	784CIP2B_116	4142
443	2229	4015	5801	784CIP2B_117	4149
444	2230	4016	5802	784CIP2B_118	4196
445	2231	4017	5803	784CIP2B_119	4202
446	2232	4018	5804	784CIP2B_120	4274
447	2233	4019	5805	784CIP2B_121	4304
448	2234	4020	5806	784CIP2B_122	4306
449	2235	4021	5807	784CIP2B_123	4311
450	2236	4022	5808	784CIP2B_124	4321
451	2237	4023	5809	784CIP2B_125	4323
452	2238	4024	5810	784CIP2B_126	4332
453	2239	4025	5811	784CIP2B_127	4488
454	2240	4026	5812	784CIP2B_128	4588
455	2241	4027	5813	784CIP2B_129	5569
456	2242	4028	5814	784CIP2B_130	5573
457	2243	4029	5815	784CIP2B_131	5577
458	2244	4030	5816	784CIP2B_132	5579
459	2245	4031	5817	784CIP2B_133	5582
460	2246	4032	5818	784CIP2B_134	5583
461	2247	4033	5819	784CIP2B_135	5584
462	2248	4034	5820	784CIP2B_136	5585
463	2249	4035	5821	784CIP2B_137	5591
464	2250	4036	5822	784CIP2B_138	5593
465	2251	4037	5823	784CIP2B_139	5594
466	2252	4038	5824	784CIP2B_140	5594
467	2253	4039	5825	784CIP2B_141	5598
468	2254	4040	5826	784CIP2B_142	5602
469	2255	4041	5827	784CIP2B_143	5605
470	2256	4042	5828	784CIP2B_144	5608
471	2257	4043	5829	784CIP2B_145	5617
472	2258	4044	5830	784CIP2B_146	5620
473	2259	4045	5831	784CIP2B_147	5622
474	2260	4046	5832	784CIP2B_148	5623
475	2261	4047	5833	784CIP2B_149	5624
476	2262	4048	5834	784CIP2B_150	5625
477	2263	4049	5835	784CIP2B_151	5627
478	2264	4050	5836	784CIP2B_152	5628
479	2265	4051	5837	784CIP2B_153	5630
480	2266	4052	5838	784CIP2B_154	5632
481	2267	4053	5839	784CIP2B_155	5640
482	2268	4054	5840	784CIP2B_156	5641
483	2269	4055	5841	784CIP2B_157	5643
484	2270	4056	5842	784CIP2B_158	5647
485	2271	4057	5843	784CIP2B_159	5649
486	2272	4058	5844	784CIP2B_160	5658
487	2273	4059	5845	784CIP2B_161	5659
488	2274	4060	5846	784CIP2B_162	5667
489	2275	4061	5847	784CIP2B_163	5672
490	2276	4062	5848	784CIP2B_164	5674
491	2277	4063	5849	784CIP2B_165	5678
492	2278	4064	5850	784CIP2B_166	5680
493	2279	4065	5851	784CIP2B_167	5684

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
494	2280	4066	5852	784CIP2B_168	5686
495	2281	4067	5853	784CIP2B_169	5694
496	2282	4068	5854	784CIP2B_170	5698
497	2283	4069	5855	784CIP2B_171	5699
498	2284	4070	5856	784CIP2B_172	5712
499	2285	4071	5857	784CIP2B_173	5719
500	2286	4072	5858	784CIP2B_174	5720
501	2287	4073	5859	784CIP2B_175	5727
502	2288	4074	5860	784CIP2B_176	5730
503	2289	4075	5861	784CIP2B_177	5734
504	2290	4076	5862	784CIP2B_178	5738
505	2291	4077	5863	784CIP2B_179	5739
506	2292	4078	5864	784CIP2B_180	5740
507	2293	4079	5865	784CIP2B_181	5744
508	2294	4080	5866	784CIP2B_182	5748
509	2295	4081	5867	784CIP2B_183	5749
510	2296	4082	5868	784CIP2B_184	5750
511	2297	4083	5869	784CIP2B_185	5750
512	2298	4084	5870	784CIP2B_186	5750
513	2299	4085	5871	784CIP2B_187	5761
514	2300	4086	5872	784CIP2B_188	5762
515	2301	4087	5873	784CIP2B_189	5767
516	2302	4088	5874	784CIP2B_190	5773
517	2303	4089	5875	784CIP2B_191	5783
518	2304	4090	5876	784CIP2B_192	5784
519	2305	4091	5877	784CIP2B_193	5788
520	2306	4092	5878	784CIP2B_194	5798
521	2307	4093	5879	784CIP2B_196	5807
522	2308	4094	5880	784CIP2B_197	5818
523	2309	4095	5881	784CIP2B_198	5819
524	2310	4096	5882	784CIP2B_199	5827
525	2311	4097	5883	784CIP2B_200	5828
526	2312	4098	5884	784CIP2B_201	5842
527	2313	4099	5885	784CIP2B_202	5853
528	2314	4100	5886	784CIP2B_203	5861
529	2315	4101	5887	784CIP2B_204	5864
530	2316	4102	5888	784CIP2B_205	5865
531	2317	4103	5889	784CIP2B_206	5871
532	2318	4104	5890	784CIP2B_207	5873
533	2319	4105	5891	784CIP2B_208	5873
534	2320	4106	5892	784CIP2B_209	5875
535	2321	4107	5893	784CIP2B_210	5878
536	2322	4108	5894	784CIP2B_211	5879
537	2323	4109	5895	784CIP2B_212	5880
538	2324	4110	5896	784CIP2B_213	5880
539	2325	4111	5897	784CIP2B_214	5880
540	2326	4112	5898	784CIP2B_215	5880
541	2327	4113	5899	784CIP2B_216	5885
542	2328	4114	5900	784CIP2B_217	5895
543	2329	4115	5901	784CIP2B_218	5898
544	2330	4116	5902	784CIP2B_219	5902
545	2331	4117	5903	784CIP2B_220	5904
546	2332	4118	5904	784CIP2B_221	5918
547	2333	4119	5905	784CIP2B_222	5921
548	2334	4120	5906	784CIP2B_223	5927
549	2335	4121	5907	784CIP2B_224	5932
550	2336	4122	5908	784CIP2B_225	5939
551	2337	4123	5909	784CIP2B_226	5945
552	2338	4124	5910	784CIP2B_227	5946
553	2339	4125	5911	784CIP2B_228	5947
554	2340	4126	5912	784CIP2B_229	5956
555	2341	4127	5913	784CIP2B_230	5967

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
556	2342	4128	5914	784CIP2B_232	5975
557	2343	4129	5915	784CIP2B_233	5977
558	2344	4130	5916	784CIP2B_234	5978
559	2345	4131	5917	784CIP2B_235	5979
560	2346	4132	5918	784CIP2B_236	5980
561	2347	4133	5919	784CIP2B_237	5988
562	2348	4134	5920	784CIP2B_238	5989
563	2349	4135	5921	784CIP2B_239	5991
564	2350	4136	5922	784CIP2B_240	5997
565	2351	4137	5923	784CIP2B_241	5998
566	2352	4138	5924	784CIP2B_242	6003
567	2353	4139	5925	784CIP2B_243	6004
568	2354	4140	5926	784CIP2B_244	6013
569	2355	4141	5927	784CIP2B_245	6028
570	2356	4142	5928	784CIP2B_246	6028
571	2357	4143	5929	784CIP2B_247	6029
572	2358	4144	5930	784CIP2B_248	6031
573	2359	4145	5931	784CIP2B_249	6031
574	2360	4146	5932	784CIP2B_250	6032
575	2361	4147	5933	784CIP2B_251	6037
576	2362	4148	5934	784CIP2B_252	6037
577	2363	4149	5935	784CIP2B_253	6043
578	2364	4150	5936	784CIP2B_254	6044
579	2365	4151	5937	784CIP2B_255	6046
580	2366	4152	5938	784CIP2B_256	6048
581	2367	4153	5939	784CIP2B_257	6049
582	2368	4154	5940	784CIP2B_258	6051
583	2369	4155	5941	784CIP2B_259	6053
584	2370	4156	5942	784CIP2B_260	6060
585	2371	4157	5943	784CIP2B_261	6063
586	2372	4158	5944	784CIP2B_262	6066
587	2373	4159	5945	784CIP2B_263	6067
588	2374	4160	5946	784CIP2B_264	6068
589	2375	4161	5947	784CIP2B_265	6073
590	2376	4162	5948	784CIP2B_266	6076
591	2377	4163	5949	784CIP2B_267	6076
592	2378	4164	5950	784CIP2B_268	6077
593	2379	4165	5951	784CIP2B_269	6079
594	2380	4166	5952	784CIP2B_270	6082
595	2381	4167	5953	784CIP2B_272	6088
596	2382	4168	5954	784CIP2B_273	6091
597	2383	4169	5955	784CIP2B_274	6094
598	2384	4170	5956	784CIP2B_275	6101
599	2385	4171	5957	784CIP2B_276	6103
600	2386	4172	5958	784CIP2B_277	6104
601	2387	4173	5959	784CIP2B_278	6108
602	2388	4174	5960	784CIP2B_279	6112
603	2389	4175	5961	784CIP2B_280	6121
604	2390	4176	5962	784CIP2B_281	6125
605	2391	4177	5963	784CIP2B_282	6126
606	2392	4178	5964	784CIP2B_283	6128
607	2393	4179	5965	784CIP2B_284	6129
608	2394	4180	5966	784CIP2B_285	6133
609	2395	4181	5967	784CIP2B_286	6133
610	2396	4182	5968	784CIP2B_287	6135
611	2397	4183	5969	784CIP2B_288	6139
612	2398	4184	5970	784CIP2B_289	6141
613	2399	4185	5971	784CIP2B_290	6145
614	2400	4186	5972	784CIP2B_291	6146
615	2401	4187	5973	784CIP2B_292	6148
616	2402	4188	5974	784CIP2B_293	6149
617	2403	4189	5975	784CIP2B_294	6149

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
618	2404	4190	5976	784CIP2B_295	6153
619	2405	4191	5977	784CIP2B_296	6159
620	2406	4192	5978	784CIP2B_297	6164
621	2407	4193	5979	784CIP2B_298	6167
622	2408	4194	5980	784CIP2B_299	6172
623	2409	4195	5981	784CIP2B_300	6173
624	2410	4196	5982	784CIP2B_301	6190
625	2411	4197	5983	784CIP2B_302	6194
626	2412	4198	5984	784CIP2B_303	6196
627	2413	4199	5985	784CIP2B_304	6197
628	2414	4200	5986	784CIP2B_305	6198
629	2415	4201	5987	784CIP2B_306	6198
630	2416	4202	5988	784CIP2B_308	6214
631	2417	4203	5989	784CIP2B_309	6215
632	2418	4204	5990	784CIP2B_310	6219
633	2419	4205	5991	784CIP2B_311	6226
634	2420	4206	5992	784CIP2B_312	6229
635	2421	4207	5993	784CIP2B_313	6234
636	2422	4208	5994	784CIP2B_314	6237
637	2423	4209	5995	784CIP2B_315	6238
638	2424	4210	5996	784CIP2B_316	6239
639	2425	4211	5997	784CIP2B_317	6239
640	2426	4212	5998	784CIP2B_318	6239
641	2427	4213	5999	784CIP2B_319	6240
642	2428	4214	6000	784CIP2B_320	6244
643	2429	4215	6001	784CIP2B_321	6245
644	2430	4216	6002	784CIP2B_322	6250
645	2431	4217	6003	784CIP2B_323	6252
646	2432	4218	6004	784CIP2B_324	6252
647	2433	4219	6005	784CIP2B_325	6256
648	2434	4220	6006	784CIP2B_326	6260
649	2435	4221	6007	784CIP2B_327	6261
650	2436	4222	6008	784CIP2B_328	6264
651	2437	4223	6009	784CIP2B_329	6265
652	2438	4224	6010	784CIP2B_330	6266
653	2439	4225	6011	784CIP2B_331	6270
654	2440	4226	6012	784CIP2B_332	6271
655	2441	4227	6013	784CIP2B_334	6274
656	2442	4228	6014	784CIP2B_335	6276
657	2443	4229	6015	784CIP2B_336	6281
658	2444	4230	6016	784CIP2B_337	6281
659	2445	4231	6017	784CIP2B_338	6288
660	2446	4232	6018	784CIP2B_339	6292
661	2447	4233	6019	784CIP2B_340	6294
662	2448	4234	6020	784CIP2B_343	6312
663	2449	4235	6021	784CIP2B_344	6312
664	2450	4236	6022	784CIP2B_345	6312
665	2451	4237	6023	784CIP2B_346	6322
666	2452	4238	6024	784CIP2B_347	6324
667	2453	4239	6025	784CIP2B_349	6329
668	2454	4240	6026	784CIP2B_350	6331
669	2455	4241	6027	784CIP2B_351	6333
670	2456	4242	6028	784CIP2B_352	6334
671	2457	4243	6029	784CIP2B_353	6337
672	2458	4244	6030	784CIP2B_354	6339
673	2459	4245	6031	784CIP2B_355	6346
674	2460	4246	6032	784CIP2B_356	6348
675	2461	4247	6033	784CIP2B_357	6348
676	2462	4248	6034	784CIP2B_358	6350
677	2463	4249	6035	784CIP2B_359	6351
678	2464	4250	6036	784CIP2B_360	6355
679	2465	4251	6037	784CIP2B_361	6362

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
680	2466	4252	6038	784CIP2B_362	6368
681	2467	4253	6039	784CIP2B_363	6369
682	2468	4254	6040	784CIP2B_364	6371
683	2469	4255	6041	784CIP2B_365	6376
684	2470	4256	6042	784CIP2B_366	6379
685	2471	4257	6043	784CIP2B_367	6380
686	2472	4258	6044	784CIP2B_368	6381
687	2473	4259	6045	784CIP2B_369	6392
688	2474	4260	6046	784CIP2B_370	6395
689	2475	4261	6047	784CIP2B_371	6397
690	2476	4262	6048	784CIP2B_372	6400
691	2477	4263	6049	784CIP2B_373	6401
692	2478	4264	6050	784CIP2B_374	6411
693	2479	4265	6051	784CIP2B_375	6411
694	2480	4266	6052	784CIP2B_376	6411
695	2481	4267	6053	784CIP2B_377	6416
696	2482	4268	6054	784CIP2B_378	6418
697	2483	4269	6055	784CIP2B_379	6422
698	2484	4270	6056	784CIP2B_380	6423
699	2485	4271	6057	784CIP2B_381	6426
700	2486	4272	6058	784CIP2B_382	6427
701	2487	4273	6059	784CIP2B_383	6428
702	2488	4274	6060	784CIP2B_384	6429
703	2489	4275	6061	784CIP2B_385	6430
704	2490	4276	6062	784CIP2B_386	6432
705	2491	4277	6063	784CIP2B_387	6432
706	2492	4278	6064	784CIP2B_388	6438
707	2493	4279	6065	784CIP2B_389	6441
708	2494	4280	6066	784CIP2B_390	6446
709	2495	4281	6067	784CIP2B_391	6454
710	2496	4282	6068	784CIP2B_392	6459
711	2497	4283	6069	784CIP2B_394	6461
712	2498	4284	6070	784CIP2B_395	6467
713	2499	4285	6071	784CIP2B_396	6468
714	2500	4286	6072	784CIP2B_397	6487
715	2501	4287	6073	784CIP2B_398	6491
716	2502	4288	6074	784CIP2B_399	6506
717	2503	4289	6075	784CIP2B_401	6514
718	2504	4290	6076	784CIP2B_402	6519
719	2505	4291	6077	784CIP2B_403	6521
720	2506	4292	6078	784CIP2B_404	6532
721	2507	4293	6079	784CIP2B_405	6536
722	2508	4294	6080	784CIP2B_406	6543
723	2509	4295	6081	784CIP2B_407	6544
724	2510	4296	6082	784CIP2B_408	6548
725	2511	4297	6083	784CIP2B_409	6551
726	2512	4298	6084	784CIP2B_410	6551
727	2513	4299	6085	784CIP2B_411	6552
728	2514	4300	6086	784CIP2B_412	6554
729	2515	4301	6087	784CIP2B_413	6556
730	2516	4302	6088	784CIP2B_414	6560
731	2517	4303	6089	784CIP2B_415	6563
732	2518	4304	6090	784CIP2B_416	6564
733	2519	4305	6091	784CIP2B_417	6567
734	2520	4306	6092	784CIP2B_418	6573
735	2521	4307	6093	784CIP2B_419	6575
736	2522	4308	6094	784CIP2B_420	6577
737	2523	4309	6095	784CIP2B_421	6593
738	2524	4310	6096	784CIP2B_422	6595
739	2525	4311	6097	784CIP2B_423	6599
740	2526	4312	6098	784CIP2B_424	6625
741	2527	4313	6099	784CIP2B_425	6625

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
742	2528	4314	6100	784CIP2B_426	6626
743	2529	4315	6101	784CIP2B_427	6630
744	2530	4316	6102	784CIP2B_428	6631
745	2531	4317	6103	784CIP2B_429	6632
746	2532	4318	6104	784CIP2B_430	6633
747	2533	4319	6105	784CIP2B_431	6634
748	2534	4320	6106	784CIP2B_432	6638
749	2535	4321	6107	784CIP2B_433	6641
750	2536	4322	6108	784CIP2B_434	6644
751	2537	4323	6109	784CIP2B_435	6646
752	2538	4324	6110	784CIP2B_436	6648
753	2539	4325	6111	784CIP2B_437	6652
754	2540	4326	6112	784CIP2B_438	6654
755	2541	4327	6113	784CIP2B_439	6657
756	2542	4328	6114	784CIP2B_440	6658
757	2543	4329	6115	784CIP2B_441	6663
758	2544	4330	6116	784CIP2B_442	6664
759	2545	4331	6117	784CIP2B_443	6668
760	2546	4332	6118	784CIP2B_444	6669
761	2547	4333	6119	784CIP2B_445	6673
762	2548	4334	6120	784CIP2B_446	6685
763	2549	4335	6121	784CIP2B_447	6687
764	2550	4336	6122	784CIP2B_448	6689
765	2551	4337	6123	784CIP2B_449	6693
766	2552	4338	6124	784CIP2B_450	6698
767	2553	4339	6125	784CIP2B_451	6699
768	2554	4340	6126	784CIP2B_452	6705
769	2555	4341	6127	784CIP2B_453	6711
770	2556	4342	6128	784CIP2B_454	6713
771	2557	4343	6129	784CIP2B_455	6716
772	2558	4344	6130	784CIP2B_456	6725
773	2559	4345	6131	784CIP2B_457	6726
774	2560	4346	6132	784CIP2B_458	6727
775	2561	4347	6133	784CIP2B_459	6730
776	2562	4348	6134	784CIP2B_460	6730
777	2563	4349	6135	784CIP2B_461	6730
778	2564	4350	6136	784CIP2B_462	6732
779	2565	4351	6137	784CIP2B_463	6733
780	2566	4352	6138	784CIP2B_464	6737
781	2567	4353	6139	784CIP2B_465	6745
782	2568	4354	6140	784CIP2B_466	6751
783	2569	4355	6141	784CIP2B_467	6754
784	2570	4356	6142	784CIP2B_468	6758
785	2571	4357	6143	784CIP2B_469	6761
786	2572	4358	6144	784CIP2B_470	6765
787	2573	4359	6145	784CIP2B_471	6768
788	2574	4360	6146	784CIP2B_472	6773
789	2575	4361	6147	784CIP2B_473	6776
790	2576	4362	6148	784CIP2B_474	6796
791	2577	4363	6149	784CIP2B_475	6798
792	2578	4364	6150	784CIP2B_476	6823
793	2579	4365	6151	784CIP2B_477	6825
794	2580	4366	6152	784CIP2B_478	6826
795	2581	4367	6153	784CIP2B_479	6839
796	2582	4368	6154	784CIP2B_480	6844
797	2583	4369	6155	784CIP2B_482	6849
798	2584	4370	6156	784CIP2B_483	6854
799	2585	4371	6157	784CIP2B_484	6857
800	2586	4372	6158	784CIP2B_485	6861
801	2587	4373	6159	784CIP2B_486	6873
802	2588	4374	6160	784CIP2B_487	6875
803	2589	4375	6161	784CIP2B_488	6877

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
804	2590	4376	6162	784CIP2B_489	6880
805	2591	4377	6163	784CIP2B_490	6885
806	2592	4378	6164	784CIP2B_491	6890
807	2593	4379	6165	784CIP2B_492	6890
808	2594	4380	6166	784CIP2B_493	6894
809	2595	4381	6167	784CIP2B_494	6901
810	2596	4382	6168	784CIP2B_495	6904
811	2597	4383	6169	784CIP2B_496	6907
812	2598	4384	6170	784CIP2B_497	6914
813	2599	4385	6171	784CIP2B_498	6917
814	2600	4386	6172	784CIP2B_499	6923
815	2601	4387	6173	784CIP2B_500	6929
816	2602	4388	6174	784CIP2B_501	6931
817	2603	4389	6175	784CIP2B_502	6935
818	2604	4390	6176	784CIP2B_503	6940
819	2605	4391	6177	784CIP2B_504	6945
820	2606	4392	6178	784CIP2B_505	6946
821	2607	4393	6179	784CIP2B_506	6947
822	2608	4394	6180	784CIP2B_507	6949
823	2609	4395	6181	784CIP2B_508	6959
824	2610	4396	6182	784CIP2B_509	6960
825	2611	4397	6183	784CIP2B_510	6962
826	2612	4398	6184	784CIP2B_511	6963
827	2613	4399	6185	784CIP2B_512	6967
828	2614	4400	6186	784CIP2B_513	6983
829	2615	4401	6187	784CIP2B_514	6988
830	2616	4402	6188	784CIP2B_515	6996
831	2617	4403	6189	784CIP2B_516	7003
832	2618	4404	6190	784CIP2B_517	7016
833	2619	4405	6191	784CIP2B_518	7017
834	2620	4406	6192	784CIP2B_519	7025
835	2621	4407	6193	784CIP2B_520	7025
836	2622	4408	6194	784CIP2B_521	7025
837	2623	4409	6195	784CIP2B_522	7050
838	2624	4410	6196	784CIP2B_523	7051
839	2625	4411	6197	784CIP2B_524	7055
840	2626	4412	6198	784CIP2B_525	7060
841	2627	4413	6199	784CIP2B_526	7064
842	2628	4414	6200	784CIP2B_527	7067
843	2629	4415	6201	784CIP2B_528	7071
844	2630	4416	6202	784CIP2B_529	7072
845	2631	4417	6203	784CIP2B_530	7073
846	2632	4418	6204	784CIP2B_531	7076
847	2633	4419	6205	784CIP2B_532	7088
848	2634	4420	6206	784CIP2B_533	7089
849	2635	4421	6207	784CIP2B_534	7091
850	2636	4422	6208	784CIP2B_535	7091
851	2637	4423	6209	784CIP2B_536	7104
852	2638	4424	6210	784CIP2B_537	7105
853	2639	4425	6211	784CIP2B_538	7105
854	2640	4426	6212	784CIP2B_539	7109
855	2641	4427	6213	784CIP2B_540	7109
856	2642	4428	6214	784CIP2B_541	7119
857	2643	4429	6215	784CIP2B_542	7120
858	2644	4430	6216	784CIP2B_543	7121
859	2645	4431	6217	784CIP2B_544	7126
860	2646	4432	6218	784CIP2B_545	7127
861	2647	4433	6219	784CIP2B_546	7130
862	2648	4434	6220	784CIP2B_547	7131
863	2649	4435	6221	784CIP2B_548	7144
864	2650	4436	6222	784CIP2B_549	7159
865	2651	4437	6223	784CIP2B_550	7163

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
866	2652	4438	6224	784CIP2B_551	7175
867	2653	4439	6225	784CIP2B_552	7188
868	2654	4440	6226	784CIP2B_553	7189
869	2655	4441	6227	784CIP2B_554	7190
870	2656	4442	6228	784CIP2B_555	7191
871	2657	4443	6229	784CIP2B_556	7203
872	2658	4444	6230	784CIP2B_557	7204
873	2659	4445	6231	784CIP2B_558	7208
874	2660	4446	6232	784CIP2B_559	7209
875	2661	4447	6233	784CIP2B_560	7210
876	2662	4448	6234	784CIP2B_561	7216
877	2663	4449	6235	784CIP2B_562	7221
878	2664	4450	6236	784CIP2B_563	7230
879	2665	4451	6237	784CIP2B_564	7237
880	2666	4452	6238	784CIP2B_565	7240
881	2667	4453	6239	784CIP2B_566	7245
882	2668	4454	6240	784CIP2B_567	7250
883	2669	4455	6241	784CIP2B_568	7251
884	2670	4456	6242	784CIP2B_569	7255
885	2671	4457	6243	784CIP2B_570	7260
886	2672	4458	6244	784CIP2B_571	7265
887	2673	4459	6245	784CIP2B_572	7268
888	2674	4460	6246	784CIP2B_573	7275
889	2675	4461	6247	784CIP2B_574	7279
890	2676	4462	6248	784CIP2B_575	7283
891	2677	4463	6249	784CIP2B_576	7283
892	2678	4464	6250	784CIP2B_577	7287
893	2679	4465	6251	784CIP2B_578	7301
894	2680	4466	6252	784CIP2B_579	7308
895	2681	4467	6253	784CIP2B_580	7308
896	2682	4468	6254	784CIP2B_581	7309
897	2683	4469	6255	784CIP2B_582	7319
898	2684	4470	6256	784CIP2B_583	7320
899	2685	4471	6257	784CIP2B_584	7326
900	2686	4472	6258	784CIP2B_585	7326
901	2687	4473	6259	784CIP2B_586	7334
902	2688	4474	6260	784CIP2B_587	7337
903	2689	4475	6261	784CIP2B_588	7339
904	2690	4476	6262	784CIP2B_589	7344
905	2691	4477	6263	784CIP2B_590	7355
906	2692	4478	6264	784CIP2B_591	7363
907	2693	4479	6265	784CIP2B_592	7363
908	2694	4480	6266	784CIP2B_593	7365
909	2695	4481	6267	784CIP2B_594	7368
910	2696	4482	6268	784CIP2B_595	7369
911	2697	4483	6269	784CIP2B_596	7372
912	2698	4484	6270	784CIP2B_599	7375
913	2699	4485	6271	784CIP2B_600	7381
914	2700	4486	6272	784CIP2B_601	7383
915	2701	4487	6273	784CIP2B_602	7387
916	2702	4488	6274	784CIP2B_603	7391
917	2703	4489	6275	784CIP2B_604	7393
918	2704	4490	6276	784CIP2B_605	7395
919	2705	4491	6277	784CIP2B_606	7397
920	2706	4492	6278	784CIP2B_607	7399
921	2707	4493	6279	784CIP2B_608	7405
922	2708	4494	6280	784CIP2B_609	7406
923	2709	4495	6281	784CIP2B_610	7406
924	2710	4496	6282	784CIP2B_611	7409
925	2711	4497	6283	784CIP2B_612	7410
926	2712	4498	6284	784CIP2B_613	7411
927	2713	4499	6285	784CIP2B_614	7417

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
928	2714	4500	6286	784CIP2B_615	7418
929	2715	4501	6287	784CIP2B_616	7421
930	2716	4502	6288	784CIP2B_617	7422
931	2717	4503	6289	784CIP2B_618	7422
932	2718	4504	6290	784CIP2B_619	7423
933	2719	4505	6291	784CIP2B_620	7424
934	2720	4506	6292	784CIP2B_621	7426
935	2721	4507	6293	784CIP2B_622	7427
936	2722	4508	6294	784CIP2B_623	7428
937	2723	4509	6295	784CIP2B_624	7430
938	2724	4510	6296	784CIP2B_625	7435
939	2725	4511	6297	784CIP2B_626	7437
940	2726	4512	6298	784CIP2B_627	7439
941	2727	4513	6299	784CIP2B_628	7440
942	2728	4514	6300	784CIP2B_629	7442
943	2729	4515	6301	784CIP2B_630	7450
944	2730	4516	6302	784CIP2B_631	7451
945	2731	4517	6303	784CIP2B_632	7452
946	2732	4518	6304	784CIP2B_633	7454
947	2733	4519	6305	784CIP2B_634	7457
948	2734	4520	6306	784CIP2B_635	7459
949	2735	4521	6307	784CIP2B_636	7461
950	2736	4522	6308	784CIP2B_637	7463
951	2737	4523	6309	784CIP2B_638	7466
952	2738	4524	6310	784CIP2B_639	7469
953	2739	4525	6311	784CIP2B_640	7473
954	2740	4526	6312	784CIP2B_641	7481
955	2741	4527	6313	784CIP2B_642	7482
956	2742	4528	6314	784CIP2B_643	7482
957	2743	4529	6315	784CIP2B_644	7483
958	2744	4530	6316	784CIP2B_645	7485
959	2745	4531	6317	784CIP2B_646	7486
960	2746	4532	6318	784CIP2B_647	7487
961	2747	4533	6319	784CIP2B_648	7491
962	2748	4534	6320	784CIP2B_649	7492
963	2749	4535	6321	784CIP2B_650	7494
964	2750	4536	6322	784CIP2B_651	7498
965	2751	4537	6323	784CIP2B_652	7504
966	2752	4538	6324	784CIP2B_653	7508
967	2753	4539	6325	784CIP2B_654	7516
968	2754	4540	6326	784CIP2B_655	7518
969	2755	4541	6327	784CIP2B_656	7519
970	2756	4542	6328	784CIP2B_657	7521
971	2757	4543	6329	784CIP2B_658	7529
972	2758	4544	6330	784CIP2B_659	7532
973	2759	4545	6331	784CIP2B_660	7533
974	2760	4546	6332	784CIP2B_661	7535
975	2761	4547	6333	784CIP2B_662	7545
976	2762	4548	6334	784CIP2B_663	7546
977	2763	4549	6335	784CIP2B_664	7552
978	2764	4550	6336	784CIP2B_665	7554
979	2765	4551	6337	784CIP2B_666	7567
980	2766	4552	6338	784CIP2B_667	7569
981	2767	4553	6339	784CIP2B_668	7575
982	2768	4554	6340	784CIP2B_669	7576
983	2769	4555	6341	784CIP2B_670	7577
984	2770	4556	6342	784CIP2B_671	7579
985	2771	4557	6343	784CIP2B_672	7582
986	2772	4558	6344	784CIP2B_673	7587
987	2773	4559	6345	784CIP2B_674	7589
988	2774	4560	6346	784CIP2B_675	7597
989	2775	4561	6347	784CIP2B_676	7597

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
990	2776	4562	6348	784CIP2B_677	7609
991	2777	4563	6349	784CIP2B_678	7609
992	2778	4564	6350	784CIP2B_679	7609
993	2779	4565	6351	784CIP2B_680	7613
994	2780	4566	6352	784CIP2B_681	7623
995	2781	4567	6353	784CIP2B_682	7629
996	2782	4568	6354	784CIP2B_683	7630
997	2783	4569	6355	784CIP2B_684	7633
998	2784	4570	6356	784CIP2B_685	7635
999	2785	4571	6357	784CIP2B_686	7638
1000	2786	4572	6358	784CIP2B_687	7639
1001	2787	4573	6359	784CIP2B_688	7646
1002	2788	4574	6360	784CIP2B_689	7647
1003	2789	4575	6361	784CIP2B_690	7648
1004	2790	4576	6362	784CIP2B_691	7658
1005	2791	4577	6363	784CIP2B_692	7664
1006	2792	4578	6364	784CIP2B_693	7664
1007	2793	4579	6365	784CIP2B_695	7674
1008	2794	4580	6366	784CIP2B_696	7675
1009	2795	4581	6367	784CIP2B_697	7676
1010	2796	4582	6368	784CIP2B_698	7681
1011	2797	4583	6369	784CIP2B_699	7688
1012	2798	4584	6370	784CIP2B_700	7693
1013	2799	4585	6371	784CIP2B_701	7694
1014	2800	4586	6372	784CIP2B_702	7715
1015	2801	4587	6373	784CIP2B_703	7716
1016	2802	4588	6374	784CIP2B_704	7718
1017	2803	4589	6375	784CIP2B_705	7721
1018	2804	4590	6376	784CIP2B_706	7723
1019	2805	4591	6377	784CIP2B_707	7729
1020	2806	4592	6378	784CIP2B_708	7733
1021	2807	4593	6379	784CIP2B_709	7735
1022	2808	4594	6380	784CIP2B_710	7741
1023	2809	4595	6381	784CIP2B_711	7743
1024	2810	4596	6382	784CIP2B_712	7748
1025	2811	4597	6383	784CIP2B_713	7749
1026	2812	4598	6384	784CIP2B_714	7750
1027	2813	4599	6385	784CIP2B_715	7757
1028	2814	4600	6386	784CIP2B_716	7759
1029	2815	4601	6387	784CIP2B_717	7760
1030	2816	4602	6388	784CIP2B_718	7760
1031	2817	4603	6389	784CIP2B_719	7764
1032	2818	4604	6390	784CIP2B_720	7765
1033	2819	4605	6391	784CIP2B_721	7766
1034	2820	4606	6392	784CIP2B_722	7767
1035	2821	4607	6393	784CIP2B_723	7769
1036	2822	4608	6394	784CIP2B_724	7770
1037	2823	4609	6395	784CIP2B_725	7774
1038	2824	4610	6396	784CIP2B_726	7779
1039	2825	4611	6397	784CIP2B_727	7781
1040	2826	4612	6398	784CIP2B_728	7782
1041	2827	4613	6399	784CIP2B_729	7783
1042	2828	4614	6400	784CIP2B_730	7787
1043	2829	4615	6401	784CIP2B_731	7792
1044	2830	4616	6402	784CIP2B_732	7795
1045	2831	4617	6403	784CIP2B_733	7801
1046	2832	4618	6404	784CIP2B_734	7807
1047	2833	4619	6405	784CIP2B_735	7808
1048	2834	4620	6406	784CIP2B_736	7819
1049	2835	4621	6407	784CIP2B_737	7824
1050	2836	4622	6408	784CIP2B_738	7826
1051	2837	4623	6409	784CIP2B_739	7829

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1052	2838	4624	6410	784CIP2B_740	7832
1053	2839	4625	6411	784CIP2B_741	7839
1054	2840	4626	6412	784CIP2B_743	7847
1055	2841	4627	6413	784CIP2B_744	7848
1056	2842	4628	6414	784CIP2B_745	7853
1057	2843	4629	6415	784CIP2B_746	7854
1058	2844	4630	6416	784CIP2B_747	7856
1059	2845	4631	6417	784CIP2B_748	7862
1060	2846	4632	6418	784CIP2B_749	7865
1061	2847	4633	6419	784CIP2B_750	7874
1062	2848	4634	6420	784CIP2B_751	7877
1063	2849	4635	6421	784CIP2B_752	7880
1064	2850	4636	6422	784CIP2B_753	7882
1065	2851	4637	6423	784CIP2B_754	7884
1066	2852	4638	6424	784CIP2B_755	7886
1067	2853	4639	6425	784CIP2B_756	7888
1068	2854	4640	6426	784CIP2B_757	7889
1069	2855	4641	6427	784CIP2B_758	7901
1070	2856	4642	6428	784CIP2B_759	7910
1071	2857	4643	6429	784CIP2B_760	7911
1072	2858	4644	6430	784CIP2B_761	7921
1073	2859	4645	6431	784CIP2B_762	7923
1074	2860	4646	6432	784CIP2B_763	7924
1075	2861	4647	6433	784CIP2B_764	7925
1076	2862	4648	6434	784CIP2B_765	7928
1077	2863	4649	6435	784CIP2B_766	7929
1078	2864	4650	6436	784CIP2B_767	7930
1079	2865	4651	6437	784CIP2B_768	7934
1080	2866	4652	6438	784CIP2B_769	7938
1081	2867	4653	6439	784CIP2B_770	7942
1082	2868	4654	6440	784CIP2B_771	7945
1083	2869	4655	6441	784CIP2B_772	7946
1084	2870	4656	6442	784CIP2B_773	7948
1085	2871	4657	6443	784CIP2B_774	7951
1086	2872	4658	6444	784CIP2B_775	7952
1087	2873	4659	6445	784CIP2B_776	7953
1088	2874	4660	6446	784CIP2B_777	7954
1089	2875	4661	6447	784CIP2B_778	7957
1090	2876	4662	6448	784CIP2B_779	7958
1091	2877	4663	6449	784CIP2B_780	7961
1092	2878	4664	6450	784CIP2B_781	7965
1093	2879	4665	6451	784CIP2B_782	7966
1094	2880	4666	6452	784CIP2B_783	7979
1095	2881	4667	6453	784CIP2B_784	7986
1096	2882	4668	6454	784CIP2B_785	7986
1097	2883	4669	6455	784CIP2B_786	7988
1098	2884	4670	6456	784CIP2B_787	7991
1099	2885	4671	6457	784CIP2B_788	7992
1100	2886	4672	6458	784CIP2B_789	7992
1101	2887	4673	6459	784CIP2B_790	7992
1102	2888	4674	6460	784CIP2B_791	7992
1103	2889	4675	6461	784CIP2B_792	8003
1104	2890	4676	6462	784CIP2B_793	8014
1105	2891	4677	6463	784CIP2B_794	8015
1106	2892	4678	6464	784CIP2B_795	8016
1107	2893	4679	6465	784CIP2B_796	8017
1108	2894	4680	6466	784CIP2B_797	8019
1109	2895	4681	6467	784CIP2B_798	8020
1110	2896	4682	6468	784CIP2B_799	8022
1111	2897	4683	6469	784CIP2B_800	8022
1112	2898	4684	6470	784CIP2B_801	8028
1113	2899	4685	6471	784CIP2B_802	8030

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1114	2900	4686	6472	784CIP2B_803	8038
1115	2901	4687	6473	784CIP2B_804	8042
1116	2902	4688	6474	784CIP2B_805	8045
1117	2903	4689	6475	784CIP2B_806	8045
1118	2904	4690	6476	784CIP2B_807	8046
1119	2905	4691	6477	784CIP2B_808	8047
1120	2906	4692	6478	784CIP2B_809	8051
1121	2907	4693	6479	784CIP2B_810	8059
1122	2908	4694	6480	784CIP2B_811	8064
1123	2909	4695	6481	784CIP2B_812	8069
1124	2910	4696	6482	784CIP2B_813	8074
1125	2911	4697	6483	784CIP2B_814	8077
1126	2912	4698	6484	784CIP2B_815	8078
1127	2913	4699	6485	784CIP2B_816	8079
1128	2914	4700	6486	784CIP2B_817	8084
1129	2915	4701	6487	784CIP2B_818	8088
1130	2916	4702	6488	784CIP2B_819	8090
1131	2917	4703	6489	784CIP2B_820	8091
1132	2918	4704	6490	784CIP2B_821	8099
1133	2919	4705	6491	784CIP2B_822	8099
1134	2920	4706	6492	784CIP2B_823	8100
1135	2921	4707	6493	784CIP2B_824	8102
1136	2922	4708	6494	784CIP2B_825	8103
1137	2923	4709	6495	784CIP2B_826	8103
1138	2924	4710	6496	784CIP2B_827	8104
1139	2925	4711	6497	784CIP2B_828	8108
1140	2926	4712	6498	784CIP2B_829	8110
1141	2927	4713	6499	784CIP2B_830	8116
1142	2928	4714	6500	784CIP2B_831	8117
1143	2929	4715	6501	784CIP2B_832	8123
1144	2930	4716	6502	784CIP2B_833	8130
1145	2931	4717	6503	784CIP2B_834	8130
1146	2932	4718	6504	784CIP2B_835	8143
1147	2933	4719	6505	784CIP2B_836	8143
1148	2934	4720	6506	784CIP2B_837	8154
1149	2935	4721	6507	784CIP2B_838	8155
1150	2936	4722	6508	784CIP2B_839	8162
1151	2937	4723	6509	784CIP2B_840	8163
1152	2938	4724	6510	784CIP2B_841	8172
1153	2939	4725	6511	784CIP2B_842	8173
1154	2940	4726	6512	784CIP2B_843	8179
1155	2941	4727	6513	784CIP2B_844	8182
1156	2942	4728	6514	784CIP2B_845	8183
1157	2943	4729	6515	784CIP2B_846	8184
1158	2944	4730	6516	784CIP2B_847	8185
1159	2945	4731	6517	784CIP2B_848	8187
1160	2946	4732	6518	784CIP2B_849	8188
1161	2947	4733	6519	784CIP2B_850	8190
1162	2948	4734	6520	784CIP2B_851	8190
1163	2949	4735	6521	784CIP2B_852	8192
1164	2950	4736	6522	784CIP2B_853	8193
1165	2951	4737	6523	784CIP2B_854	8197
1166	2952	4738	6524	784CIP2B_855	8197
1167	2953	4739	6525	784CIP2B_856	8199
1168	2954	4740	6526	784CIP2B_857	8202
1169	2955	4741	6527	784CIP2B_858	8203
1170	2956	4742	6528	784CIP2B_859	8208
1171	2957	4743	6529	784CIP2B_860	8209
1172	2958	4744	6530	784CIP2B_861	8211
1173	2959	4745	6531	784CIP2B_862	8214
1174	2960	4746	6532	784CIP2B_863	8217
1175	2961	4747	6533	784CIP2B_864	8223

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1176	2962	4748	6534	784CIP2B_865	8224
1177	2963	4749	6535	784CIP2B_866	8226
1178	2964	4750	6536	784CIP2B_867	8227
1179	2965	4751	6537	784CIP2B_868	8229
1180	2966	4752	6538	784CIP2B_869	8232
1181	2967	4753	6539	784CIP2B_870	8236
1182	2968	4754	6540	784CIP2B_871	8239
1183	2969	4755	6541	784CIP2B_872	8244
1184	2970	4756	6542	784CIP2B_873	8245
1185	2971	4757	6543	784CIP2B_874	8248
1186	2972	4758	6544	784CIP2B_875	8251
1187	2973	4759	6545	784CIP2B_876	8253
1188	2974	4760	6546	784CIP2B_877	8260
1189	2975	4761	6547	784CIP2B_878	8262
1190	2976	4762	6548	784CIP2B_879	8268
1191	2977	4763	6549	784CIP2B_880	8270
1192	2978	4764	6550	784CIP2B_881	8272
1193	2979	4765	6551	784CIP2B_882	8274
1194	2980	4766	6552	784CIP2B_883	8274
1195	2981	4767	6553	784CIP2B_884	8275
1196	2982	4768	6554	784CIP2B_885	8277
1197	2983	4769	6555	784CIP2B_886	8281
1198	2984	4770	6556	784CIP2B_887	8283
1199	2985	4771	6557	784CIP2B_888	8289
1200	2986	4772	6558	784CIP2B_889	8295
1201	2987	4773	6559	784CIP2B_890	8300
1202	2988	4774	6560	784CIP2B_891	8303
1203	2989	4775	6561	784CIP2B_892	8304
1204	2990	4776	6562	784CIP2B_893	8305
1205	2991	4777	6563	784CIP2B_894	8309
1206	2992	4778	6564	784CIP2B_895	8318
1207	2993	4779	6565	784CIP2B_896	8319
1208	2994	4780	6566	784CIP2B_897	8321
1209	2995	4781	6567	784CIP2B_898	8322
1210	2996	4782	6568	784CIP2B_899	8323
1211	2997	4783	6569	784CIP2B_900	8325
1212	2998	4784	6570	784CIP2B_901	8331
1213	2999	4785	6571	784CIP2B_902	8332
1214	3000	4786	6572	784CIP2B_903	8333
1215	3001	4787	6573	784CIP2B_904	8335
1216	3002	4788	6574	784CIP2B_905	8336
1217	3003	4789	6575	784CIP2B_906	8337
1218	3004	4790	6576	784CIP2B_907	8340
1219	3005	4791	6577	784CIP2B_908	8343
1220	3006	4792	6578	784CIP2B_909	8347
1221	3007	4793	6579	784CIP2B_910	8349
1222	3008	4794	6580	784CIP2B_911	8351
1223	3009	4795	6581	784CIP2B_912	8353
1224	3010	4796	6582	784CIP2B_913	8355
1225	3011	4797	6583	784CIP2B_914	8361
1226	3012	4798	6584	784CIP2B_915	8365
1227	3013	4799	6585	784CIP2B_916	8367
1228	3014	4800	6586	784CIP2B_917	8369
1229	3015	4801	6587	784CIP2B_919	8375
1230	3016	4802	6588	784CIP2B_920	8387
1231	3017	4803	6589	784CIP2B_921	8391
1232	3018	4804	6590	784CIP2B_922	8393
1233	3019	4805	6591	784CIP2B_923	8393
1234	3020	4806	6592	784CIP2B_924	8394
1235	3021	4807	6593	784CIP2B_925	8395
1236	3022	4808	6594	784CIP2B_926	8396
1237	3023	4809	6595	784CIP2B_927	8398

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1238	3024	4810	6596	784CIP2B_928	8402
1239	3025	4811	6597	784CIP2B_929	8402
1240	3026	4812	6598	784CIP2B_930	8405
1241	3027	4813	6599	784CIP2B_931	8406
1242	3028	4814	6600	784CIP2B_932	8409
1243	3029	4815	6601	784CIP2B_933	8410
1244	3030	4816	6602	784CIP2B_934	8414
1245	3031	4817	6603	784CIP2B_935	8415
1246	3032	4818	6604	784CIP2B_936	8419
1247	3033	4819	6605	784CIP2B_937	8426
1248	3034	4820	6606	784CIP2B_938	8430
1249	3035	4821	6607	784CIP2B_939	8431
1250	3036	4822	6608	784CIP2B_940	8432
1251	3037	4823	6609	784CIP2B_941	8433
1252	3038	4824	6610	784CIP2B_942	8434
1253	3039	4825	6611	784CIP2B_943	8438
1254	3040	4826	6612	784CIP2B_944	8439
1255	3041	4827	6613	784CIP2B_945	8441
1256	3042	4828	6614	784CIP2B_946	8450
1257	3043	4829	6615	784CIP2B_947	8451
1258	3044	4830	6616	784CIP2B_948	8452
1259	3045	4831	6617	784CIP2B_949	8460
1260	3046	4832	6618	784CIP2B_950	8461
1261	3047	4833	6619	784CIP2B_951	8462
1262	3048	4834	6620	784CIP2B_952	8464
1263	3049	4835	6621	784CIP2B_953	8465
1264	3050	4836	6622	784CIP2B_954	8467
1265	3051	4837	6623	784CIP2B_955	8470
1266	3052	4838	6624	784CIP2B_956	8471
1267	3053	4839	6625	784CIP2B_957	8473
1268	3054	4840	6626	784CIP2B_958	8474
1269	3055	4841	6627	784CIP2B_959	8475
1270	3056	4842	6628	784CIP2B_960	8476
1271	3057	4843	6629	784CIP2B_961	8480
1272	3058	4844	6630	784CIP2B_962	8482
1273	3059	4845	6631	784CIP2B_963	8482
1274	3060	4846	6632	784CIP2B_964	8486
1275	3061	4847	6633	784CIP2B_965	8488
1276	3062	4848	6634	784CIP2B_966	8492
1277	3063	4849	6635	784CIP2B_967	8494
1278	3064	4850	6636	784CIP2B_968	8496
1279	3065	4851	6637	784CIP2B_969	8497
1280	3066	4852	6638	784CIP2B_970	8499
1281	3067	4853	6639	784CIP2B_971	8513
1282	3068	4854	6640	784CIP2B_972	8522
1283	3069	4855	6641	784CIP2B_973	8526
1284	3070	4856	6642	784CIP2B_974	8531
1285	3071	4857	6643	784CIP2B_975	8533
1286	3072	4858	6644	784CIP2B_976	8542
1287	3073	4859	6645	784CIP2B_977	8544
1288	3074	4860	6646	784CIP2B_978	8565
1289	3075	4861	6647	784CIP2B_979	8565
1290	3076	4862	6648	784CIP2B_980	8572
1291	3077	4863	6649	784CIP2B_981	8576
1292	3078	4864	6650	784CIP2B_982	8578
1293	3079	4865	6651	784CIP2B_983	8584
1294	3080	4866	6652	784CIP2B_984	8598
1295	3081	4867	6653	784CIP2B_985	8602
1296	3082	4868	6654	784CIP2B_986	8604
1297	3083	4869	6655	784CIP2B_987	8609
1298	3084	4870	6656	784CIP2B_988	8612
1299	3085	4871	6657	784CIP2B_989	8637

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1300	3086	4872	6658	784CIP2B_990	8640
1301	3087	4873	6659	784CIP2B_991	8643
1302	3088	4874	6660	784CIP2B_992	8645
1303	3089	4875	6661	784CIP2B_993	8650
1304	3090	4876	6662	784CIP2B_994	8651
1305	3091	4877	6663	784CIP2B_995	8654
1306	3092	4878	6664	784CIP2B_996	8655
1307	3093	4879	6665	784CIP2B_997	8657
1308	3094	4880	6666	784CIP2B_998	8665
1309	3095	4881	6667	784CIP2B_999	8668
1310	3096	4882	6668	784CIP2B_1000	8671
1311	3097	4883	6669	784CIP2B_1001	8672
1312	3098	4884	6670	784CIP2B_1002	8692
1313	3099	4885	6671	784CIP2B_1003	8706
1314	3100	4886	6672	784CIP2B_1004	8716
1315	3101	4887	6673	784CIP2B_1005	8719
1316	3102	4888	6674	784CIP2B_1006	8743
1317	3103	4889	6675	784CIP2B_1007	8764
1318	3104	4890	6676	784CIP2B_1008	8764
1319	3105	4891	6677	784CIP2B_1009	8764
1320	3106	4892	6678	784CIP2B_1010	8774
1321	3107	4893	6679	784CIP2B_1011	8782
1322	3108	4894	6680	784CIP2B_1012	8796
1323	3109	4895	6681	784CIP2B_1013	8827
1324	3110	4896	6682	784CIP2B_1014	8842
1325	3111	4897	6683	784CIP2B_1015	8842
1326	3112	4898	6684	784CIP2B_1016	8858
1327	3113	4899	6685	784CIP2B_1017	8871
1328	3114	4900	6686	784CIP2B_1018	8921
1329	3115	4901	6687	784CIP2B_1019	8927
1330	3116	4902	6688	784CIP2B_1020	8942
1331	3117	4903	6689	784CIP2B_1021	8994
1332	3118	4904	6690	784CIP2B_1022	9023
1333	3119	4905	6691	784CIP2B_1023	9028
1334	3120	4906	6692	784CIP2B_1024	9058
1335	3121	4907	6693	784CIP2B_1025	9058
1336	3122	4908	6694	784CIP2B_1026	9079
1337	3123	4909	6695	784CIP2B_1027	9079
1338	3124	4910	6696	784CIP2B_1028	9082
1339	3125	4911	6697	784CIP2B_1029	9084
1340	3126	4912	6698	784CIP2B_1030	9093
1341	3127	4913	6699	784CIP2B_1031	9101
1342	3128	4914	6700	784CIP2B_1032	9103
1343	3129	4915	6701	784CIP2B_1033	9105
1344	3130	4916	6702	784CIP2B_1034	9151
1345	3131	4917	6703	784CIP2B_1035	9161
1346	3132	4918	6704	784CIP2B_1036	9172
1347	3133	4919	6705	784CIP2B_1037	9174
1348	3134	4920	6706	784CIP2B_1038	9204
1349	3135	4921	6707	784CIP2B_1039	9234
1350	3136	4922	6708	784CIP2B_1040	9235
1351	3137	4923	6709	784CIP2B_1041	9239
1352	3138	4924	6710	784CIP2B_1042	9256
1353	3139	4925	6711	784CIP2B_1043	9276
1354	3140	4926	6712	784CIP2B_1044	9345
1355	3141	4927	6713	784CIP2B_1045	9379
1356	3142	4928	6714	784CIP2B_1046	9435
1357	3143	4929	6715	784CIP2B_1047	9437
1358	3144	4930	6716	784CIP2B_1048	9469
1359	3145	4931	6717	784CIP2B_1049	9500
1360	3146	4932	6718	784CIP2B_1050	9502
1361	3147	4933	6719	784CIP2B_1051	9520

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1362	3148	4934	6720	784CIP2B_1052	9541
1363	3149	4935	6721	784CIP2B_1053	9541
1364	3150	4936	6722	784CIP2B_1054	9548
1365	3151	4937	6723	784CIP2B_1055	9556
1366	3152	4938	6724	784CIP2B_1056	9556
1367	3153	4939	6725	784CIP2B_1057	9575
1368	3154	4940	6726	784CIP2B_1058	9589
1369	3155	4941	6727	784CIP2B_1059	9599
1370	3156	4942	6728	784CIP2B_1060	9602
1371	3157	4943	6729	784CIP2B_1061	9606
1372	3158	4944	6730	784CIP2B_1062	9622
1373	3159	4945	6731	784CIP2B_1063	9623
1374	3160	4946	6732	784CIP2B_1064	9646
1375	3161	4947	6733	784CIP2B_1065	9747
1376	3162	4948	6734	784CIP2B_1066	9773
1377	3163	4949	6735	784CIP2B_1067	9785
1378	3164	4950	6736	784CIP2B_1068	9801
1379	3165	4951	6737	784CIP2B_1069	9811
1380	3166	4952	6738	784CIP2B_1070	9843
1381	3167	4953	6739	784CIP2B_1071	9854
1382	3168	4954	6740	784CIP2B_1072	9854
1383	3169	4955	6741	784CIP2B_1073	9864
1384	3170	4956	6742	784CIP2B_1074	9864
1385	3171	4957	6743	784CIP2B_1075	9871
1386	3172	4958	6744	784CIP2B_1076	9879
1387	3173	4959	6745	784CIP2B_1077	9881
1388	3174	4960	6746	784CIP2B_1078	9885
1389	3175	4961	6747	784CIP2B_1079	9901
1390	3176	4962	6748	784CIP2B_1080	9912
1391	3177	4963	6749	784CIP2B_1081	9916
1392	3178	4964	6750	784CIP2B_1082	9921
1393	3179	4965	6751	784CIP2B_1083	9925
1394	3180	4966	6752	784CIP2B_1084	9930
1395	3181	4967	6753	784CIP2B_1085	9949
1396	3182	4968	6754	784CIP2B_1086	9951
1397	3183	4969	6755	784CIP2B_1087	9959
1398	3184	4970	6756	784CIP2B_1088	9973
1399	3185	4971	6757	784CIP2B_1089	9982
1400	3186	4972	6758	784CIP2B_1090	9994
1401	3187	4973	6759	784CIP2B_1091	10021
1402	3188	4974	6760	784CIP2B_1092	10041
1403	3189	4975	6761	784CIP2B_1094	10067
1404	3190	4976	6762	784CIP2B_1095	10073
1405	3191	4977	6763	784CIP2B_1096	10112
1406	3192	4978	6764	784CIP2B_1097	10117
1407	3193	4979	6765	784CIP2B_1098	10132
1408	3194	4980	6766	784CIP2B_1099	10169
1409	3195	4981	6767	784CIP2B_1100	10217
1410	3196	4982	6768	784CIP2B_1101	10226
1411	3197	4983	6769	784CIP2B_1102	10232
1412	3198	4984	6770	784CIP2B_1103	10237
1413	3199	4985	6771	784CIP2B_1104	10279
1414	3200	4986	6772	784CIP2C_1	33
1415	3201	4987	6773	784CIP2C_2	271
1416	3202	4988	6774	784CIP2C_3	848
1417	3203	4989	6775	784CIP2C_4	849
1418	3204	4990	6776	784CIP2C_5	864
1419	3205	4991	6777	784CIP2C_6	953
1420	3206	4992	6778	784CIP2C_7	980
1421	3207	4993	6779	784CIP2C_8	1595
1422	3208	4994	6780	784CIP2C_9	1697
1423	3209	4995	6781	784CIP2C_10	1744

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1424	3210	4996	6782	784CIP2C_11	1937
1425	3211	4997	6783	784CIP2C_12	1955
1426	3212	4998	6784	784CIP2C_13	1955
1427	3213	4999	6785	784CIP2C_14	2185
1428	3214	5000	6786	784CIP2C_15	2889
1429	3215	5001	6787	784CIP2C_16	2901
1430	3216	5002	6788	784CIP2C_17	2902
1431	3217	5003	6789	784CIP2C_18	2905
1432	3218	5004	6790	784CIP2C_19	2948
1433	3219	5005	6791	784CIP2C_20	2956
1434	3220	5006	6792	784CIP2C_21	2959
1435	3221	5007	6793	784CIP2C_22	2965
1436	3222	5008	6794	784CIP2C_23	2966
1437	3223	5009	6795	784CIP2C_24	2970
1438	3224	5010	6796	784CIP2C_25	2985
1439	3225	5011	6797	784CIP2C_26	2987
1440	3226	5012	6798	784CIP2C_27	2993
1441	3227	5013	6799	784CIP2C_28	2993
1442	3228	5014	6800	784CIP2C_29	3017
1443	3229	5015	6801	784CIP2C_30	3046
1444	3230	5016	6802	784CIP2C_31	3050
1445	3231	5017	6803	784CIP2C_32	3357
1446	3232	5018	6804	784CIP2C_33	3359
1447	3233	5019	6805	784CIP2C_34	3432
1448	3234	5020	6806	784CIP2C_35	3438
1449	3235	5021	6807	784CIP2C_36	3439
1450	3236	5022	6808	784CIP2C_39	3463
1451	3237	5023	6809	784CIP2C_40	3466
1452	3238	5024	6810	784CIP2C_41	3466
1453	3239	5025	6811	784CIP2C_42	3467
1454	3240	5026	6812	784CIP2C_43	3468
1455	3241	5027	6813	784CIP2C_44	3483
1456	3242	5028	6814	784CIP2C_45	3484
1457	3243	5029	6815	784CIP2C_46	3488
1458	3244	5030	6816	784CIP2C_47	3491
1459	3245	5031	6817	784CIP2C_48	3493
1460	3246	5032	6818	784CIP2C_49	3494
1461	3247	5033	6819	784CIP2C_50	3495
1462	3248	5034	6820	784CIP2C_51	3496
1463	3249	5035	6821	784CIP2C_52	3503
1464	3250	5036	6822	784CIP2C_53	3503
1465	3251	5037	6823	784CIP2C_54	3504
1466	3252	5038	6824	784CIP2C_55	3511
1467	3253	5039	6825	784CIP2C_56	3531
1468	3254	5040	6826	784CIP2C_57	3536
1469	3255	5041	6827	784CIP2C_58	3546
1470	3256	5042	6828	784CIP2C_59	3548
1471	3257	5043	6829	784CIP2C_60	3551
1472	3258	5044	6830	784CIP2C_61	3553
1473	3259	5045	6831	784CIP2C_62	3564
1474	3260	5046	6832	784CIP2C_63	3567
1475	3261	5047	6833	784CIP2C_64	3572
1476	3262	5048	6834	784CIP2C_65	3573
1477	3263	5049	6835	784CIP2C_66	3574
1478	3264	5050	6836	784CIP2C_67	3583
1479	3265	5051	6837	784CIP2C_68	3615
1480	3266	5052	6838	784CIP2C_69	3623
1481	3267	5053	6839	784CIP2C_70	3629
1482	3268	5054	6840	784CIP2C_71	3666
1483	3269	5055	6841	784CIP2C_72	3667
1484	3270	5056	6842	784CIP2C_73	3906
1485	3271	5057	6843	784CIP2C_74	3912

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1486	3272	5058	6844	784CIP2C_75	3924
1487	3273	5059	6845	784CIP2C_76	3928
1488	3274	5060	6846	784CIP2C_77	3935
1489	3275	5061	6847	784CIP2C_78	3959
1490	3276	5062	6848	784CIP2C_79	3981
1491	3277	5063	6849	784CIP2C_80	3989
1492	3278	5064	6850	784CIP2C_81	4295
1493	3279	5065	6851	784CIP2C_82	4300
1494	3280	5066	6852	784CIP2C_83	4360
1495	3281	5067	6853	784CIP2C_84	4362
1496	3282	5068	6854	784CIP2C_85	4371
1497	3283	5069	6855	784CIP2C_86	4373
1498	3284	5070	6856	784CIP2C_87	4376
1499	3285	5071	6857	784CIP2C_89	4378
1500	3286	5072	6858	784CIP2C_90	4382
1501	3287	5073	6859	784CIP2C_91	4409
1502	3288	5074	6860	784CIP2C_92	4421
1503	3289	5075	6861	784CIP2C_93	4421
1504	3290	5076	6862	784CIP2C_94	4426
1505	3291	5077	6863	784CIP2C_95	4430
1506	3292	5078	6864	784CIP2C_96	4435
1507	3293	5079	6865	784CIP2C_97	4436
1508	3294	5080	6866	784CIP2C_98	4439
1509	3295	5081	6867	784CIP2C_99	4440
1510	3296	5082	6868	784CIP2C_100	4441
1511	3297	5083	6869	784CIP2C_101	4442
1512	3298	5084	6870	784CIP2C_102	4455
1513	3299	5085	6871	784CIP2C_103	4462
1514	3300	5086	6872	784CIP2C_104	4466
1515	3301	5087	6873	784CIP2C_105	4469
1516	3302	5088	6874	784CIP2C_106	4477
1517	3303	5089	6875	784CIP2C_107	4481
1518	3304	5090	6876	784CIP2C_108	4483
1519	3305	5091	6877	784CIP2C_109	4484
1520	3306	5092	6878	784CIP2C_110	4486
1521	3307	5093	6879	784CIP2C_111	4490
1522	3308	5094	6880	784CIP2C_112	4499
1523	3309	5095	6881	784CIP2C_113	4503
1524	3310	5096	6882	784CIP2C_114	4506
1525	3311	5097	6883	784CIP2C_115	4509
1526	3312	5098	6884	784CIP2C_116	4514
1527	3313	5099	6885	784CIP2C_117	4516
1528	3314	5100	6886	784CIP2C_118	4522
1529	3315	5101	6887	784CIP2C_119	4525
1530	3316	5102	6888	784CIP2C_120	4527
1531	3317	5103	6889	784CIP2C_121	4528
1532	3318	5104	6890	784CIP2C_122	4529
1533	3319	5105	6891	784CIP2C_123	4532
1534	3320	5106	6892	784CIP2C_124	4537
1535	3321	5107	6893	784CIP2C_125	4538
1536	3322	5108	6894	784CIP2C_126	4551
1537	3323	5109	6895	784CIP2C_127	4552
1538	3324	5110	6896	784CIP2C_128	4559
1539	3325	5111	6897	784CIP2C_129	4567
1540	3326	5112	6898	784CIP2C_130	4568
1541	3327	5113	6899	784CIP2C_132	4585
1542	3328	5114	6900	784CIP2C_133	4592
1543	3329	5115	6901	784CIP2C_134	4609
1544	3330	5116	6902	784CIP2C_135	4616
1545	3331	5117	6903	784CIP2C_136	4617
1546	3332	5118	6904	784CIP2C_137	4618
1547	3333	5119	6905	784CIP2C_138	4620

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1548	3334	5120	6906	784CIP2C_139	4624
1549	3335	5121	6907	784CIP2C_140	4632
1550	3336	5122	6908	784CIP2C_141	4634
1551	3337	5123	6909	784CIP2C_142	4638
1552	3338	5124	6910	784CIP2C_143	4639
1553	3339	5125	6911	784CIP2C_144	4643
1554	3340	5126	6912	784CIP2C_145	4644
1555	3341	5127	6913	784CIP2C_146	4655
1556	3342	5128	6914	784CIP2C_147	4668
1557	3343	5129	6915	784CIP2C_148	4677
1558	3344	5130	6916	784CIP2C_149	4677
1559	3345	5131	6917	784CIP2C_150	4677
1560	3346	5132	6918	784CIP2C_152	4682
1561	3347	5133	6919	784CIP2C_153	4690
1562	3348	5134	6920	784CIP2C_154	4691
1563	3349	5135	6921	784CIP2C_155	4727
1564	3350	5136	6922	784CIP2C_156	4730
1565	3351	5137	6923	784CIP2C_157	4734
1566	3352	5138	6924	784CIP2C_158	4757
1567	3353	5139	6925	784CIP2C_159	4764
1568	3354	5140	6926	784CIP2C_160	4786
1569	3355	5141	6927	784CIP2C_161	4793
1570	3356	5142	6928	784CIP2C_162	4825
1571	3357	5143	6929	784CIP2C_163	4826
1572	3358	5144	6930	784CIP2C_164	4850
1573	3359	5145	6931	784CIP2C_165	4853
1574	3360	5146	6932	784CIP2C_166	4855
1575	3361	5147	6933	784CIP2C_167	4856
1576	3362	5148	6934	784CIP2C_168	4867
1577	3363	5149	6935	784CIP2C_169	4869
1578	3364	5150	6936	784CIP2C_170	4878
1579	3365	5151	6937	784CIP2C_171	4880
1580	3366	5152	6938	784CIP2C_172	4942
1581	3367	5153	6939	784CIP2C_173	4945
1582	3368	5154	6940	784CIP2C_174	4950
1583	3369	5155	6941	784CIP2C_175	4952
1584	3370	5156	6942	784CIP2C_176	4954
1585	3371	5157	6943	784CIP2C_177	4958
1586	3372	5158	6944	784CIP2C_178	4961
1587	3373	5159	6945	784CIP2C_179	5590
1588	3374	5160	6946	784CIP2C_180	5599
1589	3375	5161	6947	784CIP2C_181	5692
1590	3376	5162	6948	784CIP2C_182	5732
1591	3377	5163	6949	784CIP2C_183	5765
1592	3378	5164	6950	784CIP2C_184	5771
1593	3379	5165	6951	784CIP2C_185	5774
1594	3380	5166	6952	784CIP2C_186	5793
1595	3381	5167	6953	784CIP2C_187	5806
1596	3382	5168	6954	784CIP2C_188	5852
1597	3383	5169	6955	784CIP2C_189	5892
1598	3384	5170	6956	784CIP2C_190	6057
1599	3385	5171	6957	784CIP2C_191	6061
1600	3386	5172	6958	784CIP2C_192	6109
1601	3387	5173	6959	784CIP2C_193	6160
1602	3388	5174	6960	784CIP2C_194	6297
1603	3389	5175	6961	784CIP2C_195	6398
1604	3390	5176	6962	784CIP2C_196	6398
1605	3391	5177	6963	784CIP2C_197	6415
1606	3392	5178	6964	784CIP2C_198	6448
1607	3393	5179	6965	784CIP2C_199	6469
1608	3394	5180	6966	784CIP2C_200	6476
1609	3395	5181	6967	784CIP2C_201	6561

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1610	3396	5182	6968	784CIP2C_202	6574
1611	3397	5183	6969	784CIP2C_203	6578
1612	3398	5184	6970	784CIP2C_204	6662
1613	3399	5185	6971	784CIP2C_205	6672
1614	3400	5186	6972	784CIP2C_206	6691
1615	3401	5187	6973	784CIP2C_207	6695
1616	3402	5188	6974	784CIP2C_208	6746
1617	3403	5189	6975	784CIP2C_209	6898
1618	3404	5190	6976	784CIP2C_210	6938
1619	3405	5191	6977	784CIP2C_211	6943
1620	3406	5192	6978	784CIP2C_212	7110
1621	3407	5193	6979	784CIP2C_213	7200
1622	3408	5194	6980	784CIP2C_214	7212
1623	3409	5195	6981	784CIP2C_215	7218
1624	3410	5196	6982	784CIP2C_216	7249
1625	3411	5197	6983	784CIP2C_217	7500
1626	3412	5198	6984	784CIP2C_218	7509
1627	3413	5199	6985	784CIP2C_219	7523
1628	3414	5200	6986	784CIP2C_220	7544
1629	3415	5201	6987	784CIP2C_221	7564
1630	3416	5202	6988	784CIP2C_222	7568
1631	3417	5203	6989	784CIP2C_223	7631
1632	3418	5204	6990	784CIP2C_224	7813
1633	3419	5205	6991	784CIP2C_225	7831
1634	3420	5206	6992	784CIP2C_226	7843
1635	3421	5207	6993	784CIP2C_227	7907
1636	3422	5208	6994	784CIP2C_228	7943
1637	3423	5209	6995	784CIP2C_229	8175
1638	3424	5210	6996	784CIP2C_230	8216
1639	3425	5211	6997	784CIP2C_231	8225
1640	3426	5212	6998	784CIP2C_232	8271
1641	3427	5213	6999	784CIP2C_233	8397
1642	3428	5214	7000	784CIP2C_234	8466
1643	3429	5215	7001	784CIP2C_235	8503
1644	3430	5216	7002	784CIP2C_236	8953
1645	3431	5217	7003	784CIP2C_237	9106
1646	3432	5218	7004	784CIP2C_238	9139
1647	3433	5219	7005	784CIP2C_239	9555
1648	3434	5220	7006	784CIP2C_240	9650
1649	3435	5221	7007	784CIP2C_241	9889
1650	3436	5222	7008	784CIP2C_242	9933
1651	3437	5223	7009	784CIP2C_243	9953
1652	3438	5224	7010	784CIP2C_244	9981
1653	3439	5225	7011	784CIP2D_1	746
1654	3440	5226	7012	784CIP2D_2	3558
1655	3441	5227	7013	784CIP2D_3	3558
1656	3442	5228	7014	784CIP2D_4	3633
1657	3443	5229	7015	784CIP2D_5	3658
1658	3444	5230	7016	784CIP2D_6	3732
1659	3445	5231	7017	784CIP2D_7	4004
1660	3446	5232	7018	784CIP2D_8	4700
1661	3447	5233	7019	784CIP2D_9	4703
1662	3448	5234	7020	784CIP2D_10	4774
1663	3449	5235	7021	784CIP2D_11	4894
1664	3450	5236	7022	784CIP2D_12	4918
1665	3451	5237	7023	784CIP2D_13	5159
1666	3452	5238	7024	784CIP2D_14	7443
1667	3453	5239	7025	784CIP2D_15	8673
1668	3454	5240	7026	784CIP2D_16	8679
1669	3455	5241	7027	784CIP2D_17	8727
1670	3456	5242	7028	784CIP2D_18	8734
1671	3457	5243	7029	784CIP2D_19	8756

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1672	3458	5244	7030	784CIP2D_20	8818
1673	3459	5245	7031	784CIP2D_21	8844
1674	3460	5246	7032	784CIP2D_22	8846
1675	3461	5247	7033	784CIP2D_23	8912
1676	3462	5248	7034	784CIP2D_24	8918
1677	3463	5249	7035	784CIP2D_25	8918
1678	3464	5250	7036	784CIP2D_26	8941
1679	3465	5251	7037	784CIP2D_27	8941
1680	3466	5252	7038	784CIP2D_28	8951
1681	3467	5253	7039	784CIP2D_29	8951
1682	3468	5254	7040	784CIP2D_30	9007
1683	3469	5255	7041	784CIP2D_31	9012
1684	3470	5256	7042	784CIP2D_32	9013
1685	3471	5257	7043	784CIP2D_33	9025
1686	3472	5258	7044	784CIP2D_34	9053
1687	3473	5259	7045	784CIP2D_35	9054
1688	3474	5260	7046	784CIP2D_36	9054
1689	3475	5261	7047	784CIP2D_37	9113
1690	3476	5262	7048	784CIP2D_38	9134
1691	3477	5263	7049	784CIP2D_39	9152
1692	3478	5264	7050	784CIP2D_40	9152
1693	3479	5265	7051	784CIP2D_41	9211
1694	3480	5266	7052	784CIP2D_42	9223
1695	3481	5267	7053	784CIP2D_43	9223
1696	3482	5268	7054	784CIP2D_44	9231
1697	3483	5269	7055	784CIP2D_45	9236
1698	3484	5270	7056	784CIP2D_46	9236
1699	3485	5271	7057	784CIP2D_47	9303
1700	3486	5272	7058	784CIP2D_48	9309
1701	3487	5273	7059	784CIP2D_49	9314
1702	3488	5274	7060	784CIP2D_50	9326
1703	3489	5275	7061	784CIP2D_51	9339
1704	3490	5276	7062	784CIP2D_52	9348
1705	3491	5277	7063	784CIP2D_53	9376
1706	3492	5278	7064	784CIP2D_54	9382
1707	3493	5279	7065	784CIP2D_55	9407
1708	3494	5280	7066	784CIP2D_56	9414
1709	3495	5281	7067	784CIP2D_57	9439
1710	3496	5282	7068	784CIP2D_58	9485
1711	3497	5283	7069	784CIP2D_59	9493
1712	3498	5284	7070	784CIP2D_60	9501
1713	3499	5285	7071	784CIP2D_61	9526
1714	3500	5286	7072	784CIP2D_62	9526
1715	3501	5287	7073	784CIP2D_63	9551
1716	3502	5288	7074	784CIP2D_64	9557
1717	3503	5289	7075	784CIP2D_65	9568
1718	3504	5290	7076	784CIP2D_66	9588
1719	3505	5291	7077	784CIP2D_67	9597
1720	3506	5292	7078	784CIP2D_68	9615
1721	3507	5293	7079	784CIP2D_69	9628
1722	3508	5294	7080	784CIP2D_70	9649
1723	3509	5295	7081	784CIP2D_71	9652
1724	3510	5296	7082	784CIP2D_72	9660
1725	3511	5297	7083	784CIP2D_73	9662
1726	3512	5298	7084	784CIP2D_74	9725
1727	3513	5299	7085	784CIP2D_75	9746
1728	3514	5300	7086	784CIP2D_76	9777
1729	3515	5301	7087	784CIP2D_77	9787
1730	3516	5302	7088	784CIP2D_78	9790
1731	3517	5303	7089	784CIP2D_79	9842
1732	3518	5304	7090	784CIP2D_80	9842
1733	3519	5305	7091	784CIP2D_81	9848

SEQ ID NO: of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority docket number_ corresponding SEQ ID NO: in priority application	SEQ ID NO: in U.S.S.N. 09/488,725
1734	3520	5306	7092	784CIP2D_82	9867
1735	3521	5307	7093	784CIP2D_83	10010
1736	3522	5308	7094	784CIP2D_84	10011
1737	3523	5309	7095	784CIP2D_85	10052
1738	3524	5310	7096	784CIP2D_86	10057
1739	3525	5311	7097	784CIP2D_87	10085
1740	3526	5312	7098	784CIP2D_89	10139
1741	3527	5313	7099	784CIP2D_90	10142
1742	3528	5314	7100	784CIP2D_92	10165
1743	3529	5315	7101	784CIP2D_93	10173
1744	3530	5316	7102	784CIP2D_94	10173
1745	3531	5317	7103	784CIP2D_95	10273
1746	3532	5318	7104	784CIP2E_1	3121
1747	3533	5319	7105	784CIP2E_2	3628
1748	3534	5320	7106	784CIP2E_4	3673
1749	3535	5321	7107	784CIP2E_5	4018
1750	3536	5322	7108	784CIP2E_6	4467
1751	3537	5323	7109	784CIP2E_7	4865
1752	3538	5324	7110	784CIP2E_8	4916
1753	3539	5325	7111	784CIP2E_9	4923
1754	3540	5326	7112	784CIP2E_10	4926
1755	3541	5327	7113	784CIP2E_11	4962
1756	3542	5328	7114	784CIP2E_12	4963
1757	3543	5329	7115	784CIP2E_13	4964
1758	3544	5330	7116	784CIP2E_14	4988
1759	3545	5331	7117	784CIP2E_15	5835
1760	3546	5332	7118	784CIP2E_16	7682
1761	3547	5333	7119	784CIP2E_17	7682
1762	3548	5334	7120	784CIP2E_18	7699
1763	3549	5335	7121	784CIP2E_19	7707
1764	3550	5336	7122	784CIP2E_20	7707
1765	3551	5337	7123	784CIP2E_21	7752
1766	3552	5338	7124	784CIP2E_22	8357
1767	3553	5339	7125	784CIP2E_23	9065
1768	3554	5340	7126	784CIP2E_24	9324
1769	3555	5341	7127	784CIP2F_1	2976
1770	3556	5342	7128	784CIP2F_2	3559
1771	3557	5343	7129	784CIP2F_3	4021
1772	3558	5344	7130	784CIP2F_4	4474
1773	3559	5345	7131	784CIP2F_5	4566
1774	3560	5346	7132	784CIP2F_6	4705
1775	3561	5347	7133	784CIP2F_7	4707
1776	3562	5348	7134	784CIP2F_8	4712
1777	3563	5349	7135	784CIP2F_9	5008
1778	3564	5350	7136	784CIP2F_10	5009
1779	3565	5351	7137	784CIP2F_11	5015
1780	3566	5352	7138	784CIP2F_12	5015
1781	3567	5353	7139	784CIP2F_13	7724
1782	3568	5354	7140	784CIP2F_14	7725
1783	3569	5355	7141	784CIP2F_15	8828
1784	3570	5356	7142	784CIP2F_16	8830
1785	3571	5357	7143	784CIP2F_17	9739
1786	3572	5358	7144	784CIP2F_18	9896

TRADOC:1416247.1(%CS7011.DOC)

TABLE 7

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5359	337	1131	AHLSARLSALILDEVAILPAPQNL SVLSTNMKHLMLMNSPVIAPG ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTGEPEDVTDITDITA TVPNLNRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI TKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVEQGEAIP VLALFAFVGFMILLVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW KITQF
5360	2	1115	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIA RPVGSSVRLK CVASGHPRPDITWMKDDQALTRPEAAEPKKKWTLSLKNLRPED SGKYTCRVSNRAGAINATYKVDVIQRTSRKPVLTGTHPVNTTVD FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSIDVGGQKF VVLPTGDVWSRPDGSYLKLLITRARQDDAGMYICLGANTMGYS FRSAFLTLPDPKPPGPFVASSSSATSLPWPVVIGIPAGAVFIL GTL LLWLCAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPSL AALSAGPGVGLCEEHGSFAAPQHLLGPGPVAGPKLYPKLYTGHS TPHTYTHPPFSCQLNSSHS
5361	3	925	HEGSISSANILLDDQFQKLTDFAMAHFRSHLEHQSCITNMSTSS SSKHLWYMPEEYIRQGLSITDVSFGIVIMEVLTGCRVVLDD PKHIQLRDLRLRELMKRGDLSCLSLDKKVPCCPRNFSAKLFCL AGRCAATRAKLRPSMDEVLTLESTQASLYFAEDPPTSLKSFRC PSPLFLENVPSIPVEDDESQNNLLPSDEGLRIDRMTQKTPFEC SQSVMFLSLDKKPKESKRNEEACNMPSSSCEESWFPKYIIVPSQD LRPYKVNIDPSSZAPGHSCRSRPVSSSCSKFSWDEYEQYKKE
5362	2	4879	SCQVEGCTRTYNSQSISGKHKMTAHPDQYAAFKMQRKSKKQKA NNLNTPNNGKFVYFLPSPVNSNPPFTSQTKANGPACSAQLQH VSPPIFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSQ MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSLPAESSSIDL FFSPADSGTNSVFSQLENNTNHYSSQIEGNTNSSFLKGGNGENA VFPSQVNVANNFSSTNAQSSAPEKVKKDRGRGTGKERKPKHKN RAKWPAILRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA EIAQELLQSNQPSLLASMLSTNAVNLLQPPQOSTFNPEACFKD PSFLQLLAENRSPAFLPNTFPRSGVTNFTSVSQEGSEIIQAL ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH TVCHPNTLLTNQRTSNTSKTSSIECSSLVPVPTNDLLKTVEN GLCSSFPNSGGSPSQNFTSNSSRSVVISGPQNTRSSHLNKKGS ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVIEPTNLH SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFECT LEIIKTAMNSQILEVKSGSQAGETSQNAQINYNIQLPVSVNTV NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL QKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVQIPVSE MINIQFNDKVNKPFVCQNGCNYSAMTKDALFKHYGKIHYQYTP MILEIKKNQLKFAPFKCVVPTCTKTFTTRNSNLRACQLVHHFTT EEMVKLKI KRPYGRKSQSENVPASRSTQVKKQLAMTEENKESQ PALELRAETQNTHSNVAVPEKQLEKKSPTKTESLQVITVTS EQCNTNALTNTQTKGRKIRRHKKKEEKKRKKPVQSLEFPTRY SPYRYPYRCVHQGCFAFTIQNLIILHYQAVHKSDDLPAFSAEVEE ESEAGKESEETETKQTLKEFRQVSDCSRIFOAITGLIQHYMKL HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD HGIGLRASKTEEDGVYKDCCEGCDRIYATRSNLLRHIFNKHNDK HKAHLIRPRRLTPGQENMSSKANQEKSXKRGTKHSRCGKBGI KMPKTKRKKKNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN DALSECTSRFVTQYPCMIKGTSTVVTSESNIIIRHYKCHKLSKAF TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSCTCVSESND NSRTTATVSQKEVEKNE*DEMDDELTELITKLINEDSTSVETQA NTSSNVSNDFQEDNLQSERQKASNLKRVNKEKNVSNQKKRKE KAEPASAAELSSVRKEEETAVAIQITIEHPASFDWSSFKPMGFE VSFLKFLEESAVKQKKNTDKDHPNTGNKKGSHSNRKNIDKTAV TSGNHVCPCKESETFVQFANPSQLQCSNDNVKIVLDKNLKDCTEL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5363	8066	703	<p>VLKQLQEMKPTVSLKKLEVHNSNDPDMVSMKDISIGKATRGQY</p> <p>RLCCTGGGEGTGPASGKRGPAATTSLVLCIPSPVPPVFPPTLWP PPSWRRQPPGGIRDFSRRLRREANLVATCLPVRASLPHRLNML RGP GPG LLL L AVLCLGTAVPSTGASKSKRQAQQMVQPSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNAIVCTCYGGSRGFNCESEK PEAEETCFDKYTGNTRYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGMVMDCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNRG EWKCEHRTSVQTTSSGSGPFTDVRAAVYQPPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQYV GNSNGEPCVLPFTYNGRTFYSCCTEGRQDGHLCSTTSNYEQDQ KYSFCTDHTVLVQTRGGNSGALCHFPFLYNNHNYTDCTSEGR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW DKQHDGMHMRCTCVGNRGGEWTCIAYSQLRDQCIQDDITYNVD DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCDSETGTIFYQI GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTPSSSGPVEVFI TETPSQPNSHPIQWNAQPSHISKYILWRPKNSVGRWKEATIP GHLNSYTIKGLKPGVYEGQLISIQQYGHQEVTRFDFTTSTST PVTSTNT\VTGETTTPSPVATSESVTEITASSFVSVWSASDTV SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEDEGEQLILSTSTQTTAPDAPPDPTVDQVDDTSIVVRWS PQAPITGYRIVYSPSVEGSSSTELNLPETANSVTLSDLQPGVQYN ITIIYAVEENQESTPVVVIQGETTGTTPRSDTVSPRDLQFVEVTDV KVTIMWTPPESAVTGYRVDVIVPNLPGEHGQRLPLSRNTF\AEN TGLSPGVYTYFVFAVSHGRESKPLTAQQTTL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVPRPSQGGAPREVTSDSGSIV VSGLTPGVEYVYTIQVLRDQGERDAP\IVNK\VVTPLSPTNLH LEANPDTGVLTVSWERSTTDPITGYRITTTPTNGQQNSLLEEV HADQSSCTF\DNLEVPGLBYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN/ILGPDTRMTW\APPPSIDLTNLFVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVSVSSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DTA\NSFT\VHW\IAPRA\TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTGTEYVV SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYRYITYGETGGNSPVQEFVTPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPIISINYRTEIDKPSQMQVTDQDNS ISVKNLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVSVYAQNPSGESQPLVQTAVTNIDRPGKGLAFTDV DVDSIKIAWESPGQVSRVRYVYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIAPPTDLKFT QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVYALKDITLTSRPAQGVVTTLENVSPRRR ARVTDATETTTITISWRTKTETITGFQVDAVPANGQTFIQRTIKP DVRSYTTIGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTNSLVSWQPPRARITGYIIKYEKPGSPPREVVRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDDEL QLVTLPHPNLHGP EILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGQQMIFEBHGFRRTTPPTATPIRHRPRPYPPNVGQB ALSQTTISWAPPQDTSEYIISCHPVGTDEEPLQFRVPCTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVTVGNSVNBGLNQPT DDSCFDPTYVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKNDROGENGQMMSCCLGNGKGEFKCDP HEATCYDDGKTYHVGQWQKEYLGAI CSCTCFGGQGRGWRCDNCR RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPICFMPDLVDQ ADREDSRE</p>
5364	8066	703	<p>RLCCTGGGEGTGPASGKRGPAATTSLVLCIPSPVPPVFPPTLWP PPSWRRQPPGGIRDFSRRLRREANLVATCLPVRASLPHRLNML RGP GPG LLL L AVLCLGTAVPSTGASKSKRQAQQMVQPSPVAVS</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESEK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGWEW CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR ITCTSRNRCDQDTRTSYRIGDTSKKNRGNLLQCICTGNRG EWKCEHRTSVQTTSSGSGPFTDVRAAVYQPPHPQPPPYGHCVT DSGVVYSVMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG GNSNGEPCVLPFTYNGRTFFYSCCTTEGRQDGHLCSTTSNYEQDQ KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW DKQHDMMHMRCTCVGNRGGEWTCIAYSQLRDQCIVDITYNVN DTFHKRHEBGMNLCTCFQGRGRWKCDPVDQCQDSETGTFFQI GDSWEKYVHGVRVYQCYCYGRGIGEWHCQPLQTPSSSGPVEVFI TETPSQPNSHPIQWNAQPSHISKYILRWPKNSVGRWKEATIP GHLNSYTIKGLKPGVVYEGQLISIQYGHQEVTRFDFTTTSTST PVTSTNT\VTGETTFFSPLVATSESVTEITASSFVSVWSASDTV SGFRVEYELSEEGDEPQYLVPSTATSV\NIP\DLLPGRKYIVN VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQDDTSIVVRNSR PQAPITGYRIVYSPSVEGSSSTELNLPETANSVTLSDLPQGVQYN ITIYAVEENQESTPVVVIQQUETGTGTPRSDTVSPRDLQFVEVTDV KVTIMWTFPESAVTGYRVDVIPVNLPGHEGQRLPLSRNTF\AEN TGLSPGVITYYFKVFAVSHGRESKPLTAQQTTL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRQPRQYVNGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETITITWTPAPRIGFKLGVRPSQGEAPREVTSDSGSIV VSGLTPGVEVYTIQVLRDQGERDAP\IVNK\VVTPLSPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN\ILGPDTRMTW\APPPSIDLTNLFVRYSVPKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSVEYQHESTP \LRGQKQGLDSP\TGIDFS\DTA\NSFT\VHW\IAPRA\TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTGTEYV SIVALNGREBSPLLIGQSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYRITYGETGGNSPVQEPVPGSKSTATISGLKPGVD YTITVAVTGRGDSPASSKPIISINYRTEIDKPSQMVDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI EGLQPTVEYVVSVAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQQQVSRVRYTYSSPEDGIHELFAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIAPPTDLKFT QVTPTLSAQWTPPNVQLTGYRVVTPKEKTGPMKEINLAPDSS SVVVSGLMVAATKYEVSVYALKDTLTSRPAQGVVTTLENVSPRR ARVTDATETITISWRKTETITGQVDAVPANGQTPIQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVRP RPGVTEATITGLEPGTEYTIYVIALKNNQSEPLIGRKKTDLP QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT SGQQPSVGVQMIFFEHGPRRTTPPTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSYIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREEVTVGNSVNEGLNQPT DDSCFDPPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQGENGQMSCTCLGNGKGEFKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCCTCFGGQGRWRCNCR RPGGEPSPGTTGQSYNQYSQRYHQRTNTNVNCPICEFMPLDVQ ADREDSRE</p>
5365	8066	703	<p>RLCCTGGGEGTPGASGKRGAATSLVLCIPSVPPVPFPTLWP PPSWRRQPPGGIRDFSRRLREANLVATCLPVRASLPHRLNML RGPGPGLLLLAVLCLGTAVPSTGASKSKRAQOMVQPSPVAVS QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESEK PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGWEW CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICITGNRG EWKCEHRTSVQTTSSGSGPFTDVRAAVYQPPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLNGVSCQETA VTQTYG GNSNGEPCVLPFTYNGRTFYSCCTEGRQDGHLCSTTSNYEQDQ KYSFCTDHTVLVQTRGGSNGALCHFPFLYNNHNYTDCSTSEGR DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDOW DKQDHMGHMMRCTCVNGRGEWTCIAYSQLRDQCI VDDI TYNVN DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCDSETGTFYQI GDSWEKYVHGVRVYQCYCYGRGIGEWHCQPLQTPSSSGPVEVFI TETPSQPNSHPIQWNAQPSHISKYILRWRPKNSVGRWKEATIP GHLSYTIKGLKPGVVEGQLISIQQYGHQEVTRFDFTTSTST PVTSTNT\VTGETTFFSPLVATSESVTEITASSFVSVWSASDTV SGFRVEYELSEEGDEPQYLVLVLPSTATSV\NIP\DLLPGRKYIVN VYQISEDEGEQSLILSTSQTTPADAPPDPTVDQVDDTSIVVRWSR PQAPITGYRIVYSPSVEGSSTELNLPELTANSVTLSDLQPGVQYN ITYAVEENQESTPVVVIQQTETGTTPRSDTVPSRDLQFVEVTDV KVTIMWTPPESAVTGYRVDVIVNLPGEHGRQLPLSRNTF\AEN TGLSPGVYTYFKVFAVSHGRESKPLTAQQTTL\DAPTNLQFVN ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYVNGPSVSKY PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGFKLGVRPSQGGAPREVTS DSGSIV VSGLTGVEYVYTIQVLRDQGERDAP\IVNK\VVTPLSPPPTNLH LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEV HADQSSCTF\DNLEVPGLYVNSVYTVKDDKESVPISDTIIPAV PPPTDLRFTN\ILGPDTRMTW\APPPSIDLTNLFVRYSPVKNE GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVS VSSVYEQHESTP \LRGRQKTGLDSP\TGIDFS\DTA\NSFT\VHW\IAPRA\TPI TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLNLTPGTEYVV SIVALNGREESPLLIQGSTVSDVPRDLEVVAATPTSLLI\SWD APAVTVRYRITYGETTGNPSVQEFVTPGSKSTATISGLKPGVD YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQM QVTDVQDNS ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGDQTEMTI EGLQPTVEYVVSVAQNPSGESQPLVQTAVTNIDRPKGLAFTDV DVDSIKIAWESPQQVSRVRYTYSSPEDGIHELFPAPDGEEDTA ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIAPPTDLKFT QVTPTSLSAQWTPPNVQLTG YRVRVTPKEKTGPMKEINLAPDSS SVVVSGLMVATKYEVSVALKDTLTSRPAQGVVTTLENVSPRR ARVTDATETITISWRTKETITITGFOVDVAVPANGQTP IQRTIKP DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS NLRFLATTNLSLVSWQPPRARITGYIIKYEKPGSPPREVVPRP RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDLEP QLVTLPHPNLHGPEILDVPS TVQKTPFVTHPGYDTGNGIQLPGT SQQQPSVGGQMIFEEHGFRRTPPTATPIRHRPRPYPPNVGQE ALSQTTISWAPFQDTSEYIIISCHPVGTDEEPLQFRVPGTSTSAT LTGLTRGATYNIIVEALKDQQRHKVREVVTVGNSVNEGLNQPT DDSCFDPTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD SSRWCHDNGVNYKIGEKWDRQENGQMMSCCTCLNGKGFEKCDP HEATCYDDGKTYHVGEQWQKEYLGAICSCCTCFGQGRGWRCNCR RPGGEPSPEGTGQSYNQYSQRYHQRTNTNVNCPICFMPPLDVQ ADREDSRE</p>
5366	8066	703	<p>RLCCTGGGEGTPGASGKRGPAATTSVLICIPSVPPVPFPPTLWP PPSWRRQPPGGIRDFSRRLRREANLVATCLPVRASLPHRLNML RGPFGGLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHQINQWERTYLGNALVCTCYGGSRGFNCESE PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRPHEGTGGYMLECVCLNGKGGEWT CKPIAEKCFDHAAGTSYVVGETWEKPYQGGMMVDCCTCLGEGSGR ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICITGNRG EWKCEHRTSVQTTSSGSGPFTDVRAAVYQPPHPQPPPYGHCVT DSGVVYSVGMQLA*KTQGNKQML\CTCLNGVSCQETA VTQTYG GNSNGEPCVLPFTYNGRTFYSCCTEGRQDGHLCSTTSNYEQDQ</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCSTSEGR</p> <p>DNMKWCGTTQNYDADQKFGFCPMAAHEBICTTNEGVMYRIGDQW</p> <p>DKQHDMGHMRCTCVGNRGGEWTCIAYSQLRDQCIVDDITYNVN</p> <p>DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFTYQI</p> <p>GDSWEKYVHVGRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI</p> <p>TETPSQPNSHPIQWNAQPSHISKYILRWKPKNSVGRWKEATIP</p> <p>GHLNSYTIKGLKPGVVYEGQLISIQYGHQEVTRFDFTTTSTST</p> <p>PVTSNT\VTGETTTPFSPLVATSESVTEITASSFVSVWSASDTV</p> <p>SGFRVEYELSEEGDEPQYLVLPLSTATSV\NIP\DLLPGRKYIVN</p> <p>VYQISEDGEQSLILSTSQTTPADAPPDPTVDQVDDTSIVVRWSR</p> <p>PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN</p> <p>ITIYAVEENQESTPVVVIQOETTGTTPRSDTVPSRDLQFVEVTDV</p> <p>KVTIMWTPPEAVTGYRVDVIPVNLPGHEGQRLPLSRNTF\AEN</p> <p>TGLSPGVTYFYKVFVAVSHGRESKPLTAQQTTL\DAPTNLQFVN</p> <p>ETDSTVLVRWTPPRAQITGYRLTVGLTRRQPRQYVNGPSVSKY</p> <p>PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN</p> <p>TEVTETTIVITWTPAPRIGFKLGVRPSQGGAPREVTSDSGSIV</p> <p>VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VTPLSPPTNLH</p> <p>LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQNSLEEVV</p> <p>HADQSSCTF\DNLEVPGLYVNVSVYTVKDDKESVPISDTIIPAV</p> <p>PPPTDLRFTN\ILGPDTRMTW\APPPSIDLNFVRYSPVKNE</p> <p>GRMLQSLSIFFLSDN\AVVLNLLPGTEYVSVSVYBQHESTP</p> <p>\LRGQKTGLDSP\TGIDFS\DTA\NSPT\VHW\IAPRA\TPI</p> <p>TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLNLTPGTEYVV</p> <p>SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD</p> <p>APAVTVRYRYITYGETGNSPVQEFVTPGSKSTATISGLKPGVD</p> <p>YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS</p> <p>ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI</p> <p>EGLQPTVEYVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV</p> <p>DVDSIKIAWESPOGQVSRYRVYSSPEDGIHELFPAPDGEEDTA</p> <p>ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIAPPTDLKFT</p> <p>QVTPTSLSAQWTPPNVQLTGYRVVTPKEKTGPMKEINLAPDSS</p> <p>SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR</p> <p>ARVTDATETTITISWRKTETITGQVDAVPANGQTPIQRTIKP</p> <p>DVRSYTTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS</p> <p>NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP</p> <p>RPGVTEATITGLEPGTEXTIYVIALKNNQKSEPLIGRKKTDEL</p> <p>QLVTLPHPNLHGPEILDVPSTVQKTFFVTHPGYDTGNGIQLPGT</p> <p>SGQQPSVGQQMIFEEHGFRTTPTTATPIRHRPRPYPPNVGQE</p> <p>ALSQTTISWAPQDTSYIISCHPVGTDDEPLQFRVPGTSTSAT</p> <p>LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT</p> <p>DDSCFDPTYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD</p> <p>SSRWCHDNGVNYKIGEKWDRQENGQMMSCCTCLGNGKGFEKCDP</p> <p>HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR</p> <p>RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVCPIECFMPDLVQ</p> <p>ADREDSRE</p>
5367	235	3591	<p>KKILNMLCKKNIVIEYLADILYEYLYGFCPSGIKKYLIHVLRL</p> <p>ILELWMTRLLEKSVSLQTQYLLLIIVKILSWFPKEMRHHLQIM</p> <p>EVMMRKQDS/RIVNGNSEQQLOKELADVLMDPPMDQPGKEKLV</p> <p>KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEMSLPVKPGQ</p> <p>GDSEASSPFTFPAVEDSVVFSKLTYLGCASVNAPRSEVEALRM</p> <p>SILRSQCQISLDVTLSPVNVSEGIIVRLDPQNTIANYPIYKI</p> <p>LFVCRGHDGTPESDCFAFTESHYNALFRIHVFRCEIQEAVSRI</p> <p>LYSFATAFRRSKQTPLSATAAPQTPDSDIFTFSVSLIEKEDDG</p> <p>KGYFSAVPKDKRQCFKLKRGIDKKIVYVQQTINKELAIERCF</p> <p>GLLLSPGKDVNRNMDHLLDLESMDGSSDGKSYVITGSWNPKSPH</p> <p>FQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLETKVRVCS</p> <p>NERLFWPFSKRSTTENFLLKLKQIKQRERKNNTDTLYEVVCL</p> <p>ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDEEEDNDEPLL</p> <p>SGSGDVSKECAEKILETWGELLSKWHNLNVRPKQLSLVRNGV</p> <p>PEALRGEVWQLLAGCHNNDHLVEKYRILITKESPDQSAITRDIN</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RTFPAHDYFKDGTGGDQDLSLYKICKAYSVDDEETGYCQGSFLA AVLLHMPPEEQAFSVLVKIMFDYGLRELFKQNFEDLHCKFYQLE RLMQEYIPDLYNHFLDISLEAHMYASQWFLTLFTAKFPLYMVPH IIDLLLCBGISVIFNVALGLLKTSKDDLLLTDFEGALKFFRVQL PKRYRSEENAKKLMELACNMKISQKLLKYEKEYHTMREQQAAQ EDPIERFERENRRLEQANMRLEQENDDLAHELVTSKIALRKDLD NAEEKADALNKEMLMTKQKLIDAEEEKRRLLEESAHLKMKCRRE LDKAESEIKKNSSIIGDYKQICSQLSERLEKQQTANKVEIEKIR QKVVDCERCREFPNKEGRVKGISSTKEVLDEDTDEKETLKNQL REMELELAQTKL\QLVEAECKIQD\LEHPF*GLPFNE\VQAA\K KTWFNRTLSSIKTATGVQGGKTC
5368	573	2014	GAAAGAADPRGSLGGRTMLDFAIFAVTFLALLVGVAVLYLYPAS RQAAGIPGITPTEKDGNLDPDIVNSGSLHEFLVNLHRYGPVVS FWFGRRLVSLGTVDLVKQHINPNKTLT/LF*NHAEVLIKVSIN WWQCE*KP\QRKLYENGVTDSLKSNFALLKLPEELLDKNLSY PETQH\VPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHG TVWSEIGKGLDGLDKNMTRKKQYEDALMQLESVLRNIIKERK GRNFSQHIFIDSLVQGNLNDQILEDMSIFSLASCIITAKLCTW AIWFLTTSEEVQKKLYEINQVFGNGPVTPEKIEQLRYCQHVLC ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETVLVYALGVVLQDP NTWPSPHKPDPRFDDDELVMKTFSSLGFSGTQCEPELRFAYMVT TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREAWITVSKRY
5369	1	6622	PRSLCFSLWAAEAVLADGGLRRRRRLLRGTMSASFVNGASLED CHCNLFCLADLTGIKWKYVWQGPTSAPILPVTEEDPILSSFS RCLKADVLG/VWRRDQRPERR*L*IFWGGEDP/VLLTLFTMTY QKKMECGRMDPMPNAVLCFKAVHNLLECLMNRNFRVIRGKWF VKPYEKDEKPKINKSEHLSCSFTFFLHGDSNVCTSVINQHQPVY LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK LIGEWKQFYFISCCLEKEMSEKQEDMDWEDDSLAABEVLVAGVR MIYPACFVLVPQSDIPTPSPVGSTHCSLGVHQPASTRDPH MSSVTLTPTSPPEEVQTVDPQSVQKWKVFSVSDGFSNDSTSHH GGKIPRKLHNVVDRVWQECNMNRQNKRYSSSSGGLCEEATA AKVASWDFVEATQRTNCSCLRHKNLKSRLNAGQQAQPSLGGQQQ ILPKHKTNEKQEKSEKPKRPLTPFHHRVSVSDVGM\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHTEMANSPO PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEDEANLAWKYYK FPKKKDVLELPPQLPSDKFDDPVGFQGESVTSVTELMVQCKK PLKVSDELVQYQIKNQCLSATASDAEQEPKIDPYAFVEGDEEF LFPDKDRQNSEREAGKKHVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLNLFNSDEDEL PGSKRSANGSDDKASCKRSKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNKEYGSMDDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSKIDFSYVYKPCNCQILVGCMSFAPLKTLPSSQY LPLIKLPEECIYRQSWTVGKLELLSSGSPMPFIKEGDSNMDE YGTAYTPQHTSCGMPSSAPPSSNGAGILPSPSTPRFPTPTPT RTPRTPRGAGGPASAQGSVKYENS DLYSPASTPSTCRPLNSVEP ATVPSIPEAHSYLVNLLSESVMNLFKDCNSDSCCICVCMNMIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFDELD IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSPFGAADQDFPKSGVISNWRVVEERDCNDCCYL LEHGRQFMDNMSGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLDALQKRTVRPWGVQGPLTWQGFHKMAGRGSYG TDESPEPLIPTFLLGYDYDYLVLSPFALPYWERLMLPEYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRL TDGIMRVGSTASKKLEKLVAEWFSQAADGNNEAFSKLKYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTASTSSSSS SNLNSGVSSNKLSPFPFPGSMNSNAAGSMSTQANTVQSGQLGGQ QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPDTGDSH AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAF TQCRRLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC TDLYGELLETCIINIDVPNRARRKSSARKFGLQKLWEWCLGLV QMSSLPWRVVGRLGRIGHGELKDWSCLLSRRNLQSLSKRLKDM CRMCGISAADSPSILSACL VAMEPQGSFVIMPDVSTGVSFVGRS TTLNMQTSQNLTPQDTSCTHILVFPTSASVQVASATYTTENLDL AFNPNNDGADGMGIFDLDLTDGDDLDPDIIINILPASPTGSPVHSP GSHYPHGGDAGKGQSTDRLSTEPHEEVPNILOQPLALGYFVST AKAGPLPDWFWSSACPAQYQCPLFLKASLHLHVPVSQSDLELHS KHSHPDLSNQTSDVLRVFLVLEQYNALSWLTCDPATQDRRSCLPIH FVVLNQLYNFIMNML
5370	1226	716	RWSRKLRLRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN ANDVETVQQLLEDGADPCAADDKGR TALHFASCNGNDQIVQLLL DHGADPNQRDGLGNTPLHLAACTNHVPVITTLRGGARVDALDR AGRTPLHLAKSKLNLQEGHAQCLKAVR/HGGEADHPYAEVGSV APRAT*AAACSGVFPSPSRNLGSAWPSRSSCTIWSLPLHEAKCR AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACSTLPVG GCISWL
5371	1331	167	IAAMLWKLRLRSQSCRLCSFRKMRSPPKYRPFACFTYTTDKQS SKENTRTVEKLYKCSVDIRKIRR*KDGYF*RMKPMKKLRI/P LQELGADETAVASILERCEAIVCSPTAVNTQRKLWQLVCKNEE ELIKLIEQFPESFFTIKDQENQKLVQFPQELGLKNVVISRLLT AAPNVFHNPEVKNKQMVRIQESYLDVGGSEANMKVWLLKLSQ NPFIILNSPTAIKETLEFLQEQGFTSFELIOLLSKLKGLFOLC PRSIQNSISFSKNAFKCTDHDLLKQVLKCPALLYSVPVLEERM QGLLREGISIAQIRETPMVLELTPQIVQYRIKLNSSGYRIKDG HLANLNGSKKEFEANFGKIQAQKVRPLFNPVAPLNVEE
5372	51	857	SPGAQFLWAAPDMPDPLFSAVQGGDEILHKALCFPCPWLGRGGM FLRLILFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR RKANCRQLGEGKPCQRRVSTHNLWLLSLRRWNGSTAITDDTLG GLTITLRLNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLD HRDAGDLWFPGLDLRASRMPMWSTASPGASWKEKSPSHPLPSFS SWPASFSRPF*QPAPSGQLQPGMDRSQGHHPVNWTVAMTQGISS KLCQG
5373	2814	346	VKKTKSIFNSAQEMEYVENIRRKFGVFNYSFFRTPYTPNSQY QMLLDPTNPSAGTAKIDKQEKVKNFDMTASPKILMSKPVLSGG TGRRIISLSDMPSPMSTNSSVHTGSDVEQDAEKKATSSSHFSASE ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD KTSTTGSILNLDNRKAEMDLKELSESVOQQSTPVPLISPKRQ IRSRFQLNLDKTIIESCKAQLGINEISEDVYTAVEHSDSEDEKS DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGRAKPS PHPIKDKLKGKDETDSPVHLGLDSDSE\NELVIDLGEDHSGRE GRKNKKEPKPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ TSAAGATATTSTSTVTVTAPAPATGSPVKKQRPLLPKE\TAP AVQRSCGTSSTVQKKEITQSPSTSTITLVTSTQSSPLVTSSGSM STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIGKTM\TEI YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQL\SEMKNH LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAQVDETCKKQWC ANFKKBAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ \QADAE\VNTETLNKSSQSSSTQSAPSETASA\SKEKETS EKSKEGSLDLGSGRETSSILGNSQGS DHSR\SNKSSWSSS DEKRGSL\TRSDHN\TPSTQHGRLSLPGKESRAGTFFLGTSK
5374	2814	346	VKKTKSIFNSAQEMEYVENIRRKFGVFNYSFFRTPYTPNSQY QMLLDPTNPSAGTAKIDKQEKVKNFDMTASPKILMSKPVLSGG TGRRIISLSDMPSPMSTNSSVHTGSDVEQDAEKKATSSSHFSASE ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD KTSTTGSILNLDNRKAEMDLKELSESVOQQSTPVPLISPKRQ IRSRFQLNLDKTIIESCKAQLGINEISEDVYTAVEHSDSEDEKS DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TNPVEIKKELKSTSFASEKADPGAVKDKASPEPEKDFSGKAKPS PHPIKDKLKGKDETDSPVHGLGDSSE\NELVIDLGEDHSGRE GRKNKKEPKSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ TSAAGATATTSTSTVTVPAPAPATGSPVKQRPLLPKE\TAQ AVQRSCGTSSSTVQKEITOSPSTSTITLVTSTQSSPLVTSSGSM STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDA\KGTM\TEI YNDLSKN\TTWKAQLAEDSQGLRIE\IEKLQWLHQQL\SEMKN LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAQVDETKKKQWC ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCQTQSATAPQ \QEADAE\VNTETLNKSSQSSSSSTQSAPSETASA\SKEKETSA EKSKESGSTLDLSSGRET\SSILLGSNQGSDHSR\SNKSSWSS DEKRG\TRSDHN\TPSTQHGRSLPLPGKESRAGTPFLGTSK
5375	2907	1116	HI FLAEEEPMLERRCRGLAMGPAQPRLLSGPSQESPTLGKES RGLRQQGTSVA\QSGAQAPGRAHRCACHRRHFGWVA\LWLHTR RCQA\RGLPLPCPECGRRFRHAPFLALHRQVHAAATPDWGFACH LCCGQFRGWVALVLHLRAHSAKAGPFACPKMADAFWRRKAAS SSILRRCHPSRPRGPRPFICGNCGRSILPTWDQ/LKVAHKRVHV SRRP*ERGPPAKVFWGPRPRGPPPTGDTPPGPGGDAVDRPF\QCA CCGKRFRHK\PNLIRSHAACSTGERPHQ/CSRECG\KRFTNKP LTS\HRRITHTARQPYPCKECGRRFRHKPNLLSHSKIHKRSEGS AQAPGPGSPQLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP QDPIEAPPSLYSCDDCGRSFRLEFLRAHQHQHTGERPFTCAEC GKNFGKTHLVAHSRVHSGERPFRLARKCGRRFLPRASQSGGRN SAEPNAPRFGPFVCPDCGKAFRHKPYLAHRPIATPAEKPVYCP DCRKAFSQKSNL\VSHRIHTGERPYACPDCCDRSFSQKSNLITH RKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV
5376	4504	591	VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSAEAS ARPLRVGSRVEVIGKGRGTVAIVGATLFBATGKWVGVLDEAKG KNDGTVQGRKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDS SASKVLKREGTDTTAKTSKLRLKPKKAPTARKTTTRRPKPTRP ASTGVAGASSSLGPSASAGELSSSEPSTPAQTPLAAPIIPTP VLTPGAVPPLPSPSKEEGLRAQVRDLBEKLETLRLKRAEDKA KLKELEKHKIQLEQVQEWKSKMQBQADLQRRLEKARKBAKEAL EAKERYMEEMADTADAIEMATLDKEMAEEAERESLQOEVEALKER VDELTDLLEILKAEIEEKGSAGAASSYQLKQLEEQNARLKDALV RMRDLSSSEKQEHVK\LQKLMKKNQLELVVRQQRERLQEEELSQ AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEKVRERLRET DLEAMNEMNDELQENARETELELRQQLDMAGARVREAKRVAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQOEASVERQQQPPP ETFDKIKFAETKAHAKAIEMLRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLMPRLICKAELIRKQAEKFESENCE RPLRGAGGQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQDETUNVEPLT KAICYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLOGGQEQATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAFGPQVSDTLDCRKHLTWVAVLQEVAAAAAQLI APLAENEGLLVALEELAFKASEQIYGTSPSSPYECLRQSCNLI ISTMNK\LVAMQEGEYDAERPSPKPP\VELRAALRAEITDA EGLGLKLEDRETVIKELKSKLKIKEELSEANVRLTLEKKLDS AAKDADERIEKVQTRLEETOALLRKKEKEFEETMDALQADIDQL EAEKAEKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPLVKDPSLLQQLISAMRLHISQLQHENSIL KGAQMKASLASLPLHVAKLSHEGPGSELPAVALYRKTSQLEET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVKEL KDEVLKETVSQRPGATVPTDFATFPSSAFPLRAKEEQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQQLHQLHSRLIS
5377	762	1106	DVPCRVLPAAEQEKQTLTSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK SS*WPGYDGGWGGQYIFIFRGMREWEBQ
5378	2009	664	QASGTTLRPLPDLPQLKREATSRNRALKPRGRVLMTSCLPAL RFIATPRLSAMPHIDNDVKLDFKDVLLRPRKSTLKSSEVDLTR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD VPQMGCVFLIYKLFITLKWMLLSVLLPASILVAEKFSLFTAVH KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP QVKYICLDVANGYSEHFVEFVKDVRKRFPPQHTIMAGNVVTGEMV EELILSGADI IKVGIGPGSVCTTRKKTGVGPQLSAVMECADA HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV PFKGDVEHTIRDILGGIRSTCTYVGAALKELSRRTTIFIRVTQQ VNPIFSEAC
5379	2009	664	QASGTTLRPLPDLPLQKREATSRNRALKPRGRVLMTSCLPAL RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSREVDLTR SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD VPQMGCVFLIYKLFITLKWMLLSVLLPASILVAEKFSLFTAVH KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP QVKYICLDVANGYSEHFVEFVKDVRKRFPPQHTIMAGNVVTGEMV EELILSGADI IKVGIGPGSVCTTRKKTGVGPQLSAVMECADA HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV PFKGDVEHTIRDILGGIRSTCTYVGAALKELSRRTTIFIRVTQQ VNPIFSEAC
5380	2	2050	PSRAGGAERGAAAAARSPPGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSSESQKPCALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSSKKLIRQAAPRRPPRGRTRPAPGGCQIP RGPI\EQVYQELIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKLSEDAQRFYFQDLIKGIEYLYQKII H\RDIKPSNLLVGEDGHIKIADPGVSNFEGSDALLSNTVGTFA FMAPESLSETRKIFSGKALDVWAMGVTLVCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPPI KLHPWVTRHGAEPPLSEDNCTLVEVTEEBVENSVKHIPS LATV ILVKTMIKRKSFNGPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPPLSTSWL PDLVGAAGSHFCFLNIALLRYSHTM
5381	2	2050	PSRAGGAERGAAAAARSPPGSAAGWECPSVLDEAGACTMSSCVS SQPSSNRAAPQDELGGRGSSSSSESQKPCALRGLSSLSIHLGME SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP RLPRRPTVESHHSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA YNENDNTYYAMKVLSSKKLIRQAAPRRPPRGRTRPAPGGCQIP RGPI\EQVYQELIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV F\ELVNQGPVMEVPTLKLSEDAQRFYFQDLIKGIEYLYQKII H\RDIKPSNLLVGEDGHIKIADPGVSNFEGSDALLSNTVGTFA FMAPESLSETRKIFSGKALDVWAMGVTLVCFVFG*CPFMDERIM CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPPI KLHPWVTRHGAEPPLSEDNCTLVEVTEEBVENSVKHIPS LATV ILVKTMIKRKSFNGPFEGSRREERSLSAPGNLLTKKPTRECESL SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPPLSTSWL PDLVGAAGSHFCFLNIALLRYSHTM
5382	1536	203	GARGSQQDAPALQEAEBVRGPERRAQPARGMTKARLFRLLVLG VFILLIIVYWSAGAAHFYLTFSRPHTPPLPTPGDRDRRE LTADSDVDFLDKFLSAGVKQSDLPKETEQQPAPGSMESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFFPTKERPF DIPNSELSHLIVDDRHAICYVFKVACTNWKRVMLVLSGSLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRRAHAAV RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAFFNEH WRQVYRLCHPCQIDYDFVGKLETLDDEAAQLQLLQVDLAAPLP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PELPGTGPPSSWEEDWFAKIFLAWRQQLYKLYEADFLVFGYPKP ENLLRD
5383	45	5250	<p>VERLLGCRNSKRTWRMLISKNPWRRLQGISFGMYSAEELKKLS</p> <p>VKSITNPRYLDLSGNPSANGLYDLALGPADSKEVCSTCVQDFSN</p> <p>CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCTPRAVI</p> <p>HLLLCQLRVLEVGAQAVYELERILSRFLEENADPSASEIREEL</p> <p>EQYTTIEIVQNNLLGSQGAHVKNVCESSKLIALFWKAHMNAKRC</p> <p>PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLGIEEAQ</p> <p>IGKRGYLTPTSAREHLSALWKNEGFFLNLYLFSGMDDDGMESRPN</p> <p>PSVFFLDPLVPPSRSRPVSRLGDQMTNGQTVNLQAVMKDVL</p> <p>IRKLLALMAQEOKLPEEVATPTTDEEKDSLIAIDRSPLSTLPQG</p> <p>SLIDKLYNIWIRLQSHVNIIVFDEMDKLMMDKYPGIRQILEKKE</p> <p>GLFRKHMGMKRVDAARSVICPDMYINTNEIGIPMVFATKLTYP</p> <p>QPVTWNVQELRQAVINGPNVHPGASMVINEDGSRALSADVMT</p> <p>QREAVAKQLLTPATGAPKPGQTKIVCRHVKNQDILLNRQPTLH</p> <p>RPSIQAHRARILPEEKVLRRLHYANCKAYNADFDGDEMNAHFPQS</p> <p>ELGRAEAYVLACTDQQLVLPKDGQPLAGLIQDHMVSGASMTTRG</p> <p>CFFTREHYMELVYRGLTDKVGKRVKLLSPSILKPPPLWTGKQVVS</p> <p>TLLINIIPEDHIPLNLGKAKITGKAWKBTPRSVPGFNPDSMC</p> <p>ESQVIIREGELLCGVLDKAHYGSSAYGLVHCCEYIYGGETSGKV</p> <p>LTCARLFTAYLQLYRGFTLGVEDILVKPKADVQRQRIIEESTH</p> <p>CGPQAVRAALNLEAASYSYDEVRGKWQDAHLGKDQDFNMIDLKF</p> <p>KEEVNHSYNEINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT</p> <p>MQISCLLGQIELEGRSTPLMASGKSLPCFEPYFTPRAGGFVTG</p> <p>RFLTGIKPPPEFFHFCMAGREGLVDTAVKTSRSGYLQRCIIKHLE</p> <p>GLVVQYDLTVRSDSGSVVQFLYGEDGLDIPKTQFLQPKQFPFLA</p> <p>SNYEVIMKSQHLHEVLSRADPKKALHHPRAIKKQSKHPNTLLR</p> <p>RGAFLSYSQKIQEAVKALKLESENRRGR/RPWDS/G/RMLRMWY</p> <p>ELDEESRRKYQKAAACPDPSLSVWRPDIYFASVSETFETKVDD</p> <p>YSQEWAAQTEKSEKSELSLDRLLRLQL/KWQRSLECEPGEAVG</p> <p>LLAAQSIGEPSTQMTLNTFHFAGRGEMNVTGIPRLREILMVAS</p> <p>ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ</p> <p>ESFCMEKQKQFQVYQLRFQFLPHAYYQOEKCLRPEIDILRFMET</p> <p>RFFKLLMESIKKNNKASAFRNVNTRATQRDLNAGELGRSRG</p> <p>EQEGDEEEEGHIVDAEABEGDADASDAKRKEKQEEVDYSEEE</p> <p>EEREGEENDDMDQERNPHREGARKTQEQQDEEVGL/GH*GGPV</p> <p>PSRPPDAAPETHPQPGAPGA/EAMERRVQAVREIHPFIDDYQYD</p> <p>TEESLWCQVTVKLPLMKINFDMSSLVSVSLAHGAVIYATKGITRC</p> <p>LLNETTNKNEKELVLNTEGINLPELFKYAEVLDLRLRLYSNDIH</p> <p>AIANTYGLAALRVIEKEIKDVFAVYGLAVDPRHLSLVADYMCF</p> <p>EGVYKPLNRFGIRSNSSPLQOMTFETSQFLKQATMLGSHDEL</p> <p>SPSACLVGKVVRRGGTGLFELKQPLR</p>
5384	196	886	<p>QSCGQRLPTVL*L*GPPGSCPCILSLF/PGRPHALPEIRPYINI</p> <p>TILKGDGDPGPMGLPGYMGREGPQGPQSGKDGKMGSPG</p> <p>APCOKRFFAFSVGRKTALHSGEDFQTLFVRVFNLDGCFDMAT</p> <p>GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS</p> <p>ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF</p> <p>SGHLIKAEDD</p>
5385	326	799	<p>LMVPRTKKEAPAPPKAEAKAKAL/KAKKAVLKDVHSHKKNKIHM</p> <p>SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHVIKFPPLTTE*A</p> <p>VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ</p> <p>SDGERKAYVRLAPDYDALVVATKIGIT</p>
5386	326	799	<p>LMVPRTKKEAPAPPKAEAKAKAL/KAKKAVLKDVHSHKKNKIHM</p> <p>SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHVIKFPPLTTE*A</p> <p>VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ</p> <p>SDGERKAYVRLAPDYDALVVATKIGIT</p>
5387	2	2117	<p>FVVAASGGCWFVLGERRAGSLLSASYGTFAFPMGMVLFGRRNAIA</p> <p>SDDLVPFGFELVVRVLWVIGILTLYLMHRGKLDCAAGALLSSY</p> <p>LIVLMILLAVVICTVSAIMCVSMRGTCNPGPRKSMKLLYIRL</p> <p>ALFFPEMVWASLGAAWVADGVQCDRTVVNGIATVVVSWIIIAA</p> <p>TVVSIIVFDPLGGKMA PYSSAGPSHLDSHSSQLNLGKXTAAT</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SVWETRIKLLCCCGKDDHTRVAFSSSTAELFSTYFSDTDLVPSD IAAGLALLHQQDNIRNNQEPAPQVCHAPGSSQEAADLDAELKNC HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGCCRSKNPQTMT/M VGGDQLQL/CTSAPILHTRAAVQGLHPRQLPWRTRFTLPFLVA LDHRKESVAVVAVRGTMQLDVLTDLSAESEVLDECEVQDRLAH KGISQAARYVYQRLINDGILSQAFSAIEPYRLVIVGHSLSGGGAA ALLATMVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIIVSLVLG KDVIPRLSVTNLEDLKRIRLVVAHCNPKPKYKILLHGLWYELFG GNPNNLPTELDDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSDSPL DSSPKYPLYPGRRIHLQEBGASGRFGCCSAAHYSAKNSHEAE FSKILIGPKMLTDHMPDILMRALDSVVSRAACVSCPAQGVSSV DVA
5388	1569	753	TADGGAGGGRRQAGVRRHYLYPFTGGYRRRRAACQAEPAARS KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMCLSTGCGFYGNPR TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSAIDST SSSMQSPVSNQSLLESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLGLNAGVEMF TVVYTVTQMYTIALTITKQMLKNFVFQOEFKSPGSHQQLLEYK ILEHLQTKN
5389	1569	753	TADGGAGGGRRQAGVRRHYLYPFTGGYRRRRAACQAEPAARS KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMCLSTGCGFYGNPR TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSAIDST SSSMQSPVSNQSLLESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLGLNAGVEMF TVVYTVTQMYTIALTITKQMLKNFVFQOEFKSPGSHQQLLEYK ILEHLQTKN
5390	217	1332	EDPRKLMEKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI EGGADDSITRDDNIAAFKRIRLRPRYLDRVSEVDTRTTIQGEEI SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS LEDIVIAAPEGLRWFLYVHPDLQLNKQLIQRVESLGFKALVIT LDTFVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAPYFQMTPIS TSLCWNDSLWFSITRLPIILKGILTKEDAELAVKHNVQGIIVS NHGGRQLDEVLASIDALTEVVAVKGKIEVYLDGGVRTGNDVLK ALALGAKCIFLGDAILWALASKEHGVKEVLNLTNEFHTSMA\ LTGCRSVAEINRNVLQFSRL
5391	1	1292	VKKAAGRSRGPPPTAGGQRCEAPGTMERRLGVRWVKNRGSF QPPVCNKLHQEQKLVKMFVGGPNTRKDYHIEEGEEVYQLEBDM VLRVLEQGHKRDVIRQGEIFLLPARVPHSPQRFANTVGLVVER RRLETELDGLRYVVDGTDMDVLFKWFYCKDLGTOLAPIIQEFFF SEQYRTGKPIPDQLLEKPPFLSTRSIMEPMSLDWLDSHREL QAGTPLSLFGDTYETQVIAYGQSSSEGLRQNVVWLWQLEGSSV VTMGRRRLSLGPWMDSLVLVSWGPSY\AW\ERTQGSVALSVT\Q DPACKKSPWGEPSCHGLKAATGVPTSTLEVPSLPNNSPSPHYLSV YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLWQTQPTAL PVLPGGLPPAPLLPIPLSLQTCSTSTPRRPSIKAS
5392	1	1623	IRGSNAQKVVGASGGAGPQDPDPAGPGGVPAALAAVLAGCBPR CAAPCPLPALSRCRGAGSRGSRGGAAGSGDAAAAAEWIRKGS FIHKPAHGWLHPDARVLGPGVSYVVRMGCI EVLRSMRSLDFNT RTQVTREAINRLHEAVPGVRGSKKKAPNKALASVLGKSNLRF GMSISIHISTDGLSLSPATRQVIANHHMPSISPAAGGDDMTD YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYNISPGEKPP GGLVDSRLALTQPCALTALDQGPSPLRDACSLPDVVGSTGAP PGDGYVQADARGPPDHEEHLVNTQGLDAPEPEDSPKKDLDFDMR PFEDALKLHECSVAAGVTAAPLPLEDQWSPPTRRAPVAPTEEQ LRQEPWYHGRMSRRAERMLRADGDFLVRDSVTNPGQYVLTGMH AQPKHLLLVDPBGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP
5393	2	982	GGDSAGMTMETQMSQNVCPRLNWLLOPLTVLLLLASADSQAAAP PKAVLKLEPPWINVLQ\EDSVTLTCQGAQP/ERSDSIQWFHNG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>\NLIPHTHTQPS\YRFKANN\DSGEYTCQTGQTS\SDPVHLTVLSEWLVLTQPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK SQKFSHLDPFTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVITIV QVPSMGSSSPMGIIIVAVVIATAVAIIVAAVVALIYCRKKRISAN STD PVKAAQFEPFGROMIAIRKRQLEETNNDYETADGGYMTLNP RAPTD DDKNIYLTLPNDHVNNSN</p>
5394	2	982	<p>GGDSAGMTMETQMSQNVCPNRLWLLQPLTVLLLASADSQAAP PKAVLKLEPPWINVLQ\EDSVTLTQCGAPQ/ERSDSIQWFHNG \NLIPHTHTQPS\YRFKANN\DSGEYTCQTGQTS\SDPVHLTVLSEWLVLTQPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK SQKFSHLDPFTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVITIV QVPSMGSSSPMGIIIVAVVIATAVAIIVAAVVALIYCRKKRISAN STD PVKAAQFEPFGROMIAIRKRQLEETNNDYETADGGYMTLNP RAPTD DDKNIYLTLPNDHVNNSN</p>
5395	3135	531	<p>RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRRTKKRPPSLKKQTTK KPTETPPVKETQOEPEDESLVPSGENLASETKTESAKTEGSPPA LLEETPLEPAAGPKAACPLDSESVGGVPPASGGGRVQNSPPVG RKTLP LTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDNPNFNFSSSTSKMQESP KL PQQSYNFDPTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME ANGVDGDLNPKAKKKKTPLKTDTRFVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCTMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSSEPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHQVPEKSSQKELEAMGLGTP SEAIEITAPEGFSASADALLSRLAHPVSLCGALDYLEPD LAEKN PPLFAQKLQREAAHPTDVSISKALYSRIGTAEEVEKPAGLLFQQ PDLDLALQIARAEIITKEREVSEWKDYEESSRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTQQVLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKKEVLEGFKNNEVLKRCQAEYLSRVKKEEQ R YQALKVHA\EEKLDRANAE\IAQVRGKAQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAMGKS</p>
5396	3135	531	<p>RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRRTKKRPPSLKKQTTK KPTETPPVKETQOEPEDESLVPSGENLASETKTESAKTEGSPPA LLEETPLEPAAGPKAACPLDSESVGGVPPASGGGRVQNSPPVG RKTLP LTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDNPNFNFSSSTSKMQESP KL PQQSYNFDPTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME ANGVDGDLNPKAKKKKTPLKTDTRFVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCTMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSSEPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHQVPEKSSQKELEAMGLGTP SEAIEITAPEGFSASADALLSRLAHPVSLCGALDYLEPD LAEKN PPLFAQKLQREAAHPTDVSISKALYSRIGTAEEVEKPAGLLFQQ PDLDLALQIARAEIITKEREVSEWKDYEESSRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTQQVLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKKEVLEGFKNNEVLKRCQAEYLSRVKKEEQ R YQALKVHA\EEKLDRANAE\IAQVRGKAQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAMGKS</p>
5397	3135	531	<p>RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRRTKKRPPSLKKQTTK KPTETPPVKETQOEPEDESLVPSGENLASETKTESAKTEGSPPA LLEETPLEPAAGPKAACPLDSESVGGVPPASGGGRVQNSPPVG RKTLP LTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS SWDNQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDNPNFNFSSSTSKMQESP KL</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PQOSYNFDPDTCDSEVDPPKTSSTPSSPSKSPASFEIPASAME ANGVDGDGLNPKAKKKKTPLKTDTPRVKKSFKRSLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCTMTVDLEADKQD YPQPSDLSTFVNETHFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHQVPEKSSQKELEAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKALYSRIGTAEVEKPAGLLFQQ PDLSALQIARAEIITKEREVSEWKDYEESSREVMEMRKIVAE YEKTI AQMI EDEQREKSVS\HQT VQQLVLEKEQA\LDLNSVEK \SLADLFRRYEKMKEVLEGFKNNEEVLRCAQEYLSRVKKEEQ YQALKVHA\EEKLDRANAE\IAQVRGKAQOEQAHAQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAMGKS
5398	56	5426	SGEVCRMESNFQEGVPRFSYVFSADPIARPSEINFDGKLDLS HFESLVAPNTEANSFESKDYLVQCLIRPFTQSEKELESEGCVH ILDSQTVVLKEPQCILGRLSEKSSG\QM\AQKFSFPFGLGPAT TQKEFPQGCIMHP\VKDLLKGQSRIFTYGLTNSGKTYTFQGT ENIRILPRTLNVLPDSLQERLYTKMNLKPHRSRYLRSLSEQEK EEIASKSALLRQIKEVTVHNSDDTLYGSLTNSLNISEFEESIK DYEQANLNMANSIKFSVWVSFFEIYNEYIYDLFVPVSSKFQKRK MLRLSQDVKGYSFIKDLQWIOVSDSKEAYRLKLGKIKHQSVAF KLNNASSRSHSIPTVKILQIEDSEMSRVIRVSELSLCDLAGSER TMKTQNEGERLRETGNINTSLLTLGKCINVLKNSEKSKFQOHVP FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKFS AIAQKVCVPDTLNSSQEKLFPGPVKSSQDVSLDSNNSKILNVKR ATISWENSLEDLMEDEDLVEELENAEETED/VGETKLLDEDLK TLEENKAFISHEEKRLDLDIEDLKKKLINKEKLETLFEKIRE EVTQEFTOYWAQREADFKETLLQEREILEENAERRLAIFKDLVG KCDTREBAKDICATKVETERATACLELKFNQIKAEAKTKGEL IKTKEELKKRENESDSLIQELETSSNKIITQNRKIKELINIIDQ KEDTINBFQNLKSHMENTFKCNDKADTSSLIINNKLICNETVEV PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQKK SEEVPRNIAETEDIRVLQENNEGLRAPLLTIENELKNEKEEKA LNKQIVHFQQLSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQK SKNQEQBEKIMKLSNEIETATRSITNNVSIKLMHTKIDELRTL DSVSQISNIDLLNLRDLNSGSEEDNLPNTQLDGLGNDYLVSKQV KEYRIQBPNRENSFHSSIEAIWEECKEIVKASSKSHQIEELEQ QIEKLQAEVKGKYNRNLKEKEHKNQDDLLKEKETLIQQLKEE LQEKNVTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILE TQKVERSHSAKLEQDILEKESIILKLEARNLKEFQEHQDSVKNT KDLNVKELKLEETIQLTNNLQDMKHLQLKEEEETNRQETEK LKEELSASSARTQN\LNADLQKKEEDYADLKEKLTDAKKQIKQV QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQR\TIQQLK EQLINQKVEEAIQQYERACKDLNVKEKIIDMRMTLEBEQEQTV EQDQVL\BAKLEEVERLATELDRWRVKCNDLETQNNQRSNKEHE NNTDVLGKLTNLQDELQSEQKYNADRKKWLEEKMLITQAKEA ENIRNKEMKKYAEADRERFPKQNNEMEILTAQLTEKDSDLQKWRB ERDQLVALEIQLKALISSNVQKDNEIEQLKRIISETSKIETQI MDIKPKRISSADPKLQTEPLSTSFEISRNKIEDGSSVVLDSCEV STENDQSTRFPKPELEIQFTPLQPNKMAVKHPGCTTPVTVKIPK ARKRKSNEEEDLVKCNKNATPRTNLKFPISDDRNSSVVKKEQ KVAIRPSSKKTYSLRSQASIGVNLATKKKEGT LQKFGDFLQHS PSILQSKAKKIIETMSSSKLSNVREASKENVSQPKRAKRLYTSE ISSPIDISGQVILMDQMKESDHQIIKRRLRTKTAK
5399	705	230	GPMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG ASPTPGEVQRHLQTHGIDNGELDFSTFLTINMHMQIKQEDPKKE ILLAMLVMDKEKKGYVMSDLRSKLTSLGKLTTHKEV\DDLFRE \ADIEPNGKVYDEFIHKITSYLDGTY
5400	931	248	SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTTPHRVFEVQKVK QASMEDIPGRGHYRLKFAVEEIIQKQKVNCTAEVLYPSTGQE TAPEVNTFTBGETGNPDEEDNTFYQRLKSMKEPLEAQNI\PDN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FGNVSPMTLVHLAWVACGYIIWQNSTEDTWYKMKVIQTQVQVQRNDDFIELDYTIILLHNIAEQEIIPWQMQLVWHPQYGTQVKVHNSRLPKEVQLE
5401	3	1360	TGWSYGPPTTSLAFLAPRDFPPFPKLLIHPQAVVRLSCGAGSMGSQAAAEWRNNAWEGSSSLSGCSMGCFKDDRIVFWTWMFSTYFMEKWAPRQDDMLFYVRRKLAYSSESAGDGRKAAEPEVEVEVYRRDSKKLPGLGDPDIDWEESVCLNLIQKLDYMTCAVCTRADGGDIHIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\EE\VFSDMTVGKGMVCVELVADSKTNTFQGVIFQGSIRYEALKKVYDNRVSVAAARMAQ\MSFGFSKYSNMEF\VR\MKGPQKGHAEMAVSRVSTGDTSPCGTEEDSSPASPHERVTSFSTPPTPERNNRPAFFSPSLKRVPRNRIAEKKSHSANDSEEFFREDDGGADLHNATNLRSLSGTGRSLVGSWLKLNRAAGNFLLYAHLYTVTLPLHRI LTDILLEVRQKPIILMT
5402	3445	1563	GECFIMAADVQNDLVFEFASNMEDERQLGDPAIFPAVIVEHVPGADILNSYAGLACVEEPNDMITESSLDVAEEIIDDODDDITLTVEASCHDGETIETIEAAEALLNMDSPGPMLEKRIINNIFSSPEDDMVVAPEVTHVSVTLTGIPVEMETQQVQEKYADSPGASSPEQPKRKKGRKTKPPRPDSPATTPNISVKKKNDGKGNITLYLWEFLLALLQDKATCPKYIKWTQREKGIKFLVDSKPVSRLLWRKHKNKP\DMNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDEDPSSSIESDPSLSSSATSNRNQTSSRSRVSSSPGVKGGATTVLKPGNSKAAKPKDPVEVAQPSVLRVTQPTQSPYPTQLFRTVHVQQPVQAVPEGEAARTSTMQDETINSSVQSIR\TIQAPTQVPVVVSPRNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAI PSSQPMTVLKENVMLQSQKAGSPPSIVLGPAPV\QQVLT SNVQTCICNGTVSV\ASSPSFS\ATAPVVTFLFLGSSQLVAHPPGTVITSVIKTQETKTLTQVEKKESEDHLKENTEKTEQQQPQPYVMVSSSNGFTSQVAMKQNELLEPNF
5403	3445	1563	GECFIMAADVQNDLVFEFASNMEDERQLGDPAIFPAVIVEHVPGADILNSYAGLACVEEPNDMITESSLDVAEEIIDDODDDITLTVEASCHDGETIETIEAAEALLNMDSPGPMLEKRIINNIFSSPEDDMVVAPEVTHVSVTLTGIPVEMETQQVQEKYADSPGASSPEQPKRKKGRKTKPPRPDSPATTPNISVKKKNDGKGNITLYLWEFLLALLQDKATCPKYIKWTQREKGIKFLVDSKPVSRLLWRKHKNKP\DMNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDEDPSSSIESDPSLSSSATSNRNQTSSRSRVSSSPGVKGGATTVLKPGNSKAAKPKDPVEVAQPSVLRVTQPTQSPYPTQLFRTVHVQQPVQAVPEGEAARTSTMQDETINSSVQSIR\TIQAPTQVPVVVSPRNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAI PSSQPMTVLKENVMLQSQKAGSPPSIVLGPAPV\QQVLT SNVQTCICNGTVSV\ASSPSFS\ATAPVVTFLFLGSSQLVAHPPGTVITSVIKTQETKTLTQVEKKESEDHLKENTEKTEQQQPQPYVMVSSSNGFTSQVAMKQNELLEPNF
5404	187	1111	LPVTLIFAKMKTQLSTLLLLLVPLIKPAPPTQQDSRIIYDYGTDNFEESIFSQDYEDKYLDGKNIKEKETVIIIPNEKSLQQLQKDEAITPLPPKKENDEMTCLLCVCLSGSVYCEEVDIDAVPPLPKESAYLYARFNIKIKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKLSLVEELSIAENQLLKL PVLPPKLTFLNAYNKIKSRGIKANAFKLNNTFLYLDHNALESVPLNLPESLRVIHLQFNINIASITDDTFCKANDTSYIRDRIEERLEGNPIVLGKHPNSFICLRLPIGSYF
5405	2199	1220	QNSRSLHMDPQNQHSGSSSLVVIQPPSLDSRPRLDYERETQPTAILSLDQIKAIRGSNEYTEGPSVVRKPAPTAPRQEKHERTHEIIPINVNNNYEHRTSHLGHAVLPSNARGPILSRSTSTGSAASSGSSASSASQGLLGRSPPTRPVPGHRSERAI RTQPKQLIVDDLKGS LKEDLTQHKFICEQCGKCKGECTAPRTLPSCLACNRQCLCSAESMVEYGTMCML\VKGIFYHCSNDDGDSYSDNPCSQSHCCSRYL CMGAMSLFLPCLLCYPPAKGCLKLCRCYDWIHRPGCRCKNSNTYCKLESCPSRGGQKPS
5406	279	2732	RWRTYNVEGPLTFMDVAIEFCLEEWQCLDTAQONLYRNVMLENY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RNLVFLG/ITAVSKPDLITCLEQEKEPWEPMRRHEMVAKPPVMC SHFTQDFWPEQHIKDPFQKATLRRYKNCEHKNVHLKKDHKSVDRE CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS HTEKKLFKCECGKSFCLSHLAQHKKIHTRVNFCCKCEKCGKAF NCPSIITKHKRINTGKPYTCERCCKVFNWSSRLTTHKKNYTRY KLYKCEECGKAFNKSSILTTTHKIIRTGEKFKYKCECAKAFNQSS NLTEHKKIHPGKPKYKCEECGKAFNWPSTLTTHKRINTGKPYT CEECGKAFNQFNLTTHKRINTA\EFYKCTECGEAFSRS\SNL TKHKEIHTKPKYKCEECGKAFKWSKLTTEHKLTHTEGKPKYKCE KCGKAFNCPSSIITKHNRINTGKPYTCEECGKAFNWSRLTTHK KNYTRYKLYKCEECGKAFNKSSILTTTHKKIHTKPKYKCEECGK AFKWSKLTTEHKIHTGKPKYKCEECGKAFNHSILTTHKRINT GKPKYKCEECGKAFNQSSNLTTTHKIHTGKPKYKCEECGKAFQ SSNLTTTHKIHTGGKPKYKCEECGKAFNQSTLTTHKIHTTEKP YKCEECGKAFKWSSTLTTHKIHTGKPKYKCEECG\KAFKLSST LSTHKIHTGKPKYKCEKCGKAFNRPSNLIHKKIHTGEPQYKCE EECGKAFNYSSHLNTHKRINTKEQPKYKCEKCGKAFNQYSNLTT NKIHTGEKLYKPEDVTILTTPQTFSTNLIK
5407	3	659	RPRRRQSSCCTGWLGLLRAAPRFRCRRTETDMEQKGLAVLIL AIIILLQGTLAQSIKGNHLVKVYDYQEDGSVLLTCDAAEAKNITWF KDGKMGFLTEDKKKWNLGSNAKDPGRMYQCKGSQNKSKPLQVY YRMCQNCIELNAATISGFLFAEIVSIFDLAVGVYFFIAGTGMFR QS\RASDKQTLTP\NDPAPTQPLKDPKMTQVSHLQGN\QLRRN
5408	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAQSPQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVSVRPQGPDRDPKDSRDAKREQGS APRPVPASRGGKTLCKGYRQAPPQPPAQFQRPICSAFPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTKGTGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRTIAYAPRPNFGQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSGRPDWEVAAEAWDNHLRRNRS IVVDLFHGLRSQVKCKTCGHSVRFPDPFNFLSLPLPMDSYMHL EITVIKLDGTTVPVRYGLRLNMDEKYTGKQLSDLCGLNSQIL LAEVHGSNINKFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP TQTFSSSPSTNEMFTLTNGDLPRPIFIPNGMPTVPCGTEK NFTNGMVNGHMPSLPDSPTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTVHTRKDLVDVAVIQVSRLASPLPPQEA AQDCDSMGYQYFPTLRVVKDGNSCAWCPWYRFRGCKIDCGE DRAFIGNAYIADVWHPALHLRYQTSQERVVDEHESVEQSRAQ VEPINLDSCLRAFTSEELGENEMYCSKCKTHCLATKCLDLWR LPPILIHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCOHKPLTPQGDSEPRILAREVKVDAQSSAGEEDVLLSKS PSSLSANISSPKGSPSSSRKSGTSCPSKSNSSPNSSPRTLGRS KGRRLRPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH LVGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHVYTYAKN PNCWKYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYQFLPK TDGKKMADTSSMEDFESDY\EKYCVLQ
5409	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAQSPQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVSVRPQGPDRDPKDSRDAKREQGS APRPVPASRGGKTLCKGYRQAPPQPPAQFQRPICSAFPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTKGTGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRTIAYAPRPNFGQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSGRPDWEVAAEAWDNHLRRNRS IVVDLFHGLRSQVKCKTCGHSVRFPDPFNFLSLPLPMDSYMHL EITVIKLDGTTVPVRYGLRLNMDEKYTGKQLSDLCGLNSQIL LAEVHGSNINKFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TQTFSSSPSTNEMFTLTNGDLPRPFIIPNGMPNTVVPQCTEK NFTNGMVNCHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR PSLFPMPLIVPCTVHTRKKDLYDAVWIVQVSRLASPLFPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIGNAYIAVDWHTALHLRYQTSQERVVDEHESVEQSRRQAQ VEPINLDSCLRAFTSEEELGENEMYCCKCKTHCLATKKLDLWR LPPILIIHLKRQFVNGRWIKSQKIVKFPRESFDPFAFLVPRDP ALCQHKPLTPQGDSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISPPKGPSSSRKSGTSCPSSKNSSPNSPRTLGRS KGRRLPLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHVYTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGDIDYAFPLPK TDGKKMADTSSMEDFESDY\EKYCVLQ
5410	2	710	LRFPQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY VHQNFSHYRATIGVDFALKVLHWDPETVVRLQLWDIAGQERFG NMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNDLDSKLSLFPNG KPVSVVLLANKCDQGDVLMNGLKMDQFCKEHGFVGWPFETSAK ENINIDEASRLVKHILANECDLMESIEPDVVKPHLTSTKVASCSG\CAKILVGTFAGVW
5411	1302	289	TGPAAAGRRKALGSFGKPSVPTGLRAARRRRTRPSAPAAPSVC GKRRSDAGAGGERASVRTGSGRRGGRTMAGDSEQLQNHQPN GGEPLIGVSGGTASGKSSVCAKIVQLLQNEVDYRQKQVVLIS QDSFYRVLTSEQAKALKGQFNFDHPDAFDNELILKLTKEITEG KTVQIPVYDFVSHSRKEETVTVYPADVLFEGILAFYSQER/IR DLFQMKLFVDTADTRLRRVLKDISERGRDLEQILSSSTLRV KPA\FEEFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
5412	3180	313	QGISNFFHKEANFWFEVSGYLISPLRSPFVDFALEWSLMASFWN KMEGESSRFEIHTPVSDKKKKKCSIHKERPKQKHSHEIFRDSLLV NEQSQITRRKKRKKDFQHLISSPLKKSRI CDETANATSTLKKRK KRRYSALEVDEEAGVTVVLVDKENINNTPKHFRKDVVDVVCVMS IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR KAASWBSQRA\RDTPQSEFPQTQESWLSVGGGEITELP\ASA HKNKSKKKKKSSNREYET\LAMPEGSQAGREAGTDMQESQPTV GLDDETPQLLGPHTKKKSKKKKKSNHQEFESLAMPEGSQVGS EVGADMQES\RPVGLHGETAGIPAPAYKNKSKKKKKSNHQEF EAVAMPESLESAYPEGSQVGSVEGTVEGSTALKGFKESNSTKKK SKKRKLTSVKRARVSGDDFSVPSKNSSTLFDSVEGDGAMMEEG VKSRRPQKKTQACLASKHVQEAAPLEPANEHNVEAEDSEIRY LSADSGDADDSDADLGSVAVKQLQEFIPNIKDRATSTIKRMYRDD LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIAWPWKLIYYRA KKMFDVNNYKGRYSEGDTEKLKMYHSLGNDWKTIGEMVARRSL SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQBLK BVDKSLQENPESCLSI VREKLYKGISWVEVEAKVQTRNWMQCKS KWTIELTKRMTNGRRYYGMNALRAKVS LIERLYEINVEDTNEI DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTPEIIDYL YETTLPLLKEKLEKMMKKGTKIQTAPAPKQVFPFRDIFYEDD SEGQGHRRKRRRRRHAWFTPIVPLWEAKAGWII
5413	3753	1304	RFPAGVAPRRAMANVSKVSWSGRDRDDEEAAPLLRRRTARPGG TPLLNGAGPGAARQS PRSALFRVGHMSSVKLDDELLEP\DMDFP HPFPKEIPHNEKLLSLKYESLDYDENSENLFLLEEERRINHTAFR TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKRVIKGNID KFTEKGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ IKCFLNGVKIPHVRLKTLVIKVGSVILSVVGGVLA VKEGPMIH SGSVIAAGISQGRSTSLKRPDKIFEYLRDTEKRDVFSAGAAAG VSAAPGAPVGGVLFSLBEGASFWNQFLTWRIFASMISTFTLNF VLSIYHGNMWDLSSPGLINPGRFDSEK MAYTIEIPVFIAMGVV GGVLGAVFNALNYWLTMFIRIYIHRPCLQVIEAVLVAAVTATVA FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAFFNTPEK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SVVSLFHDPPGSGYNPLTLGLFTLVYFFLACWTYGLTVSAGVFIP SLLIGAAWGRLLFGISLSYLTGAAIWADPGKYALMGAAQGGIV RMTLSLTVMMEATSNVTYGFIMLVMTAKIVGDFIEGLYDM HIQLQSVFPLHWEAPVTSLSLTAREVMSTPVTCLRRREKVGIV DVLSDTASNHNHGFVVEHADDTPARLQGLILRSQILVLLKHKV FVERSNLGLVQRRLRLKDFRDYPRFPPIQSIHVSQDERECTMD LSEFMNPSFYTVPQEASLPRVFKLFRALGLRLHVVDNRNQVVG LVTRKDLARYRLGKRGLEELSQAQT
5414	2130	390	GVASAWDRALFSPLLSPTSRSVFRTSPPRCVSTETGRRDRARVPS QWCSVLQGLPVSGRSLACVRSILLSPASSPRKVGIVGGTGAR AGAAPRDHGRVRRHRRPSSARRMTRTTGQCLAPRGCCQPRGTRSP RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINLLNMDRFTV AGVLPDIEQFFNIGDSSSGLIQTTFISSYMLAPVFGYLGDRYN RKYLMCGGIAFWSLVTLGSSFIPEHFWLLLTGLVGVGEASY STIAPTLIADLFVADQSRRLSIFYFAIPVGSGLGYIAGSKVD MAGDWHWALRVTPGLGVVAVLLFLVVRPEPPGAVERHSDLPPL NPTSWWADLRALARNPSFVLSSSLGFTAVAVFTGSLALWAPAFLL RSRVVLGETFPCLPGDSCSSSDSLIFGLITCLTGLVGLGVEI SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIYATYIF IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD AGSPYLIGLISDRLRNWPSPFLSEFRALQFSLMLCAFGALGG AAFLGTAHLH
5415	693	2986	IPPKTKLELQKH\LTTLT\NQEQTIFEEVQKLRPRNEQRENE IISFLRCLFEBKQKEHIHIGEMKQTSQMAENIGSELPPSATRF RLDMLKNXAKRSLTESLESILSRGNKARGLQEHISISVDLSSLS STLSNTSKEPSVCEKEALPISESSFKLLGSSDLSSDSHSLPE EPAPLSPQQAFFRRRANTLSHFPIECQEPQPARGSPGVSRQKLM RYHSVSTETPHERKDFESKANHLGDSGGTPVKTTRHRSWRQIFL RVATPQKACDSSSRDYEDYSELGELPPRSPLEPVCEGPPGPPPE EKKRTSRELRELWQKAILQQIILLRMEKENQKLQASENDLLNKR LKLDYEEITPCKLEVTTVWEKMLSTPGRSKIPFMEKMHSAVGQ GVP\RHHRGEIWKFLAEQFHLKHQFPSPKQPKDVPYKELLKQLT SQQHAILIDLGRTPFTHPYFSAQLGAGQLSLYNILKAYSLLDQE VGVCQGLSFVAGILLHMESEEEAFKMLKFLMFMGLRKQYRPM IILQIMYQLSRLLDHYRDLNHLBEHEIGPSLYAAPWFLTMF ASQFPLGFVARVFDIMFLQGTEVIFKVALSLLGSHKPLILQHEN LETIVDFIKSTLPNLGLVQMEKTINQVFEMDIAKQLQAYEVEYH VLQEELIDSSPLSDNQMDKLEKTNSLRKQNLDDLEQLQVANG RIQSLIATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS AKPSDREPECTQPEPTGD
5416	27	4074	KSQLECFWGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKGNITIKRLNIQKRRKPSVPCPEPRTTSGQQGIWTSTES LSSNSDDNKQCPNPLIARSQVTSTFISKPPPLETSLPFLTIP ENRQLPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPEGF RRPRLASFGMGTTTSLSPFVGSGNHNPAKHQLQNGYQGNQDYG SYAPAAPTTSSMGSSIIRHSPSSGISTPVTNVSFPHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE AMLGVMTEADKEIELQQQTIESLKEKIYRLEVQLRETTTHDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH MDLVDTCVGTSVETNSVGISCPPECKNKVVGPELPMNWWIVKER VEMHRCAGRSVEMCDKSVSEVSVCETGSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSDVDTVCSPEKASRGVNTEAVSQVEAAV MAVPRADQDSTDLQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNVLVGLKMRTIACGPPQITVGLTASR RSVGVDGDPVGESLENPQQAFLGMMTGLDHYIERIQKLLAEQQ TLAENYSELAEAFGEPHSQMGLNSQLISTLSSINSVMKSAST EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QEVGTSECKPISSLDAPPTQEGTLPVNLTDDQIAAGLYACTNN ESTLKSIMKKKDGKDSNGAKKNLQFVGINGGYETSSDDSSSD ESSSESDDCEDVIEYPLEEEEEDEEDTRGMAEGHHAHNIEGL KSARVEDEMQVQCEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDIYAFAEI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HONKAGYTPIMLAALAAVEAEKDMRIVEELFCGCDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTS PGPTHRSFD
5417	27	4074	KSQFCFPGGKAGDILSGDQDKEQKDPYFVETPYGYQLDLDFLK YVDDIQKNTIKRLNIQKRRKPSVPCBPRTTSGQQGIWTSTES LSSSNSDDNKQCPNFIARSQVTSTPISKPPPLETSLPFLTIP ENRQLPPSPQLPKHNLHVTKTLMETRRRLQERATMQMTPEGF RRPRLASFGMGTTSSLPFVSGSNHNPAAKHLQNGYQGNQDYG SYAPAAPTTSSMGSSIRHSPSSGISTPVTNVSPMHLQHIREQM AIALKRLKELEEQVRTIPVLQVKISVLQEEKRLVLSQLKNQRAA QINVCVGRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEME TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAENMNDIVVYHRGSRSCDKAAVGLVEMRNCVSVTE AMLGVMTRADKEIELQQQTIESLKEKIYRLEVQLRETTDREMT KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMGVSH MDLVDTCVGTSVETNSVSGISQPECKNKVVGPELPMNWIVKER VEMHDCAGRSVEMCDKSVSVSVCTGTSNTEESVNDLTLLKT NLNLKEVRSIGCGDCSDVDTVCSPKECASRGVNTAASVQVEAAV MAVPTADQDSTDLQEQVHQTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTAVAGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGININDNYLVGLKMRTIACGPPQLTVGLTASR RSVGVGDDPVGESLENPPQAPLGMGTGLDHYIERIQKLLAEQQ TLAENYSELAEAFGEPSQMGSLNSQLISTLSSINSVMKSAST EELRNPDFQKTS LGKITGSLGYTCCKGGLQSGSPSSQTSQPE QEVGTSECKPISSLDAPPTQEGTLPVNLTDDQIAAGLYACTNN ESTLKSIMKKKDGKDSNGAKKNLQFVGINGGYETSSDDSSSD ESSSESDDCEDVIEYPLEEEEEDEEDTRGMAEGHHAHNIEGL KSARVEDEMQVQCEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDIYAFAEI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HONKAGYTPIMLAALAAVEAEKDMRIVEELFCGCDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTS PGPTHRSFD
5418	24	1133	SVPRAGGDMETGAELYDQALLGILQHVGNVDFLRVLFGLYR KTDIFYRLLRHPSDRMGFPFGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRKKEEEEAKTVSAAAEKEPVPVPVQIEIDSTTEL DGHQVEVEKVQPPGPVKEMAHGSQAEAPGAVAGAAEVPR\EPPI LPRIQEQQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVKHVVK GKQVSVALSSSSIRVAMLEENGERVLMGKLTHTKINTESSLWSL EPGKCVLVNLSKVGEYWNAILGEEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLGKQSQSHELKVHEMLKKGWDAGSPFR GQRFDPAMFNISPGAVQF
5419	1395	259	GTHPLDPLVSRSTVQGPLMTMACPGMSDTEESFPLGPRAAEEG SESEACEAFGRKSEEEGRSDTSGFGRSRKHKNVWVXHPERADA KDFASLPQC/LGP/DCVRPAQPSKSKYCSDDCGMKLAANRIYEL PQRIQQWQSPCIAEHEGKLLERIRREQQSARTRLQEMERRFH ELEAII LRKQAVREDEESNEGSDDTDLQIFCVSCGHPINFR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADVCGCPLVRDVPFELTGDFCRLPK RQCNRYHCWEKLRRAEVDLERVRVWYKLDLFEQERNVRTAMTN RAGLLALMLHQTIQHDLPTTDLRSSADR
5420	117	1733	NEAGGACPFKGGASGRLYLSPLRVRVSVAGCEERPLGWVWLGG GGFLPARPPRAQRHLGFSHAQSMEDPYEVLVSREQLFHERIR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPSTRL/LLELCTFTLAIALGAVLLLPFSIIISNEVLLSLPRNYIIQWLNGS LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLRV YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYLLP YLYSCISFLGVLLLVCTPLGLARMF SVTGKLLVKPRLLEDLEE QLYCSAFEEAALTRRICNPTSCWLPDLMELLHRQVLALQTORVL LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID EAAMPGRMGQTSLGQVSFSKLGSGFAGVIQVLI FYLMVSSVVG F YSSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGL TRFDLLGDGFRFNWLGNFYIVFLYNAAFAGLTTLCLVKTTAAV RAEILRAFGERE
5421	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGVWVVLGG GGFLPARPPRAQRHLGFSAEQSMEAPDYEVLSVREQLPHERIR ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPSTRL/LLELCTFTLAIALGAVLLLPFSIIISNEVLLSLPRNYIIQWLNGS LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLRV YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYLLP YLYSCISFLGVLLLVCTPLGLARMF SVTGKLLVKPRLLEDLEE QLYCSAFEEAALTRRICNPTSCWLPDLMELLHRQVLALQTORVL LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID EAAMPGRMGQTSLGQVSFSKLGSGFAGVIQVLI FYLMVSSVVG F YSSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGL TRFDLLGDGFRFNWLGNFYIVFLYNAAFAGLTTLCLVKTTAAV RAEILRAFGERE
5422	3	1263	SCGESLPTWLAGASRPGIGRKGAGGGRGSSPAQVLLSPGPVF KAGCNWHLSDQAGVQRCDLGSSQPPPLGPKRFSCLSLPSSWD YRSTVLCVSKMEADLSGFNIDAPRWDQRTFLGRVKHFLNITDPR TVFVSERELDWAKVMVEKSRMGVVPVPGTQVEQLLYAKLYDSAF HPDTGEKMNIVGRMSFQLPGGMIITGFMLQFYRTMPAVIFWQWV NQSFNALVNYTNRNAASPTSVROMALS YFTATTAVATAVGMNM LTKKAPPLVGRWVPPAAVAAANCNIPMMRQQELIKGICVKDRN ENEIGHSRRAAIGITQVVISRITMSAPGMILLPVIMERLEKLH FMQKVVL/SAPLQVMSGCFLIFMVPVACGLFPQKCELPVSYL EPKLQDTIKAKYGELEPYVYFNKGL
5423	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCREERELDIPGPMSEGEQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQ PQASD ANREPVAERSEPALSGLPATMGSGDLLLLSGESQVEKTKLSSSE EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAPSSCSISASSTGSSSLQGHQERAEPRG GSLAKVSSSLEPVVPQEPSSVVG LGPRPQWSPQVPSGSDASGL GRRRLSFQAEYWACVLPDSLPPSPDRHSPWNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVADPVLQDSGVLDLSFSVSPASTLKS P TNVSPNCPPAEATALPFSGPREPSLKQWPSRVQKQGMGLASW SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL RTRDRGWPSRPREKRTSQSARRPTCTESRWKSEEEVESDDEY LALPARLTQVSSLSVLSISTLVTLPTGDIKGQSPLEVSDSDG PASFFSSSSSQLPFGAALQSGDPEGQNPCLFRSFVRAHDSAG EGSGLSSQALGVSSGLLKTRPSLPARLDNRNPFSDPDVEGQLPRK GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGT PAR SNLTSK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLE NTPVLEDVLGRIAKQSGELES HADRLYDSILASLDMLAGCTLIP DKKPMAAMEHPCEGV
5424	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCREERELDIPGPMSEGEQ PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQ PQASD ANREPVAERSEPALSGLPATMGSGDLLLLSGESQVEKTKLSSSE EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG LSCLSQWKSVLSPGSAAPSSCSISASSTGSSSLQGHQERAEPRG GSLAKVSSSLEPVVPQEPSSVVG LGPRPQWSPQVPSGSDASGL GRRRLSFQAEYWACVLPDSLPPSPDRHSPWNPNKEYEDLLDYT YPLRPGPQLPKHLDSRVADPVLQDSGVLDLSFSVSPASTLKS P TNVSPNCPPAEATALPFSGPREPSLKQWPSRVQKQGMGLASW

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL RTDRGWPSRPPEKRTSQSARRPTCTESRWKSEEEVESDDEY LALPARLTQVSSLSVYLSISITLVTLPTGDIKGQSPLEVSDSG PASFPSSSSQSQLPFGAALQSGDPEGQNPCLRSFVRAHDSAG EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE NTPVLEDVLGRIAKQSGELESADRLYDSILASLDMLAGCTLIP DKKPMAMEHPCEGV</p>
5425	1086	115	<p>GFCPPSPSLGHQPPRVLHPTMSMAVETFGFFMATVGLLMLGVTL NSYWRVSTVHGNVITNTIFENLWFSCATDSLGVYNCWEFFSML ALSGYIQACRALMITAILGFLGLLGIAGLRCTNIGGLELSRK AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSPLYPGT KYELGPALYLGWSASLISILGGLCLCSACCGSDEDPASARRP YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA PKKRGPGRGFFPYSNLGRPRPVVAPPRPRVLSHGPSQAK NCSWEVAYLPSEAGSLIF</p>
5426	42	3435	<p>ATSSQSLGRADPPRGGMERSPGEGSPSPMDQPSAPSDPTDQ PAAHAKPDGSGGQPGAGPAAGEALAVLTSFGRRLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLDDDEQL TAKTLYMSHRELPAWVSFPDVEKAENLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPDLINWTGMTNLLDIPGLSSLS TMIMDSIAAPLVLPNRLVPLVPLDQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHVEVPGQIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFFLQGGQGVHLRLLEWLSLLSDAEKLEQVLQWNWG VSSRPDPSSAAILVVYLDRAQDLPMTSELYPPQLKKGKNEPNP MVQLSIQDVTQESKAVYSTNCPVWEAFRFLQDPQSQELDVQV KDDSRALTGLALTPLARLLTAPELILDQWFQSSSGPNSRLYM KLVMRILYLDSSIECFPTVPGCPGAWDVSENPGRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLLAGRSFRSHVVRDLNPRWNEVEFIVTSPVQGELEVEVF DKDLDDKDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL ERLTPTPTAAELEEVQVNSLIQTQKSAELAAALLSIYMERAE LPLRKGTKHLSPYATLTVGDSHKTITISQTSAPVWDESASFLI RKPHTESLELQVRGEGTGVLSLSLPLSELLVADQLCLDRWFTL SSGQGVLLRAQLGILVSQHSQVGAHSHSYSHSSSSLSSEPELS GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTWYYSE ERKLVSIVHGCRSLRQNGRDPDPYVSLLLLPDKNRGTKRRTSQ KKRTLSPFNERFEWELPLDEAQRRLDVSVKSNSSFMSSREREL LGKVQLDLAETDLSQGVARWYDLMNDKDKGSS</p>
5427	42	3435	<p>ATSSQSLGRADPPRGGMERSPGEGSPSPMDQPSAPSDPTDQ PAAHAKPDGSGGQPGAGPAAGEALAVLTSFGRRLVLIPVYLA GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLDDDEQL TAKTLYMSHRELPAWVSFPDVEKAENLNKIVAQVWPFLGQYMEK LLAETVAPAVRGSNPHLQTFTRVELGEKPLRIIGVKVHPGQR KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL EPLIGDLPFVGAVSMFFIRRPDLINWTGMTNLLDIPGLSSLS TMIMDSIAAPLVLPNRLVPLVPLDQDVAQLRSPLPRGIIRIHL LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN PQWGETYEVMVHVEVPGQIEVEVFDKDPDKDDFLGRMKLDVGKV LQASVLDDWFFLQGGQGVHLRLLEWLSLLSDAEKLEQVLQWNWG VSSRPDPSSAAILVVYLDRAQDLPMTSELYPPQLKKGKNEPNP MVQLSIQDVTQESKAVYSTNCPVWEAFRFLQDPQSQELDVQV KDDSRALTGLALTPLARLLTAPELILDQWFQSSSGPNSRLYM KLVMRILYLDSSIECFPTVPGCPGAWDVSENPGRGSSVDAPPR PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY VKLLAGRSFRSHVVRDLNPRWNEVEFIVTSPVQGELEVEVF DKDLDDKDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ERLTPRPTAAEEVLQVNSLIQTQKSAELAAALLSIYMERAE LPLRKGTKHLSPYATLTVDSSHKTKTISQTSAPVWDESASF LIRKPHTELELQVRGEGTGVLSLSLPLSELLVADQLCDRWF TLSSGQGVLLRAQLGILVSQHSQVGAHSHSYSHSSSSLS EEPGLSGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQV KLTWLYSEERKLVSIHVHGRSLRQNGRDPDPYVSLLLP DKNRGTRKRTSQKKRTLSPEFNERFEWELPLDEAQR RKLDSVSKNSFSMRERELGKVQLDLAETDLSQGV ARWYDLMDNKKDGSS
5428	3	1839	SSRSERLSACAIAPFWLVSSRPAPQALQRPQGMVEDGA EELEDLVHFSVSELPSRGYGVMEIIRQGLCDVTLKIGD HKFSAHRIVLAASIPYFHAMFTNDMMCKQDEIVMQGMD PSALEALINFAYNGNLAIQQNVQSLMGASFLQLQSI KDACCFTFLRERLHPKNCGLVRQFAETMMCAVL YDAANSFIHQHFVEVSMSEEFLLPLEDLVLEL VSRDELNVKSEEQVFEAALAWRYDREQRGTFL\RN LQSNIRLLFCRPQFLSDRVQDDLVRCCHKCRDLV DEAKDYLLMPERRPHLP AFRTTRPCCTS IAGLI YAVGGLNSAGDSLNVVEVDFDIANCWERCRPMT TARSRGVAVVNGLLYAIGGYDGLRLSTVQAYNT ETDTWTRVGSMMNSKRSAMGTVVLDGQIYVCGGYD GNSLSVETYSPE TDKWTVTSMSSNRSAA\GV TVFEGRIYVSGGHDGLQIFSSVEH YNHTATW HPAAGMLNKRCHGAASLGSKMFVCGGYDGS GFLSIAEMYSSV\ADQWCLIVPM\HTRR\SRV SLGGPAVGRLYAVWGVTTGQSNL\SSVGDVLT PETDCWTFM\APMACHEGGVGVGCIPLLT I
5429	828	202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPT DRLAVPPFAQRERFHRFQPTYPYLQHEIDLPTISL SDGEBPPPYQGPCTLQLRDPEQQLELNRESVRAP PNRTIFDSDLMDSARLGGPCPPSSNSGISATCYG SGGRMEGPPP\TYSEVIGHYPGSSFQHQSSGPPSL LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL
5430	441	1507	QKRKRKRKRKTKTKTQPKMHNSTSWAIFTGLAALC LFQGVVRS GDATFPKAMDNVTVRQGESATLRCTI DNRVTRVAVLNRSITLYAGNDKWCLDPRVLLSNT QTQYSIEIQNVVDVDEGPYTCVQTDNHPKTSR VHLIVQVSPKIVEISSDISINEGNISLT CIATGRPEPTVTRWHISPKAVGFVSEDEYLEIQ GITREQSGDYECASNDV\APV\VRVVKTVNYP PYISEAKGTGVFVGQKGTQCEASAVPSA EFQWYKDDKRLI/EGKKGVKVENRPFLSKLI FFNVSEHDYGNVTCVASNKLGHNTASIMLFGP GAVSEVSNGTSSRRAGCVLLPLLVLLHLLKF
5431	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPAPRSP AWRARSKPV\LPGITINP\TIAEGPSP\TSEGA SEANLVDLQKKLELELDEQQKKRLEAFLTQAK VGELKDDDFERISELGAGNGGVTKVQHRPS GLIMARKLIHLEIKPAIRNQIIRELQVLHECNS PFIYGFYGFYSDGEISICMEHMDGGS LDQVLKEAKRIPEEILGKVSIAVLRLGLA YLREKHQIMHRDVKPSNILVNSRGEIKL CDFGVSGQLIDSMANSFVGTRSYMAPERLQ GTHYSVQSDIWSMGLSLVELAVGRYP IPPPDAKELEAIFGRPVVDGEGEPHSISPR PRPPGRPVSGHGMDSRP AMAIFELLDYI VNEPPPKLPNGVFTPDFQEFVNKCLIKNPA ERALDKMLTNHTFIKRSEVEEVD FAGWLCKTLRLNQPGTPTRTAV
5432	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPAPRSP AWRARSKPV\LPGITINP\TIAEGPSP\TSEGA SEANLVDLQKKLELELDEQQKKRLEAFLTQAK VGELKDDDFERISELGAGNGGVTKVQHRPS GLIMARKLIHLEIKPAIRNQIIRELQVLHECNS PFIYGFYGFYSDGEISICMEHMDGGS LDQVLKEAKRIPEEILGKVSIAVLRLGLA YLREKHQIMHRDVKPSNILVNSRGEIKL CDFGVSGQLIDSMANSFVGTRSYMAPERLQ GTHYSVQSDIWSMGLSLVELAVGRYP IPPPDAKELEAIFGRPVVDGEGEPHSISPR PRPPGRPVSGHGMDSRP AMAIFELLDYI VNEPPPKLPNGVFTPDFQEFVNKCLIKNPA ERALDKMLTNHTFIKRSEVEEVD FAGWLCKTLRLNQPGTPTRTAV
5433	360	1885	SVQEDKVGFEPLHLCSWRARACPCTWPHC/CTG LLECLGFAGVLFGWPSLVFVFNEDYFKDL CGPDAGPIGNATGQADCKAQDERF SLIFTLGSFMNFMFTFTGYIFDRFKTTVAR LIAIFFYTTATLI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			IAFTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI ITLYNGAFDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLQYLAC STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QQLSMKT GSYSQSSSFQRRKRPGQGRSRNSAPSGATL/CSRRFAWHLVWL SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL CAPWNGLLMDRLKQYKQKEARKTGSSTLAVALCSTVPSLALTSL LCLGFALCASVPILPLQYLTPILOVISRSPFLYGSNAFLTLAFP SEHFGKLFGLVMALSAVVSLLQFPITFLIKGSLQNDPFYVNVMF MLAILLTFHFPFLVYRECRTWKESPSAJA
5434	66	652	RYAALIISLIQHLLWRNQHCSRVCIMSPAQSAGLNWLF/GSGK HGPFLLGCSQYPACDYVRPLKSSADGHIVKVLGQVCPACGANLV LRQGRFGMFIGCINYPECEHTELIDKPDETAITCPQCRTHLVQ RRSRYGKTFHSCDRYPECQFAINFKPIAGHCPECHYPLLIEKKT AQGVKHFCAKQCGKPVSAE
5435	4704	1597	PODSSQRLAEMSNAKERKHAKKMRNOPTNVTLLSSGFVADRGVKH HSGGKEKPFQAKQEPHPTSRQRQTRVNPVHSLPDPEVNEQSSSK GMFRKKGWKGAGPEGTSEIPIKYITASTFAQARAAEISAMLKAV TQKSSNSLVFQTLFRHMRMRAMSHNVKRLPRRLQEIQAQKAEKA VHQKKEHSKNKCHKARRCHMNRTEFNRRQKKNIWLETHIWHAK RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYCCLE LKGKEEELKALSGMCNIDTGLTFAAVHCLSGKRQGSLLVLYRVN KYPREMLGPVTFIWKSRQTPGDPSESRLWILHPTLKQDILEE IKAACQCVBPIKSAVCIADPLPTPSQEKSCTELPDEKIGKKRRR KDDGENAKPIKKIIGDGTDRDCLPYSWISPTTGIIISDLTMEMN RFRLLIGPLSHSILTEAIIKAASVHTVGEDTEETPHRWIETCKKP DSVSLHCRQEAIFELLGGITSPAETPAGTILGLTVGDPRINLPQ KKSALPNPEKQDNEKVRQLLEGVVPECTHSFIWNQDICKSV TENKISDQDLNMRSELVPGSQLILGPHESKIPILLIQPGVK TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVVRVGLKESAVH SQYKRSPNVPGDFPDPCAGMLFAEQAKNLEKYKRRPPAKRPN YVKLGTLPFCCPWEQLTQDWESRVQAYEPEPSSVSSPNGKESDL RRSEVP/CAPMPKKTHQPSDEVGTSIEHPREAEVMDAGCQESAG PERITDQEASENHVAATGSHLCVLRSRKLLQLSANCSPSSDS RGGRRAPGRGQGLTREACLILGHFPALVWVLSLLSKGSPE PHTMICVPAKEDFLQLHEDWHYCGPQESKHSDFRSKILKQKEK KKREKRQKP\GRASSDGPAGEEPVAGQEALTLGLWSGFLFRVTL HCSRTLLGFVTQGDFFMAVGCGEALGFVSLTGLLDMLSQPAAQ RGLVLLRPPASLQYRFARIAIEV
5436	1781	635	ASDSIPWSEARTTRKLAQRGCQWLSLPERMPLVVFGLPYSGKSR RAEELRVALAAEGRVYVDDAAVLGAEDPAVYGDSAREKALRG ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA GSSVLRELHTADSVVNGSAQADVPEKELEREBSGAARSPALVTPD SEKSAKHGSGAFYSPELLEALTFRFEAPDSNRNRDRLFTLVGL EEPLPLAGIRSALFENRAPPHQSTQSQPLASGSFLHQLDQVTS QVLGLMEAQKSAVPGDLLTLPGTTEHLRFRTRPLTMAELSRRLR QFISYTKMHPNNENLPQLANMFLQYLSQSLH
5437	739	1672	CQEAASEFGGPLHTPAMFLRLGGWLPRPWGRRKPMRPDPPEPE PRRDSSSENSGSDWDSAPETMEDVGHPKTKDSGALRVRAASE PSKEEPQVEQLGSKRMDSLKWDQPISTQESGRLEAGGASPKLR WDHVDGGTRRPGVSPGGL\GVPGPGAPLEKPGRREKLLGWLR GEPGAPSRYLGGPEECQISTNLTLLHLELLASALLALCSRPLR AALDTLGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEQRGDPG KGL
5438	2443	1152	TKPRKRRRHQPASQRQRPWSSDSTGDLARGKGRKEENKGS DRV LAPPSLRPPMCCQSEARQGPFLRAAKWLHFPQLALRRRLGQLSC MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGRVPSRVVALYKS VPTRLLSRAWGRNLNQVELPHWLRRPVYSLYITWFGVNMKEAAVE DLHHYRNLEFFRRKLKQARPVCGLHSHVISPDSGRILNFGQVK NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSPKNQLVT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			REGNELYHCVIYLA PGDYHCFHSPTDWTVSHRRHFPGSLMSVNP GMARWIKELFCHNERVVLTDGDKHGFFSLTAVGAT\NWSGIRIY FDRDLHTNSPRHSGSYNDFSFTVHTNREGVPMALRGEHLG/QS FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGALGSL
5439	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLARGKGRKEENKGS DRV LAPPSLRPPMCQSEARQGP ELRAAKWLHFPQLALRRRLGQLSC MSRPALKLRSWPLTVLYLLPFGALRPLSRVGRFPVSRVALYKS VPTRLLSRAWGRLNQVELPHWLRPPVYSLYIWTFGVNMKEAAVE DLHHYRNLSEFFRRRLKPQARPVCGLSHSVISP SDGRILNFGQVK NCEVEQVQGVITYSLESFLGPRMCTEDLPFPFPAAS CDSFKNLVT REGNELYHCVIYLA PGDYHCFHSPTDWTVSHRRHFPGSLMSVNP GMARWIKELFCHNERVVLTDGDKHGFFSLTAVGAT\NWSGIRIY FDRDLHTNSPRHSGSYNDFSFTVHTNREGVPMALRGEHLG/QS FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGALGSL
5440	693	253	EPIPVTPDHLRLVTMTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA MLGAPHNPAPPMSTVIHIRSETSVPDHVVWSLFTNLFMNTCCLG FIAFAYSVKSRDRKMVG DVTGAQAYASTAKCLNIWALILGIFMT ILLIIIPVLVVQAQR
5441	2	2054	CRDGGKNGFMVSPMKPLEIKTQC SGPRMDPKICPADPAFFSFIN NSDLWVANIETGEERRLTFC HQGLSNVLD DPKSAGVATFVIQEE FDRFTGYWWCPTASWEGSEGLKTLRILYEEVDESEVEVIHVSP ALEERKTDSYRYPRTGSKNPKIALKLA EFQ TDSQGIKIVSTQKE LVQPPSSLPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVL PPALFIPSTENEEQ\RLASARAVFRNVQPYVVEVTNVWINVH DIFYPPQSEGEDEL CFLRANECKTGFC HLYKVTA VLK SQGYDW SEPFSPGEQEGLTNAIWVNEETKL VYFQGT KDTPLEHHLVYVS YRAAGEIVRLTTPGF SHSCMSQNFDMFVSHYSSVSTPPCVHVY KLSGDDDDPLHKQPRFWASMMEEAAKIFHFHTRSDVRLYGMIIKP HALQPGKKHPTVLVYGGPQVQLVNNSFKGIKYLRNLTLASLGY AVVVIDGRGSCQRGLRFE GALKNQMGQVEIEDQVEGLQFVAEKY GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVM AYDTGYTERYMDVPENNOHGYEAGSVALHVEKLPNEPNRLILH GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER HSIRCPESGEHYEVTLLHFLQEYL
5442	1	3474	CGQSRRRSPDMPEAKPAKAPKGDAPKGPAPKEAPPKEAPAE APKEAPPEDQSPTAE EPTGVFLKKPDSVSVETGKDAVVAVKNG KELPDKPTIKWFKGKWELE GSKSGARFSPKESHNSASNVYTVEL HIGKVVLDGRGYRLEVKA KDTCDSCGFNIDVEAPRQDASGQSL ESFKRTSEKSDTAGELDFSGLLKREVV EEEKKKKKDDDDDLG IPPEIWELLKGAKKSEYEKIAFYQGITDLRGMLKRLKKAKVEVK KSAAFKKLDPAYQVDRGNKIKLMVEISDPDLTLKWFKNQGEIK PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFV KEPPVLIVTPLEDQQV FVGDRVEMAVEVSBEGAQVMWMDGVEL TREDSEFKARYRFKDKGRHILIFSDVVD EDRGRYQVITNGGOCE AELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWKY NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDTFVPDGYAL GSLSAKLNFL EIKVEYVPKQ\EP PKIPLGFASGGKTSENAD/IV VVAGNKLRLDV\ SITGEAPSPFAT\WLKG\DEVFTTTEGRTRIE KRVDSSFFVIESAQREDEGRYTIKVTNP IGEDVASIFLQVVDVP DPPEAVRITSVGEDWAILVWEPMPYDGGKPV TGYLVERKKKGSQ RWMKLNFEVFTETT YBESTKMEGILYEMRVFAVNAIGVSQPSMN TKPFMPIAPTSEPLHLIVEDVDTDTTTLKWRPPNRI GAGGIDGY LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVGVN IAGRSEPATLAQPV TIREIAEPPKIRLPRHLRQTYIRKVGEQLN LVVPFQGKPRPVVWTKGGAPLDSRVHVRTSDFDTVFFVRQAA RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC TVSDLIVGNEYFYFRVY TENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVAGYSAALNCAVRGHKPKPV VWMKNKMEIREDPKFLITNYQGVLTNIRRPSPFDAGTYTCRAV NELGEALAECKLEVRVPQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5443	66	1003	SRGQLDAGQSSEQHGGNRQPEQSRSSSSSSSSSPRRSRAAEFAMALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMIWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFSEVKTDV NKIEEFLBEVLCPPKYLKLSPKHPESNTAGMDIFAKFSAYIKNS RPEANEALERGLLKTQLKLDYLNLSPLPDEIDENSMEDIKFSTR KFLDGNEMTLADCNLLPKLHIVKVVAKYRNFDIPKEMTGIWRY LTNAYSRDEFTNTCPSDKEVEI\AYS DVAKRHLHQVKSRLLEKVS FMSSP
5444	2	344	SGPIGVTGAQMAKWLRLDYLSFGGRRPPPPQPTPDYTESDILRAY RAQKNLDFEDPY*DSESRLEPDAGPGDSKNPGDAKYGSPKHRL IKVEAADMARAKALLGGPGEELEADTEYLDPFDAQPHAPPDDG YMEPYDAQWVMSLPGRGVQLYDTPYEEQDPETADGPPSGQKPR QSRMPQEDERPADBYDQPEWKKDHISRFAVQFDSPEWERTPG SAKELRRPPRSPQPAERVDPALPLEKQPFHGLNRADEALL SLCKEGSYLVRLSETNPQDCSLSLRSSQGLHLKFARTRENQVV LGQHSGLFPSPVPELVLYSSRPLPVQGAHLALYPVVTQTP*Q *PDWGDRRPNGQVATGLPELWGAEPASAAHPGLHRRHRHPEGLP RAEKPLRGPLLGLREPLGAGPRCPWGLQEPRRQCQVWFSQAPAH QGGGCGYGQSQGSGRPRGGAGSRH
5445	2364	486	ILSRGFLGSVEICIQPLPASEPVLLLTWARRRRWRETSRREPT TLRAQSVCPWWI*ETRMNRSIPVEVDESEYPQSLLKPIPEYSP EESEPPAPNIRNMAPNSLSAFTMLHNSSGDFSAHSTLKLANH QRPVSRQVTCRLTQVLEDSQSFCCRHPGLGKAFPSGCSAVSEP ASESVVGALPAEHQFSFMEKRNQWLVSQLSAASPDTHGDSKSD QSLPNASADSLGGSQEMVQRQPQPHRNAGLDLPTIDTGYDSQPQ DVLGIRQLERPLTSCYCPQDLPLPLRSREFPQFEPQRYPACA QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDPYRAAYQQVIQ ALPGQPLPGASVRGLHPVQKVLNYPSPWDQEEERPAQRDCSFPGLRHQDQPHHQPNNRAGAPGESLECPAELRPQVPQPPSPAAPVR PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVVFVFNLLV NGFQTAIDIFEDRIRGDI IKWMERYLRDKTVM IIVAI SPKYQ DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMMFRFIPVLF PNAKKEHVPTWLQNTHVYSWPKNKNKILLRLLREEEYVAPPRGP LPTLQVVPL
5446	972	161	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEEKYLKEGO TLDVKCDYTLKFASSQKAWQI IRDGEMPKTLACTERPSKNSHP VQVGR IILEDYHDHGLLRVMNVLQVEDSGLYQCVIYQPPKEPH MLFDRIRLVVTKGFSGTGSGNSNENSTQNVYKIPPTTKALCLYT TFRVTQTAPPKSTADVSTPDSEINLTNVTDI IRVPVFNIVILLA GGFLSKSLVFSVLPFAVTLRSFVP* AHEPTRMSSDFQPHPSGSCA KGGRR
5447	207	617	MTARTLSLMASLVAYDDSDSEATEHAGSFNATGQQKDTSGVAR PPGQDFASGTLDPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR GSCPSQRLQWPGKEPQVTFPIKEPSCSSLWTSHVPASHMPLAAA RFKQVKLSRNFPKSSFHAQSESETVGKNGSSPQKKCEDCVVPY TPRRLRQRQALSTETGKGDVEPQPPAGRAPAPLYVGPVSEF IQPYLNSHYKETTVPKVLPHLRGHRGPVNTIQWCPVLSKSHML LSTSMKTFKVVNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL SGGFDFAHLHLDLETGTQLFSGRSDFRITTLKFHPKDHNIIFLCG GFSSEMKAWDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTD ASTRDSADRTI IAWDFRTSAKISNQIFHERFTCPSLALHPREP V FLAQTNNGYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG GDLLVTGSADGRVLMYSFRTASRACTLQHTQACVGTITYHPVLP SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL KSPSPSKSLVLLCGRAMFPQATCPWQLPALSK
5448	194	1833	MASKVTDALVWYQKKIGAYDQOIWEKSVEQREIKGLRNKPKKTA HVKPDLDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF RWLQVTSKVIFFWLLVLYLLQVAAIVLCSTSSPHSIPLTEVI GPIWMLLLGTVHCQIVSTRTPKPLSTGGKRRRLKRAAHLEV HREGDSSSTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAFFLS GSKAKNSIDKSTETDNGYVSLDGKTKVSGEDGIQNHQPQCT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			IRPEETAWNTGTLRNGPSKDTQRTITNVSEVSSEEGPETGYSL RRHVDRTESEGLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSRR QDSEARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIWEGNDCCKADMS VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI FFFLLCVAERTYKQVGIM*TSEGLRNRKSHHYKKHYPNEDAPK SGTSCSSRCSRRQDSEARPESETEDVLWEDLLHCAECHSSCT SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI WEGNDCCKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5449	194	1833	MASKVTDIAVYQKKIGAYDQQIWEKSVQRRITKGLRNPKKTA HVKPDLDVLDLVRGSFAKAKPESPTSLTTKGIVRVVFPPFF RWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI GPIWMLLLGTVHCQIVSTRTPKPLSTGGKRRRKLKAAHLEV HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAFFLS GSKKAKNSIDKSTETDNGYVSLDGKTKVSGEDGIQNHQPQCT IRPEETAWNTGTLRNGPSKDTQRTITNVSEVSSEEGPETGYSL RRHVDRTESEGLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSRR QDSEARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIWEGNDCCKADMS VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI FFFLLCVAERTYKQVGIM*TSEGLRNRKSHHYKKHYPNEDAPK SGTSCSSRCSRRQDSEARPESETEDVLWEDLLHCAECHSSCT SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI WEGNDCCKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5450	8136	1242	GQQFASFFG*NHPEVTVMALTDIDLQLFMSQPEALLLLAAG PADHLLQLYSGHLQVRLVLGQELRLQTPAETLLSDSIPTTV LTVVEGWATLSVDGFLNASSAVPGAPLEVYPGLFVGGTGLGLP YLRGTSRPLRGCLHAATLNGRSLRLPLTPDVHEGCAEEFASDD VALGFSGPHSLAAPPANGTQDEGTLEFLLTQSRQAPLAFQAGG RRGDFIYVDIFEGHLRAVVEKGGQTVLLHNSVPVADGQPHEVSV HINAHRLAISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEASR HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALTRNMA AGCRLEEEYEDDAYGHYAFSTLAPPAWPAPELPEPCVPEPGL PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAE LRK SQVLFVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPP HIIFFPHGSLMVILEHTQKPLGPEVFQAYDPPDSACEGLTFQVLGT SSGLPVERRDQGPATEFSCREAGSLVYVHCGGPAQDLTFR VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQSAMPILPAN LSVETNAVGGQDVSVLFRVTGALQFQELQKHSTGGVEGAEWATQ AFHQRDVEQGRVRYLSTDPQHAYDTVENLALEVQVQSEILSNL SFPVTIQRATVWMLRLEPLHTQNTQOETLTAAHLEATLEEAGPS PPTFHYEVVQAERKGNLQOGTRLSDGOGFTQDDIQAGRVTYGA TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNV LLVVPEGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRG TQDKTMTVTSFTNEDLLRGLVYQHDDSETTEDDIPFVATRQGE SSGDMAWEVEVRGVFRVAIQPVNDHAPVQTIISRIHVARGGRRLL TTDDVAFSDADSGFADAQLVLRKDLLFGSIVAVDEPTRPIYRF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP YLRVANGSSLVPPQGGGTIDTAVLHLDTNLDIRSGDEVHYHVT AGPRWGQLVRAGQPATAFSQDLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLEAAQEA VPPADIVFSVKSPPSAGYLVMSRGALADEPPS LDPVQSFSQEA VDTGRVLYLHRSPEAWSDAFSLDVASGLGAPLE GVLVELEVLPAAIPLEAQNFSVPEGGSLTLAPPLLRVSGPYPT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVBEQLIRYV HDGSETLTDSEFVLMAASEMDRQSHPVAFVTVLPVNDQPPILT TNTGLQMWEGATAPIPAEALRSTDDGSGSEDLVYTIEQPSNGRV VLRGAPGTEVRSFTQAQLDGGVLVLFSHRGTLDDGGFPFRLLSGEH TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS SAGTDPQLLLYRVVRGQPLGRLFHAQQDSTGEALVNFTQAEVYA GNILYEHMPPEPFWEAHDTELEQLSSPPARDVAATLAVAVSFE AACPQRPSHLWKNKGLWVPEGQRARITVAALDASNLLASVSPSQ RSEHDVLFQVTQFPSRGQLLVSEEPHAGQPHFLQSQLAAGQLV YAHGGGGTQQDGFHRAHLQGPAGASVAGPQTSEAFITVRDVN ERPPQPQASVPLRLTRGSRAPISSRAQLSVVDPDSAPGEIEYEQ RAPHNGFLSLVGGGLGPVTRFTQADVDSGRFAFVANGSSVAGIF QLSMSDGAAPPLPMSLAVDILPSAIEVQLRAPLEVQALGRSSL SQQLRVVSDREEPEAYRLIQGPQYGHLLVGGRPSTAFSQFI DQGEVVFATNFSSSHDHFRLALARGVNASAVNVTVRALHVV WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLLEGPRHGR VVRVPRARTEPGGSQLEVEQFTQDDLEDGRLGLEVGPRPEGRAPGP AGDSLTLLELWAGQVPPAVASLDFATEPYNAARPYSVALLSVPEA ARTEAGKPESSTPTGEPGPMASPEPAVAKGGFLSFLEANMFVS IIPMLCVLLLLALILPLLFLYLRKRNTKGHDVQVLTAKPRNGLA GDTETFRKVEPGQAIPLTAVPGQPPPGGQPDPELLQFCRTPNP ALKNGQYVW
5451	1	2274	RDSSEQGRGTDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR KNSEPGSPHSLEALRDAAPSQGLNLLFTKMLFI FNFLFSLP TPALICILTFGAALFLWLTIRFPQVPLPLDLNQSVEGGARK GVSQKNNDLTSCCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQ PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW IISELACYTSMVAAPLYDTLGPEAIVHIVNKADIAMVICDTPQ KALVLIGNVEKGFPSLKVII LMDPFDDDLKQRGEKSGIEILSL YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHQN IVSNAAAFKLCVEHAYEPTPDDVAISYLPPLAHMFERIVQAVVS CGARVGFQGDIRLLADDMKTLKPTLFPAPVRLNRIYDKVQNE AKTPLKKFLLKLAVSSKFELQKGIIRHDSFWDKLIFAKIQDSL GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAQGTECTGGCT FTLPGDWTSGHVGVPACNYVKLEDVADNMNYFTVNNEGEVCIKG TNVFKGYLKDPEKTQEALDSGWLHTGDI GRWLPNGTLKIIDRK KNIFKLAQGEYIAPEKINIYNRSPVLQIFVHGESLRSSSLVGV VVPDTDVLPFAAKLGVKGSFEELCQNQVREAILEDLQKIGKE SGLKTFEQVKAI FLHPEFFSIENGLLTPTLKA KRGE LSKYFRTQ IDSLYEHIQD
5452	1833	1138	SRVPSLCLSLSLSPSPREP VAGAPGCGTAGPPAMATLWGGLLR LGSLLSLSLCLSLVLLLAQLSDAAKNFEDVRCKCICPPYKENS HIYNKNISQKDCDLHVPEPMPVRGPDVEAYCLRCECKYEBRSS VTIKVTII IYLSILGLLLYMVYLTVEPILKRRLFGHAQLIQS DDDIGDHQPFANAHDLARSRSRANVLNKVEYAAQQRNKLQVQE RKSVFDRHVLS
5453	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQPPAAAAAPGEQAV AGPAPSTVPSSSTSKDRPVSQPSLVGSKEEPPPARSGSGGSAKE PQEERSQQQDDIELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCELODRKLTKEERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLTELMTSGTLKTYLKRKFKVMKIKVL RSWCRQILKGLQLHTRTPPI IHRDLKCDNIFITGPTGSGVIGD LGLATLKRAFSKSVIGTPEFMAPEMYEEKYDESVDVYAFGCM LEMATSEYPYSECNAAQIYRRVTSGVKPAFDKVAIPEVKEII EGCIRQNKDERYSIKDLNLHAFQEETGVRVELAEBDDGEKIAI KLWLRIEDIKKLGKDYKDNIAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRKRQRL*
5454	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQPPAAAAAPGEQAV AGPAPSTVPSSSTSKDRPVSQPSLVGSKEEPPPARSGSGGSAKE PQEERSQQQDDIELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCELODRKLTKEERQRFKEEAEMLKGLQHPNI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>VRFYDSWESTVKGKRCIVLVTLMSTGTLKTYLKRPKVMKIKVL RSWCRQILKGLQLHTRTPPIIHRDLKCDNIFITGPTGSKVIGD LGLATLKRAFAKSVIGTPEFMAPEMEEKYDESDVDVYAFGMCM LEMATSEYPYSECQNAQIYRRVTSQVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQETGVRVELAEEDDGEKIAI KLWLRIEDIKKLGKGYKDNEAIEFSFDLERNVPEDVAQEMVESG YVCEGDHKTMAKAIKDRVSLIKRKRQRL*</p>
5455	1359	377	<p>LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCLGVFGLFRLLQ WVRGKAYLRNAVVIITGATSLGKCEAKVFYAAGAKLVLCGRNG GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAEIL QCFGYVDILVNNAGISYRGTIMDTTVDVDRVMETNYFGPVALT KALLPSMIKRRQGHIVAISISQKMSIPRSAYAASKHATQAFF DCLRAEMEYQIEIVTVISPGYIHTNLSVNAITADGSRYGVMDDT TAQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRLTAPG LFFSLMASRARKERKSKNS</p>
5456	2	2332	<p>CGAGLVAAGAVLVLYPASRAGERTVPGSPAPSSPLHSPGACG TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQPLSGSRLKRRPD QMEDGLEPEKKRTRGLGATTKITTSHPVPSLTTPVQTQGGTTA QKVSCKTGPSTALATGLKNQKVPVAVPVQKSGTSGVPPMAGG KKPSKRPAPDLKGLCDLNAELKRCRERTQTLDQENQQLQDQLR DAQQVQKALGTERTTLEGLAKVQAQAEQGGQELKNLRACVLEL EERLSTQEGVLQELQKKQVELQEERRGLMSQLEEKERRLQTS ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRLHNLQ QELKGNIRVFCRVRPVLPGEPPTPPGLLLPSPGPGSDPPTRL SLSRSDERRGTLGAPAPPTRHDFSFDRVFPSPGSGQDEVFEEIA MLVQSALDGYPVCIFAYGQTGSGKFTMEGGPGGDPQLEGLIPR ALRHLSFVAQELSGQGWTSYFVASVYVETYNETVRDLLATGTRK QGGECEIRRAGPGSEELTVTNARYVPVSCKEVDALLHLARQNR AVARTAQNERSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG SERLDPLGALGPGERERLRETQAINSSLTGLVIMALSNEKESH VPYRNSKLTLYLLQNSLGGSAKMLFVNISPLEENVSESLNSLRF ASKVEPSVLFGTASQNRKWKTDPPDLVCVCVCVCVCVCVCVP MSMYRVRGGRVAGGCFIGWRAPCPRAIK</p>
5457	2	1540	<p>DDFVERRRWRTRTCLVRSPPHVPVCGHACSWNGGSLDPLKGT LLRSAERLMRKVKLLRLDKENTGSWRSFSLNSEGAERMATTGP TADRGDAATDDPAARFQVQKHSWDGLRSIIHGSRYSGSLIVNK APHDFQFVQKTDESGPHSHRLYYLGMYPGSRNSLLYSEIPKKV RKEALLLSWKQMLDHPQATPHHGVSREEELLRERKRLGVFGI TSYDFHSEGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANETGEER RLTFCHQGLSNVLDPPKSAGVATFVIEEFDRFTGYWNCPTASW EGSEGLKTLRLIYEEVDESEVEVIHVPSPALEERKTDSYRYPT GSKNPKIALKLAEFQTDSSQKIVSTQEKELVQPFSSLPKVEYI ARAGWTRDGKYAWAMFLDRPQQLVLLPPLFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLLQCS</p>
5458	6642	4022	<p>FVPGLEPQWEPAPQPSATMSAPSEEEYARLVMEAPEWLRAEV KRLSHELAETTREKIQAAEYGLAVLEEKHQLKQFEELEVDYEA IRSEMEQLKEAFQQAHTNHKKVAADGESREESLIQESASKEQY VRKVLQELQELKQLRNVLNTQSENERLASVAQELKEINQVET QRGRRLDDIKYKFREARLLQDYSELEENISLQKQVSVLRNQ VEFEGLKHEIKRLEETEYLSQLEDAIRLKEISERQLEEALET LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLLDGLKFSDDAA EPNNDAAELVNGFEHGGAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYVEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAA HAEKGRYEAEGQALTEKVSLEKASRQDRELLARLEKELKVS DVAGETQGSLSVAQDELVTFSLEELANLYHHVCMCNETPNRVML DYYREGQGGAGRTSPGGRTSPAGRRSPILLPKGLLAPEAGRA DGGTGDSSPSPGSSLPSPLSDPREPMNIYNLIAIIRDQIKHLQ AAVDRTTELSRQRIASQELGPAVDKDEALMEEILKLKSLSTK</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			REQITTLRTVLKANKQTAEEVALANLKSXYENEKAMVTETMMKLR NELKALKEDAATFSSLRAMPATRCDEYITQLDEMQRQLAAAEDE KKTLSLLRMAIQKQLALTQRLELLELDHEQTRRGRKAAPKTK PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGMASNFNDIVKQGYVRISSRLGIYQRCWLVFKKASS KGPKRLEKFSDERAAYFRCHYKVELNNVKNVARLPKSTKKHAI GIYFNDTSKTFACESDLEADWCKVLQMECVGTRINDISLGE DLLATGVEREQSERFNVYLMPSPLNGCYMGECALQITYEYICLW DVQNPVRVLIWPLSALRRYGRDTTWFTFEAGRMCEGTGEGLFIF QTRDGEAIYQKVHSAALAAIEQHERLLQSVKNSMLQMKMSERAA SLSTMVPLPRSAWQHITRQHS TGQLYRLQDVSSPLKLHRTET PAYRSEH
5460	45	2097	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL GRLGTFTETQILQRAPLRSFTETPAYFASKDGISKDGS DGNKKS ASEGSSKSGSGNSGKGNQLRCPKCGDLCTHVETVSSSTRFVK CEKCHHFFVVLSEADSKKSIKEPESAAEAVKLAFFQKPPPPPK KIYNYLDKYVVGQSPAKKVLVAVYNYHYKRIYNNIPANLRQQA VEKQTSLSLTPRELEIRREDEYRFTKLQTAGISPHGNALGASMQ QQVNVQIPQEKRGGEVLDSSHDDIKLEKSNILLGPTGSGKTL AOTLAKCLDVFAICDCTTLTQAGYVGEDI ESVIKLLQDANYN VEKAQQGIVFLDEVKIGSVPGIHQLRDVGGEGVQQGLLKLLEG TIVNVPEKNSRKLGETVQVDTTNILFVASGAFNGLDRIISRRK NEKYLGFPTPSNLGKRRAAAAADLANRSGESNTHQDIEEKDRL LRHVEARDLIEFGMIPEFVGRPLVVVPLHSLDEKTLVQILTEPR NAVIPQYQALFSMDKCELVNTEADKAIARLALERKTGARGLRS IMEKLLLEPMFEVPSNDIVCVEVDKEVVEGKKEPGYIRAPTKES SEEEYDSGVVEEGWPRQADAANS
5461	1481	160	INPPPPPKSPCGRARKWRRRRRFGAPEAAVMELPSGPGPERLFD SHRLPGDCFLLLVLLLYAPVGFCLLVLRFLGIHVLVSCALPD SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLSNHVTPFDH NIVNLLTCTPLNSPPSFVCSRGFMENGRGELVESLKRFC ASTRLPPTPLLLFPPEEATNGREGLLRFSSWFFSIQDVVQPLTL QVQRPLVSVTVSDASWVSELLWSLFVFPFTVYQVRNLRPVHRQLG EANEFFALRVQQLVAKELGQTGTRLTPADKAEHMKRQRHPLRP QSAQSSFPSPGSPDVQLATLAQRVKEVLPVPLGVIQRLAK TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASAKFPSSGPV TPQPTALTFAKSSWARQESLQERKQALVEYARRRFTERRAQEAD
5462	663	3353	KIKERQMSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSA RLNGSFSAPSLTNSRGSVHTVSFLLQIGLTRESVTIEAQELSL SAVKDLVCSIVYQKFPCEGFFGMYDKILLFRHDMNSENILQLIT SADEIHEGDLVEVLSALATVEDFQIRPHTLYVHSYKAPTFCDY CGEMLWGLVRQGLKCEGCGLNHYKRCAPKIPNNCSGVRKRRLSN VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI WMEKVMVCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDIDIPMDIN NDINSDSSRGLDDTEEPSPEDKMFLLDPSDLVERDEEAVKTI SPSTSNIPLMRVVQSIIKTKRKSSTMVKEGWMVHYTSRDNLRK RHYWRDLSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS QGSNPHCFEIIITDMVYFVGENNGDSSHNPLAATGVGLDVAQS WEKAIRQALMPVTPQASVCTSPGQGDHDKDLSTSISVSNQIQE NVDISTVYQIFADEVLGSGQFGIVYGGKHKRTGRDVAIKVIDKM RFPKQESQLRNEVAILQNLHHPGIVNLECMFETPERFVVMK LHGDMLEMILSSEKSLRPERITKFMVTQILVALRNLFKNIVHC DLKPVNLLASAEPPQVKLCDFGFARIIIGKSPRRSVVGT PAYLAPEVLRSGYNRSLDMWSVGVIYVLSGTFPFNEDEDINDQI QNAAFMYPPNPWREISGEAIDLINLLQVKMKRYSVDKSLSH WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYP KHFIAPNPDDMEEDP
5463	237	1012	LLSVTMTTSSRCSHLPEVLFDCTSSAAPVVKTVEDCGSLVNGQPQ YVMQVSAKDQQLSTVVRTLATQSPFNDRPMCRICHEGSSQEDL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCHFRFAVERKPR PLVEWLRNPGPQHEKRTLFGDMVCFITPLATISGWLCLRGAV DHLHFSSRLAEVGLIALTVALFTIYLPWTLVSFRYHCRLYNEWR RTNQVRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
5464	195	677	SPSMNPRKKVDLKLITVGAIGVGKTSLLHQYVHKTFYEYQTTL GASILSKIIILGDTTLKLQIWDTGQQRVSRMVSTFYKSGDGI LAFDVTDLSEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA DRKYQSILENHLTESIKLSPDQSRSRCC
5465	5278	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQGGPAAVEA VNVFHHLFYEGQVDIYNINDPLKETATIGFINNFGQIPKQLEFK PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHLDNLRPSLTPV KELKEPVGQIVCTDKGILAVEQNKVLIPTWNKTFWAGYADLSC RLGTYESDKAMTVYECLSEWQILCAICPNKLVITGGTSTVVC VWEMGTSKEKAKTVTLQALLGHTDTVTATASLAYHIIVSGSR DRTCIWDLNKLSTLTLRGRHAPVSALCINELTGDIVSCAGTY IHVWSINGNPVSVNTFTGRSQIICCCMSEMNEWDTONVIVTG HSDGVVRFWRMEFLQVPETPAPEPAEVLMEQEDCEAQIGQEAQ DEDSSDSEADEQSIQDPKDTSPQPSSTSHRPRASCRATAAWC TDSGSDSRWSQLSLDEKDGFI FVNYSEGQTRAHLQGPLSHP HPNPIEBVRNYSRLKPGYRWERQLVFRSKLTMHTAFDRKDNAP EVTALGISKDHSLILVGDSRGRVFSWSVSDQPGRSAADHWVDE GGDSCSGCVRFSLTERRHHCRCNGQLFCQKCSRFQSEIKRLKI SSPVVRCQNCYYNLQHERGSEDPGRNC
5466	3	992	HACAHASAHASGRVLRWRKRKRSVMGIQTSPLVLLASLGVLVTL LGLAVGSYLVRSSRPQVTLDPNEKYLRLLDXTTVSHNTKRF RFALPTAHTLGLFPVGKHIYLSSTRIDGSLVIRPYTPVTSDEDDQ YVDLVIKVYLKGVHPKFPEGGKMSQYLDLKVGDVVEFRGPSGL LTYTGKGFNIQPNKSPPEPRVAKLGMIAAGTGITPMLQLIR AILKVPEDPTQCFLLFANQTEKDIILREDEELQARYPNRFLW FTLDHPPKDWAYSKGFVTADMIREHLPAAGDDVLVLLCGPPPMV QLACHPNLDKLGYSQKMRFTY
5467	2103	4	GEALRVGTGRCRRDLDPQARIFIQKKDLEEDSVTAHLKSRG RSPRKIDQCNSSNMVHGSVTFRDVAIDFSQBEWECLQPDQRTL YRDVMLENYSHLISLAGSSISKPDVITLLEQKEPVMVVRKETS RRYPDLLELYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY FRNDEYRQFEGQLQGYQEGNINQKMISYEKLPTHTPHASLICNT HKPYECKECGKYFSCGNSLIQHQS IHTGEKPYKCECGKAFQLH IQLTRHQKFHTGEKTFECKECGKAFNLPTQLNRHKN IHTVKLF ECKECKGSFNRSSNLQHQSIHAGVKPYQCKECKGAFNRGSNLI QHOKIHSNEKPFVCKECKMAFRYHYQLIEHCQIHTGEKPFCKE CGKAFLLTLKVRHQIHTGEKPFCECKGKAFSLNLQNRHKN IHTGEKPFCECKGKSFNRSNLVQHQS IHAGIKPYECKECKGK FNRGAHLIQHQIHSNEKPFVCRECEMAFRYHCQLIEHSRIHTG DKPFCEQDCGKAFNRGSSLVQHQS IHTGEKPYECKECKGAFRLY LQLSQHQKTHTEKPFCECKGKFFRRGSNLNQHRS IHTGKPF ECKECKGKAFRLHMLIRHQKLHTGEKPFCECKGKAFRLHMLI RHQKLHTGEKPFCECKGKVFSLPTQLNRHKN IHTGEKAS
5468	225	2976	SFLTDLFQSLAQLENLCKQLYETDTTTLQAEKALVEFTNSPD CLSKCQLLLERGSSSYQLLAATCLTKLVSRINNPLPLEQRIDI RNYVNLNLTATRPKLFATVQALIQLYARITKLGFDCQKDDYVF RNAITDVTRFLQDSVEYCIIGVTILSOLTNEINQVSATAFLIEA DTTHPLTKHRKIASSFRDSSLDFITLSCNLLQASGKNLNLND ESQHGLLMQLLKLTHNCLNDFIGTSTDESSDDLCTVQIPTSWR SAFLDSSTLQSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEQDAMDGEL VCRVLQMLNLTDSRLAQAGNEKLELAMLFFFEQPRKIYIGDOVQ KSSKLYRRLSEVLGLNDETMLSVFIGKIITNLKYWGRCEPITS KTLQLLNDLSIGYSSVRKLVLKSAVQFMLNNTSEHPSFLGINN QSNLTDLMCRRTTFYALGRLLMVDLGEDEDDQYEQFMLPLTAFA AVAQMFSTNSFNBQEAKRTLVGLVRDLRGIAFAFNAKTSFMMLF EWIYPSYMPILQRAIELWYHDFACTTFLVCLKMAELVHNRSQLQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FDVSSPNIGILLFRETSKMITMYGNRILTLGEVFKDQVYALKLKG ISICFSLKKAALSGSYVNFVFRLYGDDALDNALQTFIKLLLSI PHSDLLDYPKLSQSYSLLEVLTQDHMFIALEPHVIMYILSS ISEGLTALDTMVCTGCCSCLDHIVTYLFKQLSRSTKKRTTPLNQ ESDRFLHIMQQHPMIQQMLSTVLNIIIFEDCRNQWSMSRPLLG LILLNEKYFSDLRNSIVNSQPPEKQAMHLCFENLMEGIERNLL TKNRDRFTQNLASAFREVNDMSKNSTYGVNSNDMMMS
5469	134	2653	DOEFETSLVPWHLPMGWLCGSLFPVSCVLVLQVASSGNMKVLQ EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLEAHTC VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSKPS EHVKPRAPGNLTVHTNVSDTLTLLTWSNPYPDPNYLYNHLTYAVN IWSENDPADFRIYNTYLEPSLRIAASTLKSGISYRARVRAWAQ CYNTTWSEWSPSTKWHNSYREPFQHLGLGVSVCIVILAVCLL CYVSIKIKKEWWDQIPNPARSLVAIIQDAQGSQWEKRSRGQ EPAKCPHWKNCCLTKLPCLFHNMKRDEDPHKAAKEMPFQSGSK SAWCPVEISKTVLPESISVVRCELPEAPVECEEEEEVEEEKQ SFCASPESSRDDFQEGREGIVARLTESLFDLLGEENGFCQDQ MGESCLLPSPGSTSAHMPWDEFPSSAGPKEAPPWGKEQPLHLEPS PPASPTQSPDNLTCTETPLVIAGNPAYRSFNSLSQSPCPRELQ PDPLLARHLEEEVEPEMPCVPQLSEPTTVQPEPETWEQILRRNV LQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG YKAFSSLLASSAVSPEKCGFGASSGEEGYKPPQDLIPGCPGDDPA PVPVPLFTFGLDREPPRSPQSSHLPPSSPEHLGLEPGEKVEDMP KFPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGQ QTPVMASPCCGCCCGDRASPPTTFLRAPDPSPGGVPLEASLCPA SLAPSGISEKSKSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM RVS
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMDSF KNVGLVFNKSRDRTKAVLCMVVAGATAAVFHTLIAYSDLGYI INKLHHVDES VGSKTRRAFLYLAAPFMDAMAWTHAGILLKHXY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPLISLYMGA LVRCTTLCGLYYKNIHDIIPDRSGPELGGDATIRKMSLFWWPLA LILATQIRSRPIVNLVSRDLGSSAATEAVAILTATYVGHMP YGLWTEIRAVYPAFDKNPNPNKLVSTSNVTAAHIKKFTFVCM LSLTLCFVMFWTPNVSEKILIDIIGVDFAFELCVVPLRIFSPF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRRIIVLIASLVVLPYL GVHGATLGVSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPTTEVTDIVEMREENE
5471	1868	658	RSSAPPGPQRAAAATAAAAAAGVMAAAAAAGGGGGEPRTTEGV GPGVPGEVEMVKGQPFDFGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKI CDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLSKGYTKSIDIWSVGCILAEMLS NRPIFPKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAAWAKLPKSDSKALDLDRLMTFNPKNKRITVEEALAHF YLEQYYDPTDEPVAEPEPTFAMELDDLPERLKLIFQETARFQ PGVLEAP
5472	1469	753	LYVMARYLSDEEVAVSIDRLCKANGRSFSPFPGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR GSDKMPGRVVTLLLEDHEGTGWVAYVQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA IATQILACRGFSGHNLLEYLLRVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCFTEQALALV
5473	3	2119	FMNVKLLIQDLEDIEQRPVMDAQYKIIITKTAHLITKESPOQEG KEMFATMSXLKBLTKVKECYSPLLYESQQLLIPLELEKQMTS FYDSLKGKINEIITVLREAQSSALPKQKHQELLACQENCKKTLT LIEKGSQSVQKFVTLNVLKHFQDTRLQRIADIHVAFQSMVKK TGDWKKHVETNSRLMKKFESRAELEKVLRIAQEGLEBEKGDPEE LLRRHTEFFSQDQRLNLAFLKACDELTDILPEQEQQLQEA VR KLHKQWKDLQGEAPYHLHLKIDVEKNRFLASAECELTEDRET

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KLMPQEGSEKIIKEHRVFFSDKGPVHLCERLQLIEELCVKLPV RDPVRDTPGTCHVTLKELRAAIDSTYRKLMEDPDKWKDYTSRFS EFSSWISTNETQLKGIGEAIDTANHGEVRAVEEIRNGVTKRG ETLSWLKSRLLKVLTEVSSSENAQKQGDDELAKLSSSFKALVTLSS EVEKMLSNFGDCVQYKEIVKNSLEELISGSKEVQEQABKILDTE NLFEAQQLLLHHQKTKRISAKKRDVQQQIAQAQQGEGGLPDRG HEELRKLESLDGLERSRERQERRIQVTLRKWERFETNKETVVR YLFQTGSSHERFLSFSSLESLSSELEQTKEFSKRTESTIAVQAEN LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEBEYVIDK S
5474	2	780	TFDVRQLQASRRGI AVASWCSPRWFAGEEMAFVKSGLLRQSTI LKRWKKNWFDLWSDGHLIYYDDQTRQNI EDKVHMPMDCINIRTG QECRDTPPDGKSKDCMLQIVCRDGTISLCAESTDDCLAWKFT LQDSRTNTAYVGSAMVTDSTSVSSPPPYTAYAAPAVEVGRSL LQQAAYGYGPGYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLYQQ PANQVIIRERYRDNDSDLALGMLAGATGMALGSLFWVF
5475	2	506	ARGWLESLSLTCTQTPPPSSPCLLHSPETFIHTMPPNLTGYR VSQKNMEDYLQALNISLAVRKIALLLKPKDKEIEHQGNHMTVRL STFRNYTVQFDVGVEFEEDLRSVDGRKQCQITVWEEHLVCVQK GEVPNRGRWHLEGEMLYLELTARDACEQVFRKVR
5476	192	1457	SDSMSLLDCFTSRTQVESLRPEKQSETSIHQYLVDEPTLSWSR PSTRASEVLCSTNVSHYELQVEIGRFPDNLTSVHLARHTPTGT VTIKITNLENCNEERLKLKAVILSHFFRHPNITTYWTVFTVG SWLWVISPFMAYGASQLLRTYFPEGMSSETLIRNIFGAVRGLN YLHQNGCIHRSIKASHILISGDGLVTLGSLSHLSLVKHGQRHR AVYDFPQFSTSVQPNLSPPELLRQDLHGYNVKSIDIYSVGITACEL ASGQVPFQDMHRTQMLLQKLKGPYPSPLDISIFPQSESERMKNS SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC LQDDPEKRPSASSLLSHVFFKQMKESQDSILSLPPAYNKKPSI SLPPVLPWTEPECDFPDEKDSYWEF
5477	3	1044	RGNSRLRYSHEDQLPLPELFETGRQLLDEVEVATEPAGSRI VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLYLLV PAFQGALTMKQVNP SKRLDHLQRAREHF INYLTQCHCYHVAEFE LPKTMNNSAENHTANSSMAYPSLVAMASQROAKIQRKQKKELE HRLSAMKSAVESGQADDERVREYLLHLQRNIDISLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGI AKAAPBEFRKAAQQQE EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG
5478	2	835	KTVRIWVPNVKGESTVFRHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFS PDGRLIVSASDDKT LWDKSSRECVHSYCEHGGFVTVDFHPSGTCLAAAGMDNTVKVW DVRTHRLQLHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILD MEGRLLYTLHGQGPATTVAFSRTGEYFASGGSDEQVMVWKS NFDIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP
5479	2	835	KTVRIWVPNVKGESTVFRHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSQHINWVRCAKFS PDGRLIVSASDDKT LWDKSSRECVHSYCEHGGFVTVDFHPSGTCLAAAGMDNTVKVW DVRTHRLQLHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILD MEGRLLYTLHGQGPATTVAFSRTGEYFASGGSDEQVMVWKS NFDIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP
5480	444	1952	LSLSRMEEAEVLVKGRLQAITDKRKIQEBISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNNQDQHQIQVLEQSI LRLEKEIQDLEKAEQISTKERAILKKLSIBRTTEDIIRSVKV EREERAERSIEDIYANIPDLPKSYIPSLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIVYDDGQ KSVYAVSSNHSAAANGTDGLAPVEVEELLRQASERNKSPTEYH EPVYANPPYRPTTPQRETVPGPNFOSRIKIKTNGLGIGVNESI HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQAAEKLHTPQKR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LMTPEESNVMDKAPSPKRLSPRETIFGKSEHQNSSPTCQE DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSEEDKKFLT GYDGIHAELVVIDDEEEDEGEAEKPSYHPIAPHSQVYQPAKP TPLPRKRSEASPHEKHKHS
5481	3	1422	NSPGSVCLCQCVCPSLLHCLPPLLLLLLLPLLLHESQPQPALRV VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTLV QGLNEAGDDLEAVAKFLDSTGSRDYRRYADTLFDILVAGSMLA PGGTRIDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK YLEKAFEDMKKLLFLKAFSETEQTKLAMLSGILLNGTLTPAT ILTSFLTDSLVEGIAASFAVKLFKAWMAEKDANSVTSRLKAN LDKRLLELFPVNRQSVDFHAFKYFTDAGLKELSDFLRVQQLGTR KELQKELQERLSQECPIKEVVLVYVKEEMKRNLDLPEAVIGLLWT CIMNAVWVNKKEELVAEQALKHLKQYAPLLAVFSSQGSSELILL OKVQVEYCYDNIHFMKAFQKIVVLFYKADVLSEEAALKWYKEAHV AKGKSVFLDQMKKFVWELQNAEESESEGEEN
5482	1492	528	THVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSRL EGLQEKDSGYPSCSVNVQDKQKSRGHSIKTLELNLVLPAPPS CRLQGVPHVGANVTLSQCSPRSKPAVQYQWDRQLPSFQTFPAPA LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVLEVSTGP GAADVAGAVVGTGLVGLLGLVLLYHRRGKALEEPANDIKEDA IAPRTLWPWKSSDTISKNGTLSSVTSARALRPPHGPFPFGALT TPSLSSQALPSPRLPTTDGAHPQPIPIPGGVSSGLSRMGAVP VMVPAQSQAQSLV
5483	1	788	FFFFKGCRAGRGNESDYRKLEEMHQRFLVSESKDDLQRLTRA ENRIKQLETDSSEEISRYQEMIQKLQNVLESERENCGLVSEQRL KLQENKQLRKETESLRKIALEAQQKAKVKISTMEHEFSIKERG FEVQLREMEDSNRNSIVELRHLLATQQKANRWKEETKKLTESA EIRINNLKSELSRQKLHTQELLSQLEMANEKVAENKILIEHQE KANRLQRRLSQAEERAASASQOLSIVITVQRRKAASLMNLENI
5484	3	1997	IMADMEDLFGSDADSEAEKDSDSGSDSDSDQENASGSNASGS ESDQDERGDSGQPSNKLFGDDSEDEGASHHSGSDNHSERSDNR SEASERSDHEDNDPSDVDQHSQSEAPNDDDEGHRSDGGSHHSE AEGSEKAHSDDEKQWREDKSDQSDDEKIQNSDDEERAQGSDEDK LQNSDDDEKMQNTDDEBRPQLSDDERQQLSEEEKANSDDERPVA SDNDEKQNSDDEEQQLSDDEKMQNSDDERPOASDEEHRHSD EEEQDHKSESARGSDSEVLRMKRKNAIASDSEADSDTEVPKD NSGTMDLFGGADDISSGSDGEDKPPTPGQFVDENGLPQDQQEE PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVPEPRFPDQYYE DEFDEEMLEDEGRTRLKLVKVENTIRWRIRRDEEGNEIKESNAR IVKWSGDSMSLHLGNEVFDVYKAPLOGDHNHLFIRQGTGLQGQA VFKTKLTFRPHSTDSATHRKMTLSLADRCSTQKIRILPMAGRD PECQRTMIKKEERLRASIRRESQQRMRREKQHQGLSASYLE PDRYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE EDKAQRLKAKKLTSDVVRPNLFNSRGLSCTQEPPTALNEELTDQ AGTN
5485	161	1074	KRKILSSMMDSEAEKRPILTSSKQDISPHITNVGEMKHLYCG CCAAFNVAITFPIQKVLFRQOLYGIKTRDAILQLRRDGFNLY RGILPPLMQKTTTLALMPGLYEDLSCLLHKHVSAPFATSGVAA VLAGTTEAIFTPLERVQTLQDHKHDKFTNTYQAFKALKCHGI GEYRGLVPILFRNGLSNVLFGLRGPIKEHLPTATTHSAHLVN DFICGGLGLGAMLGFLFFPINVVKTRIQSQIGGEFQSFQKVI WLERDRKILINLFRGAHLNHYHRSLSISWGINATYEFLLKVI
5486	1404	142	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR PAAGKEAQKGPLLFDLLPASSTDSGSGGPLLFDLLPASSGDS GSLATSISQMVKTEGKGAKRKTSEEEKNGSEELVEKKVKCASSV IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRSY FAVFDGHGGIRASKFAAQNLHQNLIKRPKGDVISVEKTVKRCL LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG DSRAILCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGGNVR DGRVLGVLEVSRISIGDGQYKRCGVTSVPDIRCQLTPNDRFILL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ACDGLFKVFTPEEAVNFILSCLEDEKIQTRREGKSAADARYEAAC NRLANKAVQSGSADNVTVMVVRIGH
5487	535	182	AVSLEQIRGLQTPAPVPLPLQPCPSNCDMERVTALALLLAGLITA LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK CKCKSSQKQHSFVPEKAIPLITPGSATTC
5488	1072	259	AMAASGEFQRQWQEEVAVVVVGSCMTDLVSLTSRLPKTGETH GHKFFIGFGGKGANQCVQARLGAMTSMVCKVKGDSFGNDYIEN LKQNDISTEFTYQTKDAATGTASIVNNEGQNIIVIVAGANLLL NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL FNPAPAIADLDLPQFYTLSDVFCCNESEAEILTGLTVGSAADAGE AALVLLKRGCCQVVIITLGAEGCVVLSQTEPEPKHIPTKVKAVD TTVSFKI
5489	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREPEKMPPLLLGTEPELK LEHDCRSPVEPWAAASPDALACLCHCQDLSSGAFPNRGVLGGV LFPTVEMVIKVFVATSSGSIARKKQGEVVGFLANKIDFKELD IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF FSAKEENIIYSFLGLAPPPDSKSGSEKAEEGGETEAQKEGSEVVG NLPEAQEKNEEEGETATEETEIEAMEGAEGEAEETAEGEPEP GEDEDS
5490	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREPEKMPPLLLGTEPELK LEHDCRSPVEPWAAASPDALACLCHCQDLSSGAFPNRGVLGGV LFPTVEMVIKVFVATSSGSIARKKQGEVVGFLANKIDFKELD IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF FSAKEENIIYSFLGLAPPPDSKSGSEKAEEGGETEAQKEGSEVVG NLPEAQEKNEEEGETATEETEIEAMEGAEGEAEETAEGEPEP GEDEDS
5491	204	1194	GSAPRLSLGPTGAQARDPDWARPPSRPYTQSKEDRPDTEGRSE QGDMASSFLPAGAITGDSGGELSSGDDSGEVFPSPHSEIETSC LAELFEKAAHLQGLIQVASREQLLYARYKQVKGNCNTPKP SFFDFEGKQKWEAWKALGDSSPSQAMQEYIAVVKLDPGWNQPI PEKKGEANTGFGGPPVISSLYHEETIREEDKNIFDYCRENNIDH ITKAISKNVVDVNVKDEEGRALLHWACDRGHKELVTLLQHRAD INQDNEGQTALHYASACEFLDIVELLQSGADPTLRDQDGLCP EEVTGCKTVSLVLQRHTTGKA
5492	3	1896	ASKNPLSAVCTTGTIMSSLAVRDPAMDRSLRSVFGNIPYEATEE QLKDI FSEVGSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAM RNINRGREFSGRALRVDNAASEKNKEELKSLGPAAP IIDSFYGDP IDPEDAPESI TRAVASLPPEQMFELMKQMKLCVQNSHQEARNML LQNPQLAYALLQAQVVMRIMDPEIALKILHRKIHVTPLIPGKSG SVSVSGPGPGPGPLCPGPNVLNQQNP PAPQPQHLARRPVKDI PPLMQTPIQGGIPAPGPPIPAAVPGAGPGSLTPGGAMQPQLGMPG VGPVPLERGQVQMSDFRAP IPRGPVTPGGLP PRGLLGDAFNDPR GGTLLSVTGEVEPRGYLGPPHQGPPMHASGHDRGPSSHEMRG GPLQDPRLLIGEPRGPMIDQRLPMDGRGGRDSRAMETRAMETE VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGFPVSSRGP MTGGIQGPGPINIGAGGPPQGPQVPGISGVGNPGAGMQGTGIQ GTGMQAGIQGGMGAGIQGVS IQGGGIQGGGIQGASKQGGSQ PSSFSFGSQVTPQDQEKAAALIMQVLQTLADQIAMLPPEQRQSI LILKEQIQKSTGAS
5493	1	1876	RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL TDTFRVKRPHLRRSASNGHVPQTPVYREKEDMYDEI IELKKS LH VQKSDVDLMRTKLRLLEENSRKDRQIEQLDPSRGTD FVRTL A EKRPDASWVINGLQRIKLEQCKEKDGTISKLTDMKTTNLE BMRIAMETYYEEVHRLQTL LASSSETTGKKPLGEKKTGAKRQKKM GSALLSLRSVQELTEENQSLKEDLDRVLSTSP TISKTQGYVW SKPRLRLRIVELEKKLSVMESSKSHAAEPVRSHPACLAASSAL HRQPRGRDNKDHERLARGAVRDLKEERTALQEQLLQRLDLEVKQLL QAKADLEKLEKAREGEEERREEREVLREEIQTLSKQLQELQEM KKEEKEDCPEVPHKAQELPAPTSSRHCEQDWPDPSSBGLPRP RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GHLTRTKLLASKAHGSEPPSVPLPDQSSPVPRVPSFIAQATGS PVQEEAIVIIQSALRAHLARARHSATGKRTTTAASTRRRRSASAT HGDASSPPFLAALPDPSPSGQAVAPLPGDDVNSDDSDDIVIAP SLPTKNFPV
5494	71	536	RSKAKIGTPTREVPSTDMKVRRESSSSLTTHRPAPSPATPRLTGT RRVLLGVSEBGTGCADAMELVLFCLSLAPMVLASAAEKEKEMD PFHYDYQTLRIGGLVFAVVLFSVGILLILSRCKCSFNQKPRAP GDEEQVENLITANATEPQKAEN
5495	273	2168	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG ELRPASLVVLPRLAPAFERFCQVNTGPLPLLGQSEPEKWMLEPP QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL GCSFSLLEEALAKGLPRRDPAHSGAGAYKTTVPCVTHAGFCPP LVVTMRPIPKDKLEGLVRACCSLGGEQGPVHMGDPELLGIKEL SKPAYGDAMVCPPEVVPVFWPSPLTSLGAVSSCETPLAFASIPG CTVMTDLKAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQ KIRELES MIGIDPGRGIGHLLCKDELLKASLSLSHARSVLITT GPPTHFNHEPPEETDGPAGVALVAFLOALEKEVAIIVDQRAWN LHQKIVEDAVEQGVLTQIPILTYQGGSEAAQAFCKNGDPQT PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDFIDDLFLAAKK IPGISSTGVGDGNGELGMGKVKAVRRHIRHGDVIACDVEADFA VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGSPRAPGDA WTQALPSVIKEEKMGLILVQHKVRSGVSGIVGMEVDGLPFHNT AEMIQLVDVTTAQV
5496	3	2408	QDTKMHEIYKGNITPQLNKNLTLSAATDVWAVYFSQFWIDYEG MKSCKGRPISEFVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPPSSSDTFFR FSPSSSEADIHLLVHVHKKHVMQINHYQYLLLLFLHESLILLSE NLRKDVAVTGPASQTSICIGILLRSALALLHPVDQANTLK SPVSESVPVVDYLPTEGDFLSKKRQISRDINRIRSVTVNH MSDNRSMSVDLSHIPKDPPLLFKSASDTNLQKGISFMDYLSDKH LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNRYE DSNILSFDSDGNQNILSSTLTSGKNETIESIFKAEDLLPEASL SENLDISKEETPPVRTLKSSQSSLSGKPKERCPPNLAFLCVSYKN MKRSSSQMSLDTISLDSMILEEQLES DSGSDSHMFLEKGNKNS TTNYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRHYLC NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLQ CHIKNFSTEFLTSSLMNIQHFLDEDETATVMFMKIQVSNKINL KDDSPRSSTVSLPAPVTVHIDHLVVERSDDGSFHIRDHMLNT GNDLKENVKS DSVLLTSGKYDLKKQSVTQATQTS PGVPWPSQS ANFPEFSFDFTREQLMEEBLSLQELAKAKMALAEAHLEKDALL HHIKMTVE
5497	1821	3308	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASQIIREQQSPNV CFIYKYSGFPSLEQCCHFVSPHSSCYINFFSFPFFVFCQLSN GFSHYLSSESHVGPTGAGLFPCLPASRLPRVTSVHLPDYAH YYTIGPGMFPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREP PNGGGPTTASGPPAAEEAQRPRSMTVSAATRPGEEEMACEELA LALSRGLQDLTQRSSRSLQCSSGYSTQTTTPCCSEDTIPSQVS DYDYFSVSGDQEQADQEQFDKSSSTIPRNSDISQSYRRMFQAKRPA STAGLPTTLGPAMVTPGVATIRRTPTSTKPSVRRGTIGAGPIPIK TPVIPVKTPTVPDLPGVLPAPPDGPPEERGEHSPSPSVGEGPQG VTSMPSMMWGGQASVNPPLPGPKPSIPEHRQAIPESAEADQER EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKKLKT TTNDRSAPRFS
5498	2434	1492	ILTHQEIFTGKPCBCGKASIOMSHLSQKIIYSGENPFACKVCG KVFSHKSNLTHEHFHTREKPFECNECGKAFSQKQYVIKHQNT TGEKLFECNECGKSFQKENLLTHQKHTGKPFECNDCGKAFI QKSNLIRHQRTHTGKPFVCKECCGKTFSGKSNLTHEKIHIGEK PFKCECGTAFGQKKYLIKQNIHTGKPYECNECGKAFSQRST LIVHVRHSGDKPYECNVCGKAFSSSSLTVHVRSHTGKPYGC NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QKIHTH
5499	324	926	GFGQIGRGHKITTYPPSPRKSGRKGMASQGWVKRYIKAFCKGF FVAVPVAVTFLDRVACVARVEGASMQPSLNPGGSQSSDVLLNH WKVRNFEVHRGDIVSLVSPKNPEQKIKRVIALEGDIVRTIGHK NRYVKVPRGHIWVEGDHGHGSFDSNSFGPVSLGLLHAHATHILW PPERWQKLESVLPPERLPVQREEE
5500	1978	1286	KPDWRLQNLFPRLYLWRSRFGFGLHKKRLQMDFKIEHTWDGFP VKHEPVFIRLNPGRGVMMDISAPFFRDPPAPLGEFGKPFNELW DYEVVEAFFLNDITEQYLEVELCPHGQHLVLLSGRRNVWKQEL PLSPRVSRGETKWEKGAYLPWSYFPNVTKFNSFAIHGSKDKRS YEALYPVQHELOQGOQKPDFHCLEYFKSFNFNTLLGEEWKQES DLWLIEKCDI
5501	2927	2226	CRFPVSARVAPGHQGAVGSGRRPARVEVVDAAARPSRRPFLP AATMLALISRLLDWFRSLFWKEEMELTLVGLQYSGKTTFFNVIA SGQFSEDMIPTVGFNMNRKVTKGNVTIKIWDIGGQPRFRSMWERY CRGVNAIVYMIDAADREKIEASRNELHNLDDKPOLQGIPLVLG NKRDLNALDEKQLEKMNLSAIQDREICCYSSCKEKNIDIT LQWLIQHSKSRSS
5502	3	824	NSAFFVWVPERTALLTCLGAAPGSSREAPGIAGPPNSTAMSKL GKFFKGGGSSKSRAAPSQEAFLVRLRETEMLGKKQEVLENRIQ REIALAKKHGTQNKRAALQALKKKRFEKQLTQIDGTLSTIEFQ REALENSHTNTEVLRLNMGFAAKAMKSVHENMDLNKIDDLMQEIT EQQDIAQEI SEAFSQRVGFDDFDELMAELEEELEQELNKKM TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEEDDD IKQLAAWAT
5503	216	654	KGVRRGRVRSDESDSHLGYFKMSFLLPKLTSKKEVDQAIKSTA EKVLVLRFRGDEDPVCLQLDDILSKTSSDLSKMAAIYLVDDVDT AVYTYQYFDISYIPSTVFFNGQHMKVVDYGGEDPALRSIKAVRRT SPAGTLGKPKVNS
5504	58	3563	QLSFSFQAPVTFDDITVYLLQEEWVLLSQQKELCGSNKLVAPL GPTVANPELFRKFGRGPEPWLGSVQGRSLLEHHPGKKQMGMG EMEVQGPTRSGQSLPPQKKAYLSHLSTGSGHIBGDWAGNRNKL LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL IEGYTGPFVKVETLKYHAKSKAHMFCVNALAAARDPIWAARFRSIR DPPGDVLASPELPTADCFIFYPGPGPLGGFDSMAELLPSRAEL EDPPGDGAIPAMYLDICISDLRQKEITDGIHSSDINILYNDAVE SCIQDPSAEGLSSEVPVVEELPVVFEDVAVYFTREENGMLDKR QKELYRDVMRMNYELLASLGPAAPKDLISKLERRAAPWIKDPN GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARAS CSSSICEGDPRIKRTYRPRSIRSWFGQFPWLVIDPKETKL FCSACIERPNLHDKSSRLVRGYTGPFVKVETLKYHEVSKAHLRCV NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAVHSRPLN DFEKILQLLQSTGTIVLGKYNRTACTQFIKYISETLKREILED VRNSPCVSVLLDSSDTASEQACVGIYIRYFKQMEVKESYITLAP LYSETADGYFETIVSALDELDPFRKPGWVVLGTDGSAMLSCR GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLKVKCDRH IRTVKFYQSSNKRNLNELQEGAAPLEQEIIRLKDNLAVRWVASR RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMKLMRGFHF VKFCHFLDPLSIYRPLSEVCQKEI VLITEVNATLGRAYVALES LRHQAGPKKEEFNASFKDGRHLHGI CLDKLEVAEQRFQADRRTV LTGIEYLQQRFDADRPQKKNMEVFTMAWPSGIELASFGNDDI LNLARYFECSLPTGYSEALLBEWLGKLTIAQHLFPFSLMCKNAL AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRJRTDERTKL SNEVLNMLMTAVNGVAVTEYDPPQAIQHWYLTSSGRFRFSHYVT CAQVPARSPASARLRKEEMGALVVEEPRTPQKPPILPSREAAEVL KDCIMEPPERLLYPHTSQEAPGMS
5505	3312	1219	NCSPRSLSAAKMNRNNKLPNLPQLQNLIKRDPAYIEEFLQ QYNHYKSNVEIFKLQPNKPSKELAEVMPMAQISHCYPEYLSNF PQEVKDLLSCNHTVLDPLDMTFCKALILLRNKNLNPSSSLEL FFELFRCHDKLLRKTLYTHIVTDIKINAKHKNNKVNVLQNF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			YTMRLDSNATAAKMSLDVMIELYRRNIWNDAKTVNVITTACFSK VTKILVAALTFFLGKDEDEKQDSSEDDGPTARDLLVQYATG KKSSKNKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHPQDFA EKLLKQLECCKERFEVKMMLNLSRLVGIHELFLNFYFPFLQR FLQPHQREVTKILLFAAQASHHLVPEIIQSLLMTVANNPVTDK NSGEVMTVGINAIBITARCPLAMTEELLQDLAQYKTHKDKNVM MSARTLIHLFRTLNPQLQKKFRGKPTASIEARVQYEGELDAK DYIPGAEVLEVEKEENAENEDGWESTSLSEEDADGEWIDVQH SSDEEQQEISKKLNSMPMEERKAKAAAISTRVLTQEDFQKIRM AQMRELDAAPGKSQKRKYIETDSDEEPRGELLSLRDIERLHKK PKSDKETRLATAMAGKTDREKVFVRKTKTNPFSSSTNKEKKKQK NFMMMRYSQNVRSKNKRSFREKQLALRDALLKKKKRMK
5506	1	1531	FRGDLCCGQGGGSAPEGGGSSAWPAPAHPLPEREREREALCPGRS CSGGGGEETPGTTPVWSPLEGGGDEELRPNPYVRFYRWAVVV LAAPPSLGAGGETPEAPPESWTQLWFFRPVUNAAGYASFMVPGY LLVQYFRKNLYLETGRGLCFPLVKACVFGNEPKASDEVFLAPRT EAAETTPMWQALKLLFCATGLQVSYLTWGLVQERVMTRSYGATA TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY SFASLSNVLSWCOYEALKFVSFPTQVLAKASKVIPVMLMGKLV SRRSYEHWEYLTATLISIGVSMFLSSGPEPRSSPATTLISGLIL LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFSCFLTGTGSL LEQGALLEGTFRFMGRHSEFAAHALLSICSACGQLFIFYTIGQF GAAVPTIIMTLRQAFALLSCLLYGHTVTVTGGGLGVAVVFAALL LRVYARGRLKQRGKKAVPVESPVQKV
5507	3704	1271	PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGFGTAAGKK VAVADVQFGPMRFHODQLQVLLVFTKEDNQCNGFCRACKAGFK CTVTKEAQAVALACFLDKHHDIIIDHRNPRQLDAELCRSIRSS KLSENTVIVGVVRRVDREELSVMPPISAGFTRRVVENPNIMACY NELLQLEFGEVRSQKLKLRACNSVFTALENSEDAIETSEDRFTQ YANPAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSIRI KGEWQGIYAKKKNQDNIIQNVKIIPIVIGQGGKIRHYVSIIRVC NGNNKAEKISECVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT EVSSQRRHSSMARHSMTEIAPITKVINIINAAQESSMPVTEA LDRVLEILRTTELYSPQFGAKDDDPHANDLVGGLMSDGLRRLSG NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEYWDPI FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSLWQIIE ANYHSSNPYHNSTHSADVHLATAYFLSKERIKETLDPIDEVAAL IAATIHVDVHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF QLTTGDDKCNIFKNMERNDYRTLQGIIDMVLATEMTKHFEHVN KPVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMILI KCADVSNPCRPLQYCIWAARISEEYFSQTEDEKQQLGVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF KYWKGLDEMKLRLNLRPPPE
5508	1151	691	LSSVFSRRSASMFAVGCSMGPFLLHYWYLSLDRLFPASGLRGFPN VLKVLVDQLVASPLLGVWYFLGLGLEGQTVGESQCQLREKFW EFYKADWCWPAQFVNFLFVPPQFRVTYINGLTGLWDYLSYL KYRSPVPLTPPGCVLADTRAD
5509	1238	619	RKSRGQCNALSASGPAAAAAIIMVRKLKFHEQKLLKQVDFLNWE VTDHNLHELRLVRLRRLQRRREDYTRYNQLSRVRELARLRDLDP ERDQFRVRASAAALDKLYALGLVPTRGSLLELCPVTASSFCRRR LPTVLLKLRLMAQHLQAQAVFVEQGHVRVGPVVDPAFLVTRSM EDFVTWVWSSKIKRHVLEYNEERDDFDLEA
5510	96	1195	PAGAHLSGSGSEPLEVEPGRGRVGRVKGRLQASGSAPGRSKM AEGERQPPDSSBEAPPATQNFIPKKEIHTVPDMGKWKRSQAY ADYIGPILITLNEGKGGKLTFFEYRVSEAIKLVALLNTLDRWID ETPPVDQPSRFGNKAYRTWYAKLDEBAENLVATVPTHAAVVP EVAVYLKESVGNSTRIDYGTGHEAAFAFLCCLCKIGVLRVDDQ IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT GPFAHSNQLWNIISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF KPGSLPLIHPVTSG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5511	276	1980	KLSRVNLNPPENLITSISAVPISQKEEVADFQLSVDSLLEKDNH HSRPDIQVQAKRLAEKLRCDTVVSEISTGQRTVNFKNRELLTK TVLQQVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKPHVG HLRSTIIGNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQL FGYEEKLQSNPLQHLFEVYVQVNKEAADKSVAKAAQEFFQRLE LGDVQALSLWQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREK SQEVLKLLSKGKLLKTIKGTAVVDLSGNGDPSSICTVMRSDGT SLYATRDIAAIDRMDKYNFDTMIYVTDKGQKKHFPQQVFQMLKI MGYDWAERCQHVFPFVVGGMKTRRGDVTFLVDVLEIQLRMLQN MASIKTTKELKNPQETAERVGAAALIIQDFKGLLLSDYKFWSWR VFQSRGDTGVFLQYTHARLHSLSEETFGCGYLNDFNTACLQEPQS VSLQHLRLRFDEVLYKSSQDFQPRHIVSYLLTSLHAAVAHAKTL QIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITPVCRM
5512	120	1015	DPSLLLTITVTGVTVLVLKSMNSRRREPITLQDPEAKYPLPL IEKEKISHNTRFRFLGPSFDHVLGLPVGNVYQLLAKIDNELVV RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK IGETIFFRGRGRLFYHGPNGNLGIRPDQTSSEPKTLADHLGMIA GGTGITPMLQLIRHITKDPDRTRMSLIFANQTEEDILVRKELE BIARTHDPQDFLWYTLDRPPIGWKYSSGFVTADMIKEHLPPLPAK STLILVCGPPPLIQTAAHPNLEKLGTYQDMIFTY
5513	2	837	ARWRLPSDSPRIIPAGAETPGRGSCRNYLPSSSPFPPEPSPFP PPTSRGGPGSRDMSDEESQDRQLKIVVLGDGASGKTSLLTTC FAQETFGKQYKQTIGLDFLRITLPGNLNVTLQIWDIGGQTIG GKMLDKYIYGAQGVLLVYDITNYQS FENLEDWYTVVKKVSESE TQPLVALVGNKIDLEHMRITKPEKHLRFCEQENGFSHFVSAKGT DSVFLCFQKVAEILGIKLNKAEIEQSQRVVKADIVNYNQEPMS RTVNPPRSSMCAVQ
5514	1295	449	VNRPSWIMGNFRGHALPGTFFFIIGLWCTKSILKYICKKQKRT CYLGSKTLFYRLIEILGITVGMALTMAGEQFIIPGGPHMLLYD YKQGHWNQLLGWHHFTMYFFGLGVADILCFTISSLPVSLTKL MLSNALFVEAFIFYNHTHGREMLDIFVHQLLVVFLTGLVAF EPLVRNNVLELLRSSLILQGSWFFQIGFVLYPPSGGPAWDL DHENILFLTICFCWHYAVTIVIGMNYAFITWLKVSRLKRLCSS EVGLLKNAEREQESEEM
5515	1572	260	FVRLVGRGDCDPLLSVCLTTPPLYEGLSGGGEKTAVIDLGEAF TKCGFAGETGPRCIIPSVIKRAGMPKPVVVQYNINTEELYSYL KEFIHILYFRHLLVNPRDRRVIIESVLCPSHFRETLTRVLFKY FEVPSVLLAPSHLMALLTLGINSAMVLDGYSRESLVLPIYEGIP VLNCWALPLGGKALHKELETQLLEQCTVDSVAKEQSLPSVMG SVPEGVLEDIKARTCFVSDLKRLKIAAKFNIDGNNERPSPPP NVDYPLDGEKILHILGSIKSDSVVEILFEQDNEEQSVATLILDSL IQCFIDTRKQLAENLVVIGGTSMLPGFLHRLLEIRYLVEKPKY KKALGTKTFRITPPAKANCVAWLGGAI FGALQDILGSRVSKE YYNQTRIPDWCSLNNPPEMMFVVGKTPPLMKRAFSTK
5516	3	735	NSREPPQAGPGSPRKSPTASSFLFPWRPLASSFWMGAGQAGES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLTALLGGPTWAG KMYGPGGGKYPSTTEDYDHEITGLRVSVGLLVKSVQVKLGDSW DKLGLGAGNTQEVTLQPGYITKVFAVQAFLRGMVMTSKDR YFYFGKLDGQISSAYPSQEGQVLVGIYQYQLLGIKSIGFEWNY PLEEPTTEPPVNLTYANSVPGR
5517	246	499	SEIYVAMRTDSSKMTDVEGSGVANFASSARAGRNRNALPDIOSSAA TDGTSDLPLKLEALSVEKDAKEDKTTQDQLEKPNEEK
5518	3	1375	DAWADAVVRAWDLNMDFFCLWLGLLLPLVAALDFNYHROEGMEA FLKTVAQNYSSVTHLSIGKSVKGRNLWLVVGRFPKEHRIGIP EFKYVANMHGDETGRELLHLIDYLVTSDGKDEITNLINSTR IHIMPSMNPDPGEAVKKPDCYYSIGRENYQYDLNRNFPDAFEY NNVSRQPETVAVMKWLKTETVLSANLHGGALVASYPFDNGVQA TGALYSRSLTPDDDVQYLAHTYASRNPNMKKGDECKNMNFNP GVTNGYSWYPLQGGMDQYNYIWAQCFEITLELSCCKYPREKLP SFWNNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			HICPYRTNKYGEYLLLLPFSYIINVTPGHDPHITKVIPEKS QNFSALKKIDILLPFQGLDSIPVSNPSCMPILYRNLPDHSAA KPSLFLFLVSLHIFFK
5519	87	477	IKSKLNQQVEVQSEWRLEAKGPTMGKESGWDGSRRAA GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGVA AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLSPSS
5520	117	943	PTEGRQKVLKTFVPSALAMTKTSTCIYHFLVLSWYTF SQEGKDEVKPKILANGARWKYMTLLNLLQTIPYGVTC RTKGGKDIKPLTAFRDLLETTLAFVSTFVFLAFWILFLY IYPKVLDTVIPVWLNHAMHTFIPITLAEVVLPHSPSKKTGL TLAAASIAYISRLWLYFETGTWVVPVFAKLSLLGLAAFFSL YVFIASIIYLLGEKLNHWKWSVQILQRWRLESVGICFQWP PAKHQLVKNI
5521	546	911	KILNMQKSCENEGKPNMPKAEEDRPLEDVPEAGNPQ GVSEAGNPRGGPNQPGQGFEDTPVRHLDPPEMIRGVDE LREERIRVRNKFVMMHWKQRHSRSPYPVCFRP
5522	1224	637	GSRPLGQRSREKMMVFGVSLIWKVDFPYQDKLVGYIT WQGSTDHRGVPKPGRVTLVEDPAGCVWGVAYRLPVGKE AYLDFREKGGYRTTTFIYFKDPTTKPFVLLYIGTCNDP PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEA FALEKLVKERLEGGKQNLNCI
5523	3	1280	SKGKKRMGSSMSAATARRPVFDDKEDVNFDFHQLRA KVICVQKRDETKMYAMKMNKQCCIERDEVNRVRELEIL HVLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNVQFSE RLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTD ATI IKDGERATASGTPYMAPEIFHSFVNGGTGYSFEVD GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSQYVPT VALLRKLTLVNPHERLSSLQDVQAAPALAGVLWDHLSE FVPNKGRHLCDPTFELEEMILESRLHKKKRLAKNKS SSQENDYLQDCLDAIQDFVFNREKLKRSQDLPREPLPA RDAEPVEDEAERSALPMCGPICPSAGSG
5524	85	2318	RERERDHRPGESSQGGAGGCFPSPTMELRCGGLLFSS NLAHVEKVESLSSDGEVGGGASALTSGIASSPDYFNV CAETEFENGNSWFYFVSRGGMPGKLKINIMNMNKSKLY MAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRF TTFFAFCYPFSYSDCQELLNQDQRFENHPHTSSPLDTI ELLCYSLDGLRVDLLTITSCHGLREDREPRLEQLFPD REFAGKRIFLSSRVHPGETPSSFVFNGLDFILRPDDP RLFVFKLIPLNPDGVVRGHRITDSRGVNLNRQYLKPD IYGAKAVLLYHHVSRNSQSSEHQPSCLPPDAPVSDLE NLQNEAQCGHSADRHNABAWKQTEPAEQKLSNVWIMP ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFS NMLYPKLISLNSAHDFQGCNFSKNMYARDRRDQSGKE ATYKASGIIHSYTLNNTGRSVNSIPAACHDNGRASPP FPSRYTVLPEQVGRAMAIALDMAECNPWPRIVSEHSS RAWMLKHVRNSRGLSSTLVGVNKKRGLRTPPKSHNGL NTLSRARSFSTGTSAGSSSSSQNSPQMKNSPFPFHGS PGLGSSSTQKVTHRVLGFPVRGKPVVEPLQHVFGCLG CNTLDFERHLFIMGQISDQTLVINKLPEKVAKHVTLV LYEBFLGRVABLNDVTAKVASGQEKHLLFEVQPGSDSS VVRVCTKINKSSGIVEASRIMNLYQFIQLYKIDITSQA SSTSEPDENSSSVTSQASLWMGRVKQLTDEEBCCICM LILCAHSFCQKCIDKNSDRHRNCPIRLQMTGANESWV TEDDMANYILNMADEAGQPHRP
5525	105	834	SNLDFERHLFIMGQISDQTLVINKLPEKVAKHVTLV LYEBFLGRVABLNDVTAKVASGQEKHLLFEVQPGSDSS VVRVCTKINKSSGIVEASRIMNLYQFIQLYKIDITSQA SSTSEPDENSSSVTSQASLWMGRVKQLTDEEBCCICM LILCAHSFCQKCIDKNSDRHRNCPIRLQMTGANESWV TEDDMANYILNMADEAGQPHRP
5526	3	853	RRPCNPVRAAKRTGAARAPRGLEVTMLRVAWRTLSL QVLVPLPGGSAKFPFNQWGLQPRSLLLQAARGYVVRKA LDDPPPTLLKDYQNVPGIEKVDVVKRLLSLEMANKEML KQEQFMKKIVANPEDTRSLEARI IALSVKIRSYEEHLE AHKRYLLMSIDQRKKMLKNLRNTNYDVFEEKICWGLG YYRAHRRFVTKKALCIRVFQETQKLKRRRALKAAAAQKQAK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5527	3225	565	RRNPDSPAKAIPTLKDSQ LLRKYLHQNPLLLRHQPNRTCISFSATMKLKDTSRPFQSSCG KFQTKGIKVVGKWEVKIDPNMFADGQMDLVCFEELTDYQLVS PAKNPSSLSFSKEAPKKAQAVSEEEEEEGKSSSPKKIKLKKS KNVATEGSTQKEFEVKDPELEAQGDDMVCDPEAGEMTSENLV QTAPKKKKKNGKKGLEPSQSTAARKVPKAKTWIPEVHDQKADVS AWKDLFVPRPVLRLSFLGFSAPTPIQALTLAPAIRDKLDILGA AETGSGKTLAFAIPMIHVLQWQKRNAAPPPSNTAEPGETRTE AGAETRSPGKAESAEDALPDDTVIESEALPSDIAAEARAKTGGT VSDQALLFGDDDAGEGSSSLIREKPVFKQNEEENLDKEQTGN LKQELDDKSATCKAYPKRPLGLVLTPTRELAVQVKQIHDAVAR FTGIKTAILVGGMSTQKQQRMLNRRPEIVATPGRWLWELIKEKH YHLRNLRLRCLVDEADRMVEKGHFAELSQLLEMLNDSQYNPK RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDDLMMQKIGM RGKPKVIDLTRNEATVETLTETKIH CETDEKDFLYYYFLMQYFG RSLVFANSISCIKRLSGLLKVLDDIMPLTLHACHMHQKQLRLNLEQ PARLEDCVLLATDVAARGLDIPKVQVHIHYQVPRTSEIYVHRSG RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTK YMDVVKERIRLARQIEKSEYRNFOACLHNSWIEQAAAALEIELE EDMYKGGKADQGEERRQKQMKVLKKELRHLLSQPLFTESQKTK YPTQSGKPLLVSAPSKSESALSCLSKQKKKKTKPKPEQPBPQ QPSTSAN
5528	3	895	GFFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSFE YVRDEADDTCLAHCVVVRDGRNFHRAEKHNFAPKPNDSRAL QLMTKCAQTVMEELEDIVIAVQSDSEYSFVFKRKTNWFKRRASK FMTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQ LKDYLSWRQADCHINLYNTVFVWALIQSGSLTPVQAQGRQLQGT AADKNEILFSEFNINYNNEPPMYRGTVLWQKVDEVMTKEIKL PTMEGKKMAVTRTRTKPCPSHLPRAPCLRWL
5529	48	640	TFRLVSAHLKTRKLINPEAAERRWRDWSRQGWLSVKMQRVSG LSWTLRSVLWLSGLSEBGAARQPRIMEEKALEVYDLIRTI RDPE KPNTLEELEVVSSESCVEVQEIINEEYLVII RFTPTVPHCSLATL IGLCRLVKLQRCPLFPKHKLEIYISEGTHSTEDINKQINDKERV AAAMENPNLREIVEQCYLEPD
5530	4541	2606	AQIVHAISYCHKLHVGRDLKPENVVFFEKQGLVKLTDGFGFSNK FQPGKLLTSCGSLAYSAP EILLGDEYDAPVDIWSLGVILFML VCGQPPFQEAANDSETLTMIMCKYTPVSHVSKECKDLITRMLQR DPKRRASLEEIEHNHPWLQGVDPSPATKYNIPLVSYKNLSEEHN SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLP ELAGPALSTVP PASLKPTASGRKCLFRVEDEEEDKPKMSLSTQVVLRRKPS VTNRLTSRKSAVPLNQIFEEGESDDEFDMDENLPKLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSSETSDDESRRRLDKDSGF TYSWHRDSSEGGPPGSEGGGGQSKPSNASGGVDKASPSENNAG GGSPSSGGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISS GNAGQVPVAVGGIKFFSDHMDTTTELEIRIKSNLKNVQLPLC EKTISVNIQRNPKEGLLCASSPASCCHVI
5531	24	515	GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGTVLFLARLF ALEPDLPLFQYNCQFSSPEDCLSSPEFLDHIRKVMVLVIDAAV TNVEDLSSLEEYLASLGRKHRAVGVLSSFTVGESLLYMLEKC LGPAPTATRAAWSQLYGAVVQAMSRGWDGE
5532	3395	1402	SDWMVVGKRMII EDETEFCGEELLHSLVQLCKSVFVLDGEEMR RARTRANPYEMIRGVFFLNRAAMKMANMDFVDRMFTNPRDSYG KPLVKDREAELLYFADVCAGPGGFSEYVLRKKKWHAKGFGMTLK GPNDFKLEDYFASSELFEPPYGGGIDGGDITRPENISAFRN FVLNNTDRKGVHFLMADGGFSVEGQENLQELSKQLLLCQFLMA LSIVRTGGHFICKTFDLFTPFVGLVYLLYCCFRVCLFKPITTS RPANSERYVCKGLKVGIDVDYLFVAVNIKLNQLRNTSDVNL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVQDTTLSEPRQAEIRKECLRLWGIPOQARVAPSSSDPKSKFFELIQGTETDIFSYKPTLLTSKTLEKIRPVFDYRCMVSGSEQKFLIGLGSQISAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMNPIRVKEVYRLEEMEKIPVRLEMKIIKGSSGTPKLSYTGRRDRHFVPMGLYIVRTVNEPWTMGFSKSPKKKFFYNKTKDSTFDLPADSIAFFHICYGRLPFEWGDGIRVHDSQKPKDQDKLSKEDVLSFIQMHRA
5533	94	789	MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVPTVFENYTALETEEQRVELSLWDTSGSPYYDNVRPLCYSDSDAVLLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTDLSTLMELSHQKQAPISYEQGCIAIAKQLGPEIYLEGSAPTSEKSHSIFRTASMLCLNKPSPLPQKSPVRSLSKRLHLPSRSELISPTFKKEKAKXCSIM
5534	3	605	LVRGRARAANPGRVGMADGLRQRVEHFLEQRNLVTEVLGALEAKTQVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIKAIESPCKDDTVWLTYWVYALFGLAEFFSDLLLSWFPFYVVGKCAFLLLFCMAFRPWNGALMLYQRVVRPLPLRHGVAVRIMNDLSGRALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFMDSEARLCSLVLESDTQDETQKSDSENEDLKIDCLQESQELNLQKLKNSERILTEAKQKRELTVNIIKMKEDLTKELIKTGNDAKSVSKQYTLKVTKLEHDAEQAQVELTETQKQLQELNKLSDVAMKVKLQKEFRKKVDAALKRVQVLQKKQQDSKKLASLSIQNEKRANLEQSQVDHMKYQKIQLQRKLEBENEKRQLDAVIKRDQQKIKVISYIPAKYNMCK
5536	942	282	AAATAASLSFRGCRRLRTPSSDVFSFRAPPPSAAPLPTRAGQMSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVPTRPDAVYTELQPTSPPTPFADETPPQPQTQTQOLEGTDGLVTDTPETHKSTKAAHPTDDTTTLSERPSPSTDVQTDQFQTLKPSGFFHEDDPFFYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
5537	3	2391	RARVSSPQLRVFRSGRPRLRLVLRINRSTVALRLAGTGRFVAKTPGHGPGSWEMGLLTFRDVAVEFSLSEWEHLEPAQKNLYQDVMLENYRNLVSLGLVVSQPDLLTFLEQRKEPWNVKSEBTVAIQPDVFSHYNKDLLTEHCTEASFQKVISRRHGSCDLENLHLRKRKWKREECEGHNGCYDEKTFKYDQFDESSVESLFHQQILSSCAKSYNFDQYRKVFTHSSLLNQQEEIDIWGKHIIYDKTSVLFRQVSTLNSYRNVFIEKKNYHCNNSEKTLNQSSSPKNHOENYFLEKQYKCKEFEEVFLOQSMHGQEKQEQSYKCNKCEVECTQSLKHIHQHTIHIRESYSYNKYDKDLSQSSNLRKQIIHNEEKPKYKCEKCGDSLNLHSLHTQHQIIPTEEKPYKWKCEGKVFNLNCSLYLTQKQQIDTGENLYKCKACSKSTRSSNLIHVQRIHTGEKPKYKCEGKAFRCSSYLTKHKRIHTGEKPKYKCEGKAFNRSSCLTQHTQTHTGEKLYCKVCCKSYARSNNLIMHQRVHTGEKPKYKCEGKVFSRSSCLTQHRKIHTGENLYKCKVCAKPFTCFNLIVHERIHTGEKPKYKCEGKAFYPSSHLIRHRIHTGEKPKYKCKACSKSFSDSSGLTVHRRHTHTEKPKPYTCKEKGAFYSYSSDVIQHRRIHTGQRPYKCEEGKAFNYRSYLTTHQRSHTGERPYKCEEGKAFNSRSYLTTHRRRHTGERPYKCEEGKAFNSYSLTHRRSHSGERPYKCEEGKAFNSRSYLIAHQRSHTREKL
5538	926	161	HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGPIPIGTGPGDQPGTGPPIKGEKGLPGLAGDHGEFGEKGDPIGPNPGKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTINVPLRRDQTIIRFDHVI TNMNNYEPYRSGKFTCKVPGLYYPTYHASRGNLNCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVMLKLEQGENVFLQATDKNSLLGMEGANSIFSGLFLFPDMEA
5539	38	1258	HRGPSGAAAPGICALPRGQALEGPRSCRRPQMARRYDELPHYPGIVDGPAAALASFPETVPVAVPGPYGPHRPQPLPGLDSDGLKREKDEIYGHPLFPLALVFEKCELATCSPRDGAGAGLGTTPGGDVCSSDSFNEDIAAFKQVRSERPLFPSSNPELDNLVIAIQVLRFHLL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ELEKVDHLCDFCHRYITCLKGMPIDLVIEDRDGGCREDFEDY PASCPSPDQNNMIRWHDHEDSGSVHLGTPGPSSGGLASQSGDNS SDQGDGLDTSVASPSSGGEDEDLDQERRRNKRGIFPKVATNIM RAWLFQHLSPYPSEEQKQLAQDTGLTILQVNNWFINARRRIV QPMIDQSNRTGQGAASFPEGQPIGGYTETQPHVAVRPPGSVGMS LNLEGEWHYL
5540	148	1440	PPLGAGAGVHARSHPARRLPLTTAGVGGRAPDILLPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTTPPGDVCSDDS FNEDNTAFKQVRSERPLFSSNPELDNLMIAIQVLRFHLLLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSPDQNNIWRDHED SGSVHLGTPGPSSGGLASQSGDNSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSPYPSEEQKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAASFPEG QPIGGYTETEPHVAFRAPASVGDEFGRTRKEEWHYL
5541	148	1440	PPLGAGAGVHARSHPARRLPLTTAGVGGRAPDILLPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTTPPGDVCSDDS FNEDNTAFKQVRSERPLFSSNPELDNLMIAIQVLRFHLLLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSPDQNNIWRDHED SGSVHLGTPGPSSGGLASQSGDNSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSPYPSEEQKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAASFPEG QPIGGYTETEPHVAFRAPASVGDEFGRTRKEEWHYL
5542	148	1440	PPLGAGAGVHARSHPARRLPLTTAGVGGRAPDILLPTPWRQHRG PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTTPPGDVCSDDS FNEDNTAFKQVRSERPLFSSNPELDNLMIAIQVLRFHLLLELE KGKMPIDLVIEDRDGGCREDFEDYPASCPSPDQNNIWRDHED SGSVHLGTPGPSSGGLASQSGDNSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSPYPSEEQKQ LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAASFPEG QPIGGYTETEPHVAFRAPASVGDEFGRTRKEEWHYL
5543	2405	665	RWVREQWPPLRTSEAVKTPALRPFPGRGVSPFPKPDWKGSPAP KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRVPPKPTRVHG SSASRDRLARTMIVADSECRABLKDYLRFAPGGVGDSPGEGEQ RESRRRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGRV DNLAVVMGLHPDYFTSFWRLLHYLLHTDGPLASSWRHYIAIMAA ARHQCSYLVGSHMAEFLQTGGDPEWLLGLHRAPEKRLKLEINK LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSL SFVFGGILPEGDADGSPAPQAPTTPSEQSSPSPSRDPLNNSGGF ESARDVEALMERMQQLQESLLRDEGTSQEEMESRFELEKSESLL VTPSADILEPSPHPDMLCFVEDPTFGYEDFTRRGAQAPPTFRAQ DYTWEDHGYSILQRLYPEGGQLLDEKFOAAYSLTYNTIAMHSGV DTSVLRRAIWNYYIHCVPFIRYDDYDGEVNQLLERNLVYIKTV ACYPEKTTREMYNLFWRHFRHSEKVVHVNLLLEARMQAALLYAL RAITRYMT
5544	1895	514	LGGLLRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD PEGRRQEPLERRASSASVPVAGASAEGTRDRDLGSYSPTSISR QRVESLRKKRPLPPWFGLDIGGTLVKLVYFEPKDIATAEEEEEV ESLKSIRKYLTSNVAYGSTGIRDVHLELKDILCGRKGNLHFI PPTHDMPAFIQMRDKNFSSLHTVFCATGGGAYKFEQDFLTIGD LQCLKLDLDCILKILYIDSVGFNGRSQCYYFENPADSEKQK LPFDLKNPYPLLNVIGSGVSLAVYSKDNKRVGTGSLGGGT FGLCCLLTGCTTFEEALEMASRGDSTKVDKLVLDIYGGDYERF LPGWAVASSFGNMMSKEKREAVSKEDLARATLITINNIGSIAR MCALNENINQVVFVGNFLRINTIAMRLAYALDYWSKGQLKALF SEHEGYFGAVGALLELLKIP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5545	802	131	GAMWSAGRGGAAWVLLGLLLALLVPGGGAAKTGAEIVTCGSVL KLLNTHHRVRLHSHDIKYSGSGQSSVTGVEASDDANSYWRIRG GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFSPPLSNNQEV SAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFOHVGTSVFLSVT GEQYGSPIRGQHEVHGMP SANTHTWKAMEGIFIKPSVEPSAGH DEL
5546	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYANPHSFVFT RGCTGRNIRQLSLDVRVMEPLTASRLQVRKKNLSLKDCAVAVAGP LGVTHFLILSKTETNVYFKLMRLPGGPTLTQVKKYSLVRDVVS SLRRHRMHEQQFAHPFLLVLNSFGPHGMHVKLMAFMFQNLFPSI NVHKVNLNTIKRCLLDYNPDSQELDFRHYSIKVVVPVGASRGMK KLLQEKFPNMSRLQDISSELLATGAGLSESEAEPDGDHNTIETLPQ AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS FVSKTEELQAILAEAKEKKRLRLKAQRQAQQAQNVQRKQEQREAH RKKSLEGMKKARVGGSDDEASGIPSRASLELGEDDDEQEDDDI EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRPGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYANPHSFVFT RGCTGRNIRQLSLDVRVMEPLTASRLQVRKKNLSLKDCAVAVAGP LGVTHFLILSKTETNVYFKLMRLPGGPTLTQVKKYSLVRDVVS SLRRHRMHEQQFAHPFLLVLNSFGPHGMHVKLMAFMFQNLFPSI NVHKVNLNTIKRCLLDYNPDSQELDFRHYSIKVVVPVGASRGMK KLLQEKFPNMSRLQDISSELLATGAGLSESEAEPDGDHNTIETLPQ AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS FVSKTEELQAILAEAKEKKRLRLKAQRQAQQAQNVQRKQEQREAH RKKSLEGMKKARVGGSDDEASGIPSRASLELGEDDDEQEDDDI EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRPGKRVA
5548	1	2153	DQTGPETIAFTFPRSTMEPLCPILLVGFSLPLARALRGNETTA DSNETTTTSGPPDPGASQPLLAWLLPLLLLLLLVLLLAAYFFRF RKQRKAVVSTSDKKMPNGILEEQQRVMLLSRSPSGPKKYFPI PVEHLEEEIRIRSADCKQFREEFNSLPSGHIQGT FELANKEEN REKNRYPNILPNDSRVLSQLDGI PCSDYINASYIDGYKEKNK FIAAQGPQKETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY WPDQGCWTYGNIRVCVEDCVVLVDYTIKFCIQPQLPDGCKAPR LVSQHLFTSWPDFGVPTPIGMLKFLKVKTLNPNVHAGPIVVHC SAGVGRGTGTFIVIDAMMMHAEQKVDVFEFVSIRNRQRPQM VQ TDMQYTFIYQALLEYYLYGDTLVDVSSLEKHLQTMHGTTTFDK IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR VILSMRGQYETDYINASFIDGYRQKDYFIATQGPLAHTVEDFW RMIWEWKSHTIVMLTEVQBEREQDKCYQVWPTGVSHTGEITIEI KNDTLSEAISIRDVLTLNQPARQEEQVRVVRQFHFHGWPEIG IPAEKG MIDLIAAVQKQQQTGNHPI TVHCSAGAGRTGTPIAL SNILERVKAEGLLDVPQAVKSLRLQRPMMVQTLQEQYEFCKYVQ DFIDIFSDYANFK
5549	915	256	FEATGGKRLAFK MAGTARHDEMAIQAKKLTATDPIERLRLQ CLARGSAGIKGLGRVFRIMDDNNRTLDKFEMKGLNDYAVVME KEEVEELFQRFDKGNGTIDFNEFLTLRPPMSRARKEVIMQAF RKLDKTGDGVITIEDLREVYNKHHPKYQNGEWESEQVFRKFLD NFDSPYDKDGLVTPPEEFMNYAGVSASIDTDVYFIIMMRTAWKL
5550	2364	1210	RKRKVF LKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGT SLIAFTTMALLTIMEFSVYQDTWMKYEYVDKDFSSKLRLINIDI TVAMKCQYVGADVLDAETMVASADGLVYEPTVFDLSPQKQEWQ RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN ACRIHGHLYVNKVAGNFHITVGKAIHPRGHAHLAALVNHESYN FSHRIDHLSFGELVPAIINPLDGTAKIAIDHNQMFQYFITVVP KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL MVTVTEHMPFQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC CRFRLGSYKPVNSVPFEDGHTDNHLPLENNTH
5551	211	1700	MQRDHTMDYKESCPVSIFSSDEHREKKRFTVYKVLVSUGRSE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			WVFRRYAEDFKLYNTLKKQFPAMALKIPAKRIFGDNFDPDFIK QRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE DERSSQKLHSTSQNINLGPSPGNPHAKPTDFDFLKVIGKSGFGKV LLAKRKLKGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKQVVKH PFLVLGHYSFQTTEKLYFVLDVFNNGELFFHLQRRERSFPEHRAR FYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDGFLC KEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWVCLGAVLY EMLYGLPFFYCRDVAEMYDNIHLKPLSLRPGVSLTAWISILELL EKDRQNRIGAKEDFLEIQNHPPFESLSWADLVQKKIPPPFNPV AGPDDIRNFDATFETETVPYSVCVSSDYSIVNASVLEADDAFVG FSYAPPSDELFL
5552	2748	930	LGPAAGAAMGKKKKHKAWEHRSSYEDYADKPLEKPLKLVLVKVG SEVTELSGSGHDSYYDDRSHERERHKEKKKKKKKSEKEKHL DDEERRKRKEKKRKREREHCDTEGEADDFDPGKKVEVEPPDR PVRACRTQPAENESTPIQQLLEHFLRLQKQDPHGFFAFPVTD IAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA MTYNRPDVTYVYKLAKKILHAGFKMMSQAALLGNEDTAVEEPVP EVVPVQVETAKKSKKPSREVISCMFEPGNACSLTDSABEHVL ALVEHAADAEARDINRFLPGGKMGYLLKRNKGDSLLYSVVNTAEP DADEEETHPVDLSSLSKLLPGFTTLGFKDERRNKVTLSSATT ALSMQNNNSVFGDLKSDMELLYSAYGDETVQCALSLEQEFVKDA GSYSKKVVDLLDQITGGDHSRTLFQLKQRRNVPMKPPDEAKVG DTLGDSSSSVLEFMSKSYPDVSDISMLSSLGKVKKELDPDS HLNLDETTLLQLDLHEAQAERGSRPSSNLSLSNASERDQHHL GSPSRLSVGEQPDVTHDPYEFQSPPEPAASAKT
5553	74	1095	LGREAVYLVSRMDGPVAEHAQEPFHVVTPLESWALSQVAGMP VFLKCEVQPSGSKIRGIGHFCQEMAKKGRHLVCSGGNAGI AAAYAAARKLGIPATIVLPSTSLQVVRQLOGEGAELVLTGKVWD EANLRAQELAKRDGWNVPFDPHPLIWKGHASLVQELKAVLRT PGALVLAAGGGGLLAGVAGLEVGVQHVPIIAMETHGAHCFA AITAGKLVTLDPDITSVAKSLGAKTVAARALECMQVCKIHSEVVE DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRLRLQABGCL PFSLTSSVVIVCGGNNINSRELQALKTHLGQV
5554	166	2318	CSGRTGGGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL GRSFFWVLPFVLPWAVQAVEHEEVAQRVILHRGRGVAAMQSRQ WVRDSCKRLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEEKLQ VHTFEIFQKELNESENSVFQAVYGLQALQGDYKDVVNMKESS QRLEALREAAIKEETEMELLAARKHQAELKNMQHQNQSLSM DEILEDVRKAADRLBEEIEEHAFDDNKSVMGFVAVLRVEEEE ANSKQNI TKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN SIKSIVQVETLGEFGVFFTLFLVGLFESPEKLRKVWKISLQGPC YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSTPLVSRFLM GSARGDKEGDIIDYSTVLLGMLVTQDVQLGLFMAVMPPLIAGAS ASSSIVVEVLRILVLIGQILFSLAAVFLCLVIRKYLIGPYRK LHMESKGNKEILILGISAFIFMLTVTELLDVSMELGCFLAGAL VSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPFTVAYEL TVLVFLTLVVVMKFLAALVLSLILPRSSQYIKWIVSAGLAQV SEPSFVLGSRARRAGVISREVVLLILSVTTLSLLAPVLWRAAI TRCVPRPERRSSL
5555	212	1425	LSLRTRETTPAPPRCEAASQGRVGRADAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDK KAYRKLALQLHEDRNPDDPAQAEKFDLGAAYEVLSDSEKQKQY DTYGEGLKDGHQSSHGDISSHFFGDFGFMFGGTFRQQDRNIPR GSDIIVDLLEVLYAGNFVEVVRNKPVARQAPGKRKCNCRQE MRTTQLGPGRFQMTQEVGCECPNVKLVNEERTLEVEIEPGVRD GMEYYPFIGEGEPHVDGEPDLFRKIVVKHPIFERRGDDLYTNV TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL PNFDNNNIKSGSLIITFDVDFPKEQLTEAREGIIKQLLKQGSVQK VYNGLQGY
5556	5835	3346	RTRGMSQNCVPMEFEEYLLRMFGQTFYLLQKITKDNNAHTVKSR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LEELDES YIEKFTDFLRLEFVS VHLRRIESYSQFPVVEFTLLLFK YTFHQPTHEGYFSCLDIWTFLFDYLSKIKSRLGDKBAVLNRYE DALVLLLTVELNRIQFRYNQAQLEELDDDETLDDDDQQTWEQRYLR QSLEVVAKVMELLPTAFSTLFPVLQDNLEVYLGQQFIVTSGS GHRNLITAENDCRLHCSLRDLSSLLQAVGRLA EYFIGDVFAAR FNDALT VVERLVKVTLYGSOIKLYNIETAVPSVLKPDLDIVHAQ SLAALQAYSHWLAQYCEVHRQNTQQFVTLISTTMDAITPLIST KVQDKLLLSACHLLVSLATTVPVFLISIPAVQKVFNRTDASA LRLVDKAQVLVCRALSNILLPWPNLPENEQQWPVRSINHASLI SALS RDYRNLPKSAVAPQRKMPDDTKLIIHQTL SVLEDIVENI SGESTKSRQICYQSLQESVQVSLALPFAFIHQSDVTD EMLSFFL TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGCR VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIAERPS PDVKAELFELLFRTLHNNWRYFFKSTVLASVQRGIAEEQ MENEP QFSAIMQAFQSFQPDILHFKQNLFYLET LNTKQKLYHKKIFR TAMLFQFVNVLQVLVHKS HDLLQEEIGIATYNMASVD FGDGFA AFLPEFLTSCDGVANQKSVLGRNFKMDRVRRERGRAKRAEWA RKP GTC AARRGHI EASGRGLCPPCS LAAAH EMPADLV L
5557	1712	491	VILGAGLRDKDMWIPVVG LPRRLRLSALAGAGRF CILGSEAA TR KHLPARNHCGLS DSSPQLWPEPDFRNP PRKASKASLD FKRYVTD RRLAETLAQIYLGKPSRPPHLLLECNP GP GILTOALL EAGAKVV ALES DKTFI PHLES LGKNLDGKLRV IHCDFFKL DPRS GGVI KFP AMSSRGLFKNLGIEAVPWTAD I PLKVVGMPFSRGEKRALWK LAY DLYSCTSIYKFGRIEVNMFIGEKEFQKLMADPGNPDLYHVL SVI WQLACEIKVLHMEPWSSFDIYTRKGP LENPKRRELLDQLQOKLY LIQMI PRQNLF TKNLT PMN YNIF FHLLKHC FGRRSATVIDHLRS LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKD CAY KWLYDETLEDR
5558	1509	96	RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPPGGQRGPTTMI TGVFSMRLWTPVGVLTSLAYCLHQRVALAE LQ EADGQCPVDRS LLKLMVQVVRH GARS PLKPLPLEEQVEWNPQLLEVPPQTQFD YVTNLAGGPKPSPYDSQYHETTLKGGMFAGQLTKVGMQQMFA LGERLRKNYVEDIPFLSPTFNQPEVFIRSTNIFRNLESTRCLLA GLFQCQKEGPII IHTDEADSEVLYPNYQSCWSLRQTRGRQTA SLQPGISED LKKVKDRMGIDSSDKVDFFILLDNVAEEQAHN LPS CPMLKR FARMIEQRAVDTSLYILPKEDRESLQMAVGPFLLHILES NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLIMTLGIFDHKNWP FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCP LDMF LNAMSVYTLSPEKYHALCSQTQVMEVGNEE
5559	150	1983	PLAATAHFAKMSRVAKYRRQVSEDPDIDSLETLSP EEMEELEK ELD VVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFC EKETK LMQREMSMDESKQVETKTDAKNGEERGRDASKKALGPRRDS DLG KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA VDKKEAGKDGGRGEERAVATKKEEKKGS DRNTGLSRDKDKKREE MKEVAKKEDDEKVGGERNTDTRKEGEKMKRAGGNTDMKKEDEK VKRG TGNTDTKKDDEKVKKNELHEKEAKDDSKTKTPEKQTPSG PTKPSEGP AKVEEAAAPSIFDEPLERVKNNDPEMTEVNVNNSDC ITNEILVRFT EALFNTVVKLFALANTRADDHVAF AIAIM LKAN KITISLND SNHITGKGILAI FRALLQNNLT ELRFHNQRHICG GKTEMEIAKLLKENTLLKLG VHFELAGPRMTVTNLLSRNMDKQ ROKRLQEQRQAQEAKGEKDLLEV PKAGAVAKGSPKPSPPSPK PSPKNSPKKGGAPAAPPPPPPLAPPLIMENLKNLS PATQRKM GDKVLP AQEKNSRDQLLAI RSSNLKQLKKVEVPKLLQ
5560	9	921	SSVVEFSALSVSMACLSPSQLQKFPQDGFVLVLEGFLSAEECVAM QQRIGEIVAE MDPVPLHCRTEFSTQEEQLRAQGSTDYFLSSGDK IRFFFEKGVFDEKGNFLVP EKSINKIGHALHAHDPVFKSI THS FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVSPHODASFLYT EPLGRVLGVVIAVEDATLENGCLWFIPGSHTS GVSRRMVRAPVG SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEV VHKSKQNL SDRSRQAYTFHLEASGTTWSPENWLOPTAELFPFQLYT
5561	2175	1775	CYFIFQFSSFPGLHHPQTPAPLPNPGLYPPFPVMSPGQPPFPQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QLLAPTYFSAPGVMNFGNPSYPYAPGALFPFPPPHLYPNTQAPS QVYGGVTYYNPAQQQVQPKPSPPRTPQPVTIKPPPEVVSRS S
5562	342	1385	SSGKNDMAAAGAAGLVRLKAGVLSQADYLNVLQVCELTEDLKLH LQSTDYGNFLANEASPLTVSVIDDRLEKMMVFEFRHMRNHAYEP LASPLDFITYSYMIDNVILLITGTTLHQRSIAELVPKCHPLGSFE QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIET IRNTLYKAYLESFYKFTLLGGTTADAMCPILFEADRRAFIIT INSPGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQHFH GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5563	342	1385	SSGKNDMAAAGAAGLVRLKAGVLSQADYLNVLQVCELTEDLKLH LQSTDYGNFLANEASPLTVSVIDDRLEKMMVFEFRHMRNHAYEP LASPLDFITYSYMIDNVILLITGTTLHQRSIAELVPKCHPLGSFE QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIET IRNTLYKAYLESFYKFTLLGGTTADAMCPILFEADRRAFIIT INSPGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQHFH GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5564	3	914	RVRDRKRAVWTARGRRRCGDSMSGGWWAQQVGAWRGTALGLALL LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPTKFCQRTSGLC VPLTWRCRDLDCSDGSDEECRIEPCQKQGCPPPPGLPCPCT GVSDCSGGTDDKLRNCSRLACLAGELRCTLSDDCIPLTWRCDSH PDCPDSSDELGCGTNEILPEGDATMGPPVTLESVTSLRNATTM GPPVTLESVPSVGNATSSSAGDQSGSPATAYGVIAAAVLSASLV TATLALLSWLRAQERLRPLGLLVAMKESLLSEQKTSLP
5565	993	138	RWNPNPARAGSISRQAPGSVSAMVTAFFVFGCAFIAPGPA LALVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVID NKDGPTQKYLIFGAFVSUYIQEMFRFAYYKLLKKASEGLKSI NPGETAPSMRLLAYVSGLFGIMSGVFSFVNTLSDSLPGTGVGHI GDSPOFFLYSAFMTLVIILHVFVGIVFDGCEKKKWGILLIVL LTHLLVSAQTFISSYGINLASAFIILVLMGTWAFLAAGSCLRS LKLCLLCQDKNFFLLYQSR
5566	2043	1232	SHIQHGRGAQAPVMMVSWMISRAVVLVFGMLYPAYYSYKAVKT KNVKEYVRMMYIWFALYTVIETVADQTVAFVPLYELKIAFV IWLSPYTKGASLIYRKFLHPLLSKEREIDDIYQAKERGYET MVNFRQGLNLAAATAAVTAAVKSQGAITERLRSFSMHDLTTIQ DEPVGQRPYQPLPEAKKSKPAPSESAGYGIPLKDGDEKTDEEA EGPYSDNEMLTHKGPRRSQSMKSVKTTKGRKEVRYGSLKYKVK RPQVYF
5567	1554	233	EFLGSGVSPDLANEDGLTALHQCIDDREMVOQLLEAGANINA CDSECWTPHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSLQ AGADLHAPLDHGATLLHVAANGFSEAAALLLEHRASLSAKDQD GWEPLHAAAYWGOVPLVELLVAGADLNKSLMDETPLDVCDE EVRAKLLELKHKHDALLRAQSRQSLRLRRRTSSAGSRGVVRRV SLTQRTDLYRKQHAQEAIVWQQPPPTSPEPPEDNDRQTGAELR PPPPEEDNPEVVRPHNGRVGSPVRHLYSKRLDRSVSYQLSPLD STTHTLVHDKAHTLADLKRQRAAKLQRPPEGPESPEETAEP GLPGDVTVPQDCGFRAGGDPPLKLTAPAVEAPVERRPCCLLM
5568	1731	587	AEDRQFASRRGAGTTAAMAASGPGCRSWCLCEPVPSATFTALL SLLVSGPRLFLLQQPLAPSGLTALKSEALRNWQVRLVYIFVYE NPISLLCGAIIWRFAGNFERTVGTVRHCFVTIIFAIISAIIFL SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRLVFG MVVPSVLVPWLLLGASNLIPQTSFLSNVCGLSIGLAYGLTYCYS IDLSEVALKLDQTFPFSLMRRI SVFKYVSGSSAERRAAQSRKL NPVPGSYPTQSCHPHLSPSHPVSTQHASGQKLASWSPCTPGHM PTLPYQPASGLCYQNHFGPNPTSSSVYPASAGTSLGIQPPTP VNSPGTVYSGALGTPGAAGSKESSRVPM
5569	2	835	QTPCLAWERGSREDSIVPGQKFPPTCSSFSGMDVGPSSLPHLG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LKLLLLLLLLPLRGQANTGCYGIPIGMPGLPGAPGKDGVDGLPGP KGEPGIPAIPGIRGPKGQKGEPLPGHPGKNGPMGPMPGVP PMGIPGEPGEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL TNPOGDYDTSTGKFTCKVPLGYFVYHASHTANLCVLLYRSGVK VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIQ SDSVFSGFLLFPD
5570	264	946	RDRDRGGVATSTEEPAPRAPQSRGPGPVSQTGRGRERGGGDT MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT PYEGGVKVRVDLPDKYFPKSPSIGFMNKIFHPNIDEASGTVCL DVINQWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH RPEYKQKIKRYIQKYATEALKEQEECTGDSSESSMSDFSSED EAQDMEL
5571	264	946	RDRDRGGVATSTEEPAPRAPQSRGPGPVSQTGRGRERGGGDT MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT PYEGGVKVRVDLPDKYFPKSPSIGFMNKIFHPNIDEASGTVCL DVINQWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH RPEYKQKIKRYIQKYATEALKEQEECTGDSSESSMSDFSSED EAQDMEL
5572	2802	2085	RTDYRTGIPGRRFVMAAGDGVKLTGSGSESSNDGGSSESPG DAGAAAEAGGWAALALLTGGEMLLNVALVALVLLGAYRLWV RWGRRGLGAGAGAGEESPATSLPRMKKRDLSLEQLRQYDGS RNP RILLAVNGKVPDVTGSKFYGPAGPYGIFAGRDA SRGLATFCLD KDALRDEYDDLSDNAVQMESVREWEMQFKE KYDYVGRLLKPGE EPSEYTTDEEDTKDHNKQD
5573	2562	219	VPARTPNAEDQGPAAATATPCQSGGRERAGEAAEDGVKMAAF SEMGMPEIAQAVEEMDILLPTDIAESIPILIGGGDVLMAAET GSGKTGAFSIPVQIVYETLKDQEGKKGKTTIKTGASVLNKQ MNPYDRGSFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE VSHDQGLCRVWSTMQASLDLGTDFKFGFGGTGKKSHNKQFD NYGEEFTMHDITGICYLDIDKSHVKFSKNGKDLGLAFEIPPHMK NALFPACVLKNAELKFNFGEEFKFPKDFVALSKAPDGYIVK SQHSGNAQVTQTKFLPNAPKALIVEPSRELAEOQLNNIKQFKKY IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTGRLDDLST GKLNLSQVRFLVLDLADGLLSQGYSDFINRMHNQIPQVTS DGKR LQVIVCSATLHSDVKKLSEKIMHPTWVDLKGEDSV PDTVHHV VVPVNPKTDRWLERLGKSHIRTDVHAKDNTRPGANS PEMWSEA IKILKGEYAVRAIKHKMDQAIIFCRTKIDCDNLE QYFIQGGG PDKKHQFSCVCLHGDRLKPKHERKQNLERFKG DVRFLICTDVAA RGIDIHGVPYVINVTLPDEKQNYVHRIG RVGRAERMGLAISLVA TEKEKVYHVCSSRGKGCYNTRLKED GGCTIWNEMQLLSEIEE HLNCTISQVEPDIKVPVDEFD GKVITYGQKRAAGGGSYKGHVDIL APTVQELAALEKEA QTSFLHLGYLPNQLPRTF
5574	1731	952	NEGLEVFEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG LLGLLGLTVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS TGITQCDIYSTLLGLPADIQAAQAMMTSSAIISSLACIISVVG M RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWN LHGILRD FYSPLVPDSMKFEIGEALYLGIISSLSLIAGIIL CFSCSCQRN RSNYYDAYQAQPLATRSPRPGQPPKVKSEFNS YSLTGYV
5575	456	766	LLNALPCPPPTAAAVLLSSTGLMELLEKMLALTAKADSPRTAL LCSAWLLTASFSAQHKGSLQKDPLLSQACVGCLEALDYL DAR SPDIGRNSPHYLMFP
5576	249	2146	RSWGAFWFRMLRRRRHMPRLAMVGCAFVLFLFLHRDVSSR EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAP EA QTLFISINQSLCPGFYTPAELKPFWRPPQDPNAPGADG KAFQK SKWTPLETQKEEGYKHKCFNAFASDRISLQ RSLGPDTRPPECV DQKFRRCPPPLATTSVIIVFHNEA WSTLLRTVYSVLHTTPAILLK EIIIVDDASTEHLKEKLE QYVKQLQVVRVVRQEEKGLITARL LGASVAQAEVLTF LDAHCECFHGWLEPLLARIAEDKTVVVSPDI VTI DLNTFEFAKPVQGRVHSRGNFDWSTFGWETLPPHEKQRR KDETYPIKSPTFAGGLFSISKSYFEHIGTYDNQMEI NGGENVEM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SFRVWQCGGQLEIIPC SVVGHVFRTKSPHTFPKGTSVIARNQVR LAEVWMSDYKKIFYRRNLQAQMAQEKSFGDISERLQRLREQLHC HNFSWYLNHNVPEMFVDPDTPFTFYGAIKNLGTNQCLDVGENNRG GKPLIMYSCHGLGNGQYFEYTTQDRDLRHNI AKQLCLHVSKGALG LGSCHTFGKNSQVPKDEWELEAQDQLIRNSGSGTCLTSQDKKPA MAPCNPSDDPHQLWLFV
5577	3	1275	RNSDCSCGRISVHCLPWVLFILDLKVESSMFCPLKLI LLLPVLLD YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCI PKIDWTL SPGEHAKDEYVLYYYNSLSPVIGRFQNRVHLMGDILCNDGSLLL QDVQEADQGTYYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHV GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRM SVEYSQSWGHFQNRVNLVGDIFRNDGSIIMLQGVRESDDGNYTCS IHLGNLVFKKTIIVLHVSPEEPRTLVTFAALRPLVLGGNQLVII GIVCATILLLPVLLIVKKTGKNSVSNVTLVKNKTKTNPEIK EKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHFV WPSLRSDRNSLEKKSGGGMPTKQAF
5578	3	783	AVESMASPGAGRAPPPELPERNCGYREVEYWDQRYQGAADSAPYD WFGDFSSFRALLEPELRPEDRI LVLGCGNSALS YELFLGGFPNV TSVDYSSVVVAAMQARYAHVPQLRWETMDVRKLD FPSASFDVVL EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI SMTSAAPHFRTRHYAQAYYGSRLRHATYSGGFHFLYLMHKGK LSVAQLALGAQILSPRPPTSPCFLQDSHEDFLSAIQL
5579	3	1540	RNSGLARGASALARHGGGLAGGVGWDCGACASRCQGVMEGLLTR CRALPALATCSRQLSGYVPCRFHHCAFRRGRRRLLSRVFPQNL REDRVLSQLDKSDDLTKSQRMLQVGLIYPASPGCYHLLPYTV RAMEKLVVRVIDQEMQAIGGQKVNMPSLSPAELWQATNRWDLMGK ELLRLDRDRHGKEYCLGPTHEEAIT ALIASQKLSYKQLPFLLYQ VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRIA ICPRCSFSANMETLDSQMNCPACQGPLTKTKGIEVGHTFYLGT KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRI LAAAIEVLSTED CVRWPSLLAPYQACLI PPKKGSKEQAASELIGQLYDHI TEAVPQ LHGEVLLDDRTHLTIGNRLKDANKFGYPFV I IAGKRALEDPAHF EVNCQNTGEVAF LTKDGMDDLTPVQTV
5580	1681	450	ADAGTRCIPGFVVP SGAGYSAPAQRGRSSGRMRAAAAPGLTAP WRLQLQCELEAGELGMVPAAMGPSALGSGGPGSMAPWCSVSS GPSRYVLGMQELFRGHKSTREFLAHSAKVHSAVNSCDGRRLASG SPDKTASVFLLEKDRLVKENNYRGHSDSDQLCWHPSNPDLFT ASGDKTIRIWDVVRTKCIATVNTKGENINICWSPDGQTI AVGNK DDVVTPIDAKTHRSKAEQKFVEVNEISWNNDNMFFLTNGNGC INILSYPELKPVSINAHPSNCICIKFDPMGKYFATGSADALVS LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDH FIDIA EVEVGDKLWEVQCESPTFTVANHFKRPLAFACDDKDKGYDSSR EAGTVKLFGLPND
5581	54	947	GGGSGPRAPSATLLDTGESVA AVASGEDKGI AASAAAAAVFACS CSPDPQSTTMNPVYSPVPGAPYGNPKNMAYTGYP TAYPAAAF YNPSLYPTNSPSYAPFQFLHSAYATLLMKQAWPQNSSSCGTEG TFHLPVDTGTENRTYQASSA AFRYTAGTPYKVPPTQSN TAPPY SPSPNPYQTAMYP IRSAYPQNL YAQGAYYTPVYAAQPHVIH TTVPQNSIPSAIYPAPVAAPRTNGVAMGMVAGTMTAMSAGTLL TTPQHTAIGAHVSMPTYRAQGT PAYSYPVPHW
5582	5775	2739	ITNNNNV IIPLVIAHYLSGSAQARGERSPAERLMERQKRKADI EKGLQFIQSTLPLKQEEYBAFLKL VQNLFAEGNDLFREKDYKQ ALVQYMEGLNVADYASDQVALPRELLCKLHVNRACCYFTMGly EKALDESEKALGLDSEIRALFRKARALNELGRHKEAYECSSRC SLALPHDESVTQLGQELAQKGLRVRKAYKRPQELTFSLLSNG TAAGVADQGTSNGLSIDDIEDCYVDPGRSPALLPSTPTMPLF PHVLDDLAPLDSSRTLPSDSDLDDFSDGDVFGPELDTLLDSL VQGLSGSGVPSLPLIPVFPGGTLLPVPVGGSI PVSSPLPP ASFGLVMDPSKLAASVLDALDPPGPTLDPLDLPLPYSETRLDAL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DSFGSTRGSLDKPDSFMEETNSQDHRPPSGAQKPAPEPCMPEN TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCK RDILLGRRLSSEDQTKWIRIRPRPTKTSFVGSYYLCKDMINKQDC KYGDNCTFAYHQEEIDVWTEERKGTILNRDLLFDPLGGVKRGSIT IAKLLKEHQGIPTFLCEICFDSKPRIISKGTKDSFVSCSNLAAK HSFYNNKCLVHIVRSTSLKYSKIRQFQEHFQFQDVCHEVRYGCL REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWOQMEAH AGKASSMGAPRTHGPSTFDLQMKFVCGQWRNGQVVEPDKDLK YCSAKARHCWTKERRVLLVMSKAKRKWVSRPLPSIRNFPQQYD LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKNKILDMQQTY DMWLKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL CGKNSNGKKQWQHQQHSEKHEKVFTSDSDASGWAFFPMGEFR LCDRLQKQKACPDGDKCRCAHQEEELNEWLDRREVLKQKLAKAR KMDLLCPRDDDFGKYNFLQEDGDLAGATPEAPAAAATATTGE
5583	3	1265	SSGCRQGRPRGRSDRPPRRRHKMKVETRYDYILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSSPMDIFDMFFGGGGRMARERRGKNV HQLSVTLEDLYNGVTKKLALQKNVICKECGVGGKKSVEKCP CKGRGMHIHQIGPMVQIQTVCECKQGERINPKDRCESC SGAKVIREKKIEVHVKEGMDGQKILFHGEGDQEPLEPGDVI IVLDQKDSVFRRGHDLIMMKIQLSEALCGFKTKITLDNRI LVITSKAGEVIKHGDLRCVRDEGMPYKAPLEKGILIIQFLVIF PEKHWSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPEQN WRQHREAYEDEDGPQAGVQCQTA
5584	3	1265	SSGCRQGRPRGRSDRPPRRRHKMKVETRYDYILGVKPSASPEE IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD QGGEQAIKEGGSGSPSSPMDIFDMFFGGGGRMARERRGKNV HQLSVTLEDLYNGVTKKLALQKNVICKECGVGGKKSVEKCP CKGRGMHIHQIGPMVQIQTVCECKQGERINPKDRCESC SGAKVIREKKIEVHVKEGMDGQKILFHGEGDQEPLEPGDVI IVLDQKDSVFRRGHDLIMMKIQLSEALCGFKTKITLDNRI LVITSKAGEVIKHGDLRCVRDEGMPYKAPLEKGILIIQFLVIF PEKHWSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPEQN WRQHREAYEDEDGPQAGVQCQTA
5585	2619	915	LPAGTPESSLHEALDQCMTALDLFTNQFSEALSILKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEEIHAEVYAKCLLQRAALTFLQD ENMVSVIKGGIKVRNSYQTYKELDSLQSSQYCKGENHPHFEGG VKLGVGAFNLTLMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFLVLTGNVNIIEAEKLLKPYLNR YPKGAIPLFLAGRIEVIKGNIDAAIRRFEECCEAQHKKQFHHM CYWELMWCFTYKQWMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGKLKLAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNKYAVIGKQPKLTDGILEITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAENFRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESQK NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5586	2619	915	LPAGTPESSLHEALDQCMTALDLFTNQFSEALSILKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEEIHAEVYAKCLLQRAALTFLQD ENMVSVIKGGIKVRNSYQTYKELDSLQSSQYCKGENHPHFEGG VKLGVGAFNLTLMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFLVLTGNVNIIEAEKLLKPYLNR YPKGAIPLFLAGRIEVIKGNIDAAIRRFEECCEAQHKKQFHHM CYWELMWCFTYKQWMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGKLKLAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNKYAVIGKQPKLTDGILEITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAENFRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESQK NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5587	1768	148	SSAVPDGAVGRPVAVAVGGPFHSCRCRPFCLMAAIGVHLGCTSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CVAVYKDGGRAGVVANDAGDRVTPAVVAYSENEETVGLAAKQSRIRNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIEKNGKLRYEIDTGEETKFNPEDEVARLIFSKMKETAHSLVGSANDVVTVPFDGGEKQKNALGEAARAAGFNVRLRIHEPSAALLAYGIGQDSPTGKSNILVFKLGGTSLSLVMEVNSGIYRVLSTNTDDNIGGAHFTETLAQYLASEFQSRFKHDRVGNARMMKLTNSAEVAKHSLSTLGSANCFLDLSLYEGQDFDCNVSRRARFELLCSPFNKCIETAIRGLDQNGFTADDINKVVVLGGSSRIPKLQQLIKDLFPVAVELLNSIPPDEVIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDSEGSAREFTVLFPSGTPLPARRQHTLQAPGSISSVCLLEYESDGKNSAK EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET GKCEAISIEIAS
5588	3	589	TPPPEQAMVAATVAAAWLLWAAACAQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVNVASECGFTDQHYRALQQLQORDLGPHEFNVLAFCPCNQFGQEPDSNKEIESFARTYSVSFPMFSKIAVTGTGAHPAFKYLAQTSKGTEPTNFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL
5589	1884	553	LRQAWHEGGIGQTDKERGAALPGEEDPTGRSLGRASWESGSPRRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPASGLNRRSSGLWLGPDRCRPRSRCSRVMENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWKKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRLSLVSFVVRIVPSPDWFVGVDSLDLDCGDRWREQAALDLYPYDAGTDSGFTFSSPNFATIPQDVTVEITSSSPSHPANSFYYPRLKALPPPIARVTLRLRLQSPRAFIPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHGGRGLGTSRTRYVRVQPANNGSPCELEEEAECVPDNCV
5590	72	896	LCSSGALRLLPAMVAWRS AFLVCLAFSLATLVQRSGDFDDPNLEDAVKETSSVQKPDHDTTTTTNRP GTTRAPAKPPGSGLDLADALDDQDDGRRKPGIGGRERWNHVT TTTKRPVTTTRAPANTLGNDFDLADALDDRNRDDGRRKPIAGGGGFSDDKLEDIVGGGEYKPKDKGKGDGRYGSNDP GSGMVAEPGTIAGVASALAMALIGAVSSYISYQQKKFCFSIQQLNADYVKGENLEAVVCEEPQVKYSTLHTQSAEPPPPPEPARI
5591	68	1494	AGSSRRAAAERLLVSAGCRSLAGRASGVLLLP AELLPGEEAAMLVRTRNSKINAENKAKINMAGAKRVPTAPATSKPGLRPRTALGDIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVPMLVPVPSEPVPEPEPEPEPEPVKEEKLSP EPILVDTASPSMETSGCAPAEEDLCQAFSDVILAVNDVDAEDGADPNLCSEYVKDIYAYLRQLEEBQAVRPKYLLGREVTGNMRAILIDWLQVQMKFRLLQETMYMTVSTIDRFMCNNCVPKMLQLVGVTAMFLASKYEEMYPPEIGDFAFVTDNTYTKHQIRQMEMKILRALNFG LGRPLPLHFLRRASKIGEVDVEQHTLAKYLMELTMDYDMVHFPPSQIAGAFCLALKILDNGEWTPTLQHLYLSYTESLLPVMQHLAKNAAMVNQGLTKHMTVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGESKDWNQKDLLSALVLTVNCLPTPIMAKSAEVKLAIFGRAGVGKSALVVRFLTKRFIWEYDPTLESTYRHQATIDDEVVSMEILD TAGQEDTIQREGHMRWEGGFVLVYDITDRGSFEEVLPLKNILDEIKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECSECTEGGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKQAINKMLTKISS
5593	3	1113	HASGGRAANMAAERGAGQQSQEMMEVDRRVESEESGDEEGKKHSSGIVADLSEQLKDGEERGEEDPEEHLPVDMETINLDRDAEDVDLNNHYRIGKIEGFVLKKVKTCLRQNLICKIENLEELQSLRBLDLYDNQIKKIENLEALTELEILDISPNNLRNIEGVDKLTRLKKLFLVNNKISKIENLSNLHQLMLELGSNRIRAIENIDTLTNLESFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLRELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQEFWMNDNLLESWSLDLDELKGARSLETVYLERNLQKDPQYRRKV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5594	3	1113	MLALPSVRQIDATFVRF HASGGRAANMAERGAGQQSQSQEMMEVDRRVESEESGDEEGKKH SSGIVADLSEQSLKDGEERGEEDPEEEHELFPVDMETINLDRDAE DVDLNHYRIGKIEGFVLLKKVKTLCRLQNLKICLENLEELQSLR ELDLYDNQIKKIKENLEALTELEILDISFNLLRNIEGVDKLTRLK KLFLVNNKISKIENLNLHQLQMLELGSNRIRAIENIDTLTNLE SLFLGKNKITKLQNLDALTNLTVLMSQSNRLTKIEGLQNLVNL ELYLSHNGIEVIEGLENNNKLTMLDIASNRICKIENISHLTELO EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV MLALPSVRQIDATFVRF
5595	3	1476	ARWNRWVQVPAWPGPGCGTNASGERQRLPRAWRPVGRTLGSE PIALAWSPLYLFPPIPLPSWAVSQPTPTLGTMFADLDYDIEDK LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP AALDGTVAAGDEITGVNGRSIKGKTKEVAKMIQEVKGEVTHY NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC NDGLVKRLEELERTAEYKGMTEHTKNLLRAFYELSQTHRAFGD VFSVIGVREBPQAASEAFVKFADAHRSIEKFGIRLLKTIKPMPL DLNTYLNKAIPTDRLTIKKYLDVKFEYLSYCLVKEMDDEEYSC IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKME LDQKHVQDIVFQLQRLVSTMSKYNYNDYAVLRDADVFPIEVDLA HTTLAYGLNQEEFTDGEDEDEDEDETAAGEFSRDRGAAGPLDKG GSWCDS
5596	698	219	GAVLAPSSLPAAELAAQGESQSLDLSNTRPTSEVYKISFIFP NGDKVDGDCRTTSSGIYERNIGIHTTPNGIVYTGSKDDKMG FGRLEHFSGAVYEGQFKNMFHGLGTYTFNGAKYTGNFNENRV KGEGETHIQGTMRDVTTFHFTSCST
5597	3	731	ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLAYLSLSP VFVIVGFVTLIIFKRELHTISFLGGLALNEGWNWLIKNVIEPR PCGGPHTAVGTYKGMPSHSSQFMWFFSVYSFLFLYLRMHQTNA RFLDLLWRHVLSLGGLAVAPLVSYSRVLLYHTWSQVLYGGIAG GLMAIAWFIPTQEVLTPLFPRIAAMPVSEFFLIRDTSLIPNVLW FEYTVTRAERNRQRKLGTQLQ
5598	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSVPPHPPAPSPCCSGQTMKMLSKLILLALVALGFFEG DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMSQLELLSGG EMLCGGFYPRLSCLLSDSPGLGRLENKIFSVTNTECGKLEEL IKCALCSPHSQSLFHSPEREVLERDLVPLLCCKDYCKEFTYTCR GHIPGFLQTTADEFCFYARKDGGLCFPDFPRKQVRGPASNYLD QMEEDYKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGDERGGL SLAFHPNYKNGKLYVSYTTNQRWAIGPHDHLRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDM ITLDDMEEMDGLSDFTGSVLRRLDVTDMCNVPYSIPRSPNPHNS TNQPPFVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS SARILQIIKGDYSESEPSLLEFKPFSSNGPLVGGFVYRGCQSRL YGSYVFGDRNGNFTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFEDELGEVYIILSSSKSMTQTHNGKLYKIVDPKRPLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCSPGWEGDFCRTG
5599	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL VPLLGSVPPHPPAPSPCCSGQTMKMLSKLILLALVALGFFEG DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMSQLELLSGG EMLCGGFYPRLSCLLSDSPGLGRLENKIFSVTNTECGKLEEL IKCALCSPHSQSLFHSPEREVLERDLVPLLCCKDYCKEFTYTCR GHIPGFLQTTADEFCFYARKDGGLCFPDFPRKQVRGPASNYLD QMEEDYKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGDERGGL SLAFHPNYKNGKLYVSYTTNQRWAIGPHDHLRVVEYTVSRK NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDM ITLDDMEEMDGLSDFTGSVLRRLDVTDMCNVPYSIPRSPNPHNS TNQPPFVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SARILQIIKGDYSEPSLLEFKPFSNGPLVGGFVYRGCSERL YGSYVFGDRNGNFTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG HILGFGEDBLGEVYILSSSKSMTQTHNGKLYKIVDPKRLMPEE CRATVQPAQTLTSECSRLCRNGYCTPTGKCCSPGWEGDFCRTG
5600	1977	1244	SLRVLSGHLMQTRDLVQDPKSPKFIIVTLDGVPSPPGYMSDQE EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF SNAEMSELVAQKPEKLLERCKYWPACNGDECAHYHPISPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCCPTHVSRRIPLVSPKP AVAPPAPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRDC TFYHPTINVPPRHALKWIRPQTSE
5601	1977	1244	SLRVLSGHLMQTRDLVQDPKSPKFIIVTLDGVPSPPGYMSDQE EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF SNAEMSELVAQKPEKLLERCKYWPACNGDECAHYHPISPCKA FPNCKFAEKCLFVHPNCKYDAKCTKPDCCPTHVSRRIPLVSPKP AVAPPAPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRDC TFYHPTINVPPRHALKWIRPQTSE
5602	246	766	YHTSCTVWRTAKEALENTEVPVGLMVMYNNVEVVGKGRNEVNQTK NATRAEMVAIDQVLDWCQSGKSPSEVFHTVLYVTVEPCIMC AAALRLMKIPLVYGCQNERFGGCGSVLNIAADLPNTGRFPQC IPGYRAEEAVEMLKTFYKQENPNAPKS KVRKKECQQLNMF
5603	1	565	FRGRTPISGGERGCAQYFIPATPARSGENRTMPGAGDGGKAPAR WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS CFGFEDLHFRWYNSDAFKILIEGTVKNEKSDPKVTLKDDRI TLVGSTKEKRNISIVLRDLFSDTKYTCVKNPKENNLQHHA TIFLQVDDRMO
5604	1	1506	EDIFPAQLLKLQRHERVWQEPVDRHRSWGGSGAGGVAGREW DQGVVALGGHYMAEGEGYFAMSEDELAESPYPILGGDFGGDFG GGDFGGDFGGDFGGDFGGDFGGDFGGDFGGDFGGDFGGDFGG RLDGILSETIPIHGRGNFTLELQPSLIVVRRRLAEKRIQVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDPLPEGVNKEKITPLTLKEAYVQKMKVKNDSDRWSLI SLSNNSGKNVELKPVDSLRRQFEFSVDSFOIKLDSLLLFYECSE NPMTEFHPITIGESVYGDQEAFAHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQKRL ESYLQNHVFGLEDKRYEYMLTLHGUVNVESTVCLMGHERRQTNL ITMLAIRVLADQNVIPNVANVTCTCYQPAPYVADANFNSYIAQV QPVFTCQQQTYSTWLPNC
5605	35	1821	SQRSCPRSPSSPAPPWARSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFO KALRSLLRYPLPLRSGKEAKILOHFGDGLCRMLDERLQHRHTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNNGHFLTKELLQRCQAQKS PRVAP GSARPWPALRSLHLRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKPEETAVPGAASAELASEAGVQQQPLELRP GEYRVLVCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGF VWVAQETNPRDPANPGLVLDHIVERKRLDDLCSSIIDGRFREQ KFRKRCGLERRVYLVEEHGSHVNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTRLRSRPWGTTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGR QRNLGPALSRTLSQLYCSYGLT
5606	3	1099	GRSRCPGFGARGGTMSPRSCLSRLRLLVFAVFSAAAANWLYLAK LSSVGSISEETCEKLGKLIQROVQMKRNLVMSVRRGAQLA IEECQYQFRRNRWNCSTLDSLFPVFGKVVTQGTREAAFYAISA GVFAVTRACSSGELEKCGCDRTVHGVSPPGFQWSGCSDNIAYG VAFSQSFVDVRRERSKGASSSRALMNLHNEAGRKAILTHMRVEC KCHGVSGSCEVKTCSRVPVPPRQVGHALKKFDGATEVEPRRV SSRALVPRNAQFKPHTDEDLVYLEPSPDFCBQDMRSGVLGTRGR TCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCFKHWCCFVKC RQCQLVELHTCR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5607	521	141	PPVCNPAEAMPSPGTVCSSLGMLWLDLAMAGSSFLSPEHQRV QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK
5608	2	983	WFQSPLRQADPGPRHTLFMDVFVAGAIGGVCGDAVGYPDVTVKV RIQTEPKYTGIIWCVRDYHRRVWGFYRGLLPVCTVSLVSSSE VFGTYRHCLAHICRLRFNPNDAKPTKADITLSCASGLVRVFLT SPTVAKVRLQTQTAQKQRRRLSASGPLAVPPMCPVPACPEP KYRGPLHCLATVAREBGLGKLYGSSALVLRDGHSEFATYFLSYA VLCEWLSAGHSRDPVPGVLVAGGCAGVLAWAVATPMDVIKSRRL QADGGQRRYRGLLHCVITVREEGPRVLFKGLVLNCCRAPFVN MVFVAYEAVLRLARGLLT
5609	1628	304	AKGVWVLPSPPPRPGRGALVSGSLRRGRSGTSWRPRRMNHKSK KRIREAKRSARPELKDSDWTRHNYYESFSLSPAADVADNVERAD ALQLSVEEFVERVERPYKPVLLNAQEGWSAQEKWTLERLKRKY RNQFKCGEDNDGYSVMKMKYIIEYMESTRDDSPLYIFDSSYG EHPKRRKLEEDYKVPKFDDDLFQYAGEKRRPPYRWVFGPPRS GTGIHIDPLGTSANALVQGHKRWCLFPTSTPRELIKVTRDEGG NQDEAITWFNVIYPRTPQPTWPEFKPLEILQKPGETVVFVPGG WWHVVLNLDTTIAITQNFASSTNFPVWHKTVRGRPKLSRKWYR ILKQEHPELAVLADSVLDQESTGIASDSSSSSSSSSSSSSDSD SECESGSEGDGTVHRRKRRCTSMVGNDDTTSQDDCVSKERSSS R
5610	54	1196	LERTPASADMAWTKYQLFLAGLMLVTGSSINTLSAKWADNFMAEG CGGSKEHSFQHPFLQAVGMFLGEFSCLAAPYLLRCRAGQSDSS VDQQPFNPLFLPALCDMTGTSMLYVALNMTSASSFQMLRGA VIFTGLFSVAFGLRRVLVSQWLGLATLGLVVGGLADLLSKH DSQHKLESEVITGDLIIIMAIQVLEEFVYKHNHPLRA VGTEGLFGFVILSLLVPMYIIPAGSFSGNFRGTLEDALDAFCQ VGQPLIAVALLGNISIAFFNFAGISVTKELSATRMLVDSLR TVVIWALSALGWAFHALQILGFLILLIGTALYNGLHRPLLGR LSRGRPLAESEQRLLGGTRTPINDAS
5611	2	577	FVLNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG ELSNRFQGGKAFGLLKARQERRLABINREFLCDQKYSDEENLPE KLTAFFKEKYMFDLNNGEIDLSMLKRMMEKLGVPKTHLEMKKM ISEVTGGVSDTISYRDFVNMLGKRSVAVLKLMMFEGKANESSP KPVGPPPERDIASLP
5612	1	721	ASRDGYMDATIAPHRIPEMPQYGEENHIFELMQAMWLCKHLNS SLLTLENLILNEFSYTATEARRLYLQKRTVPSALLVQLIQERLA EEDCIKQGWILDGIPETREBQALRIQTLGITPRHVIVLSAPDTVL IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET AQKLEYHRNIVRVIPSYPKILKVISADQPCVDVYQALTYVQS NHRTNAPFTPRVLLGVPVGS
5613	115	1279	RGVDFALRRAEKMLPLSTKDEYKPEKFNLFKGKISGWFRSILSD KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST AILAGLAASVISKWRDNDAFSYGYVRAEVLAVGFLIPTAF FIFSEGVERALAPPDVHHERLLLSILGFVVNLIGIFVFKHGGH GSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAHSHDH AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI ASAIMMQNFGLMIADPICSILIAILIVSVIPLLRRESVGIIMQR TPPLENSLPQCYQORVQQLQGVYSLQEQHFWTLCSDVYVGTLLKL IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
5614	3	1268	LLSRNEHACPLQAGLGLTQKPKAIRGREGRATNQGGQETQNER APWGARQRLGVMAELQQLQEFPIPTGREALRGNSALLRVADYC EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRLMD LQGAALRQVEARVSTLGQVMNHMEKVARREIGTLATVQRLPPG QKVIAPENLPLTPYCRRPLNFGCLDDIGHGKIDLSQLSRTGT LSRKSIPAPATPASATIGRPPRIPEPVHLPVVPDGRLSAASSAS SLASAGSAEGVGGAPTPKGQAAPPAPPLPSSLDPPPPPAAVEVF QRPPTLEELSPPPDEELPLPLDLPPLPLDGLDELGLPPPPPGF GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5615	9	1558	SDGWCEGVSEGTGFFPGNYVEPSC ALGRRRPGDPREMEAAATPAAAGAAARREELDMVMRPLINEQNF DGTSDDEHEQEELLPVQKHQQLDDQEGISFVQTLMLHLLKGNIGTG LLGLPLAIKNAGIVLGPISLVFIGIISVHCMHILVRCSHFLCLR FKKSTLGYSDTVSFAMEVSPWSCLOKQAAWGRSVVDFFLVITQL GFCSVYIVFLAENVKQVHEGFLESKVFISSNSTSSNPCERRSDV LRIYMLCFLPFIIILLVFIRELKNLFVLSFLANVSMVSLVLIYQ YVVRNMPDPHNLPIVAGWKKYPLFFGTAVFAFEGIGVVLPLENQ MKESKRFPQALNIGMGIVTTLVYTLATLGYMCFHDEIKGSITLN LPQDVWLYQSVKILYSFGIFVTYSIQFYVPAEIIIPGITSKFHT KWKQICEPGIRSFVLSITCAGAILIPRLDIVISFVGAUSSSTA LILPLVLEILTFSKEHYNIWMVLKNISIAFTGVVGPLLGTIYITV EEIIYPTPKVAGTPQSPFLNLNSTCLTSGLK
5616	1	719	DDFVRCGPQSAAMGASARLLRAVIMGAPGSGKGTSSRTTHFE LKLHSSGDLRLDNMLRGTEIGVLAKAFIDQGLIPDDVMTRLAL HELKNLTQYSWLLDGFRTLPQAEALDRAYQIDTVINLNVFV IKRLTARWIHPASGRVYNIENFPKTVGIDDLTGEPLIQREDD KPETVIKRLKAYEDQTKPVLEYQKKGVLFTSGTETNKIWPYV YAFLOTKVPQRSQKASVTP
5617	176	765	PWRGRGSRPRGAGAMAEQVNRSAGLAPDCEASATAETTVSSVG TCEAAGKSEPKDYDSTCVFCRIAGRQDPGTLLHCENEDLCF KDIPKPAATHHYLVVPPKKHIGNCRILRKDQVELVENMVTGKTI ERNNFTDFTNVRMGPHMPPFCSISHLHLHLVAPVDQIGFLSKLV YRVNSYWFITADHLIRKLRT
5618	3	1692	YLYNINLSENKLSGKEDLWEKLQYLWKSTLNLPLEDLRVPDES LFLNSGGDSLKSIRLLSEIEKLVGTSVPGLEIILSSSILEIYN HILQTVVDEDDVTFRKSCATKRKLSNINQBEASGTSIHQA IMTPTCHNEINAFVLSRGSQILSLNSTRLTKLGHCSACPSDSVS QTNIQNLKGLNSPVLIGKSKDPCVAKVSEEGKPAIGTQKMEHL VWRSDTGKCVASPLVVIPTFDKSSSTTVYIGSHSRMKAVDFY SGKVWEQILGDRIESSACVSKCGNFIVGCGYGLVYVLKNSNG EKYWMFTTEDAVKSSATMDPTTGLIYIGSHDQAYALDIYRK VWKSCKGTVFSSPCLNLI PHLYFATLGGLLAVNPATGNVW KHSCGKPLFSSPQCCSYQICIGCVDGNLLCFTHFGEQVWQFSTS GPIFSSPCTSPSEQKIFFGSHDCFYCCNMKGHLQWKFTTSRV YATPFAFHNYSNEMLLAAASTDGKVNILESQSGQLQSVYELP GEVFPSPVLESMLIIGCRDNYVYCLDLLGNGQK
5619	2160	1477	DSPVLPTSGNVISTAQPAQFWSAVEAALRSLGSPGAGRGCP AQSLHSHQLAAWDPLKPSLRSPHLLQHPQLRSLTASSGHLGR RSCPPRPLELLRAGSSTRPQPLTSSCCGMSCMYSLGHCSVL LWGTGKRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVWGQPP TVGLRPGLLGERQRGALRAGDPQCQCLPATVREDLVGVPSPWAA ECSFPATP
5620	930	182	PLPPTLAMFLTRSEYDRGVNTFSPEGRFLQVEYAIEAIAKLGST AIGIQTSEGVC LAVEKRITSPLEMPSSIEKIVEIDAHIGCAMSG LIADAKTLIDKARVETQNHWFYNETMTVESVTQAVSNLALQFG EEDADPGAMSRPFGVALLPGGVDEKGPQLFHMDSGTFVQC DAR AIGSASEGAQSSSQEVYHKSMTLKRAIKSSLIILKQVMEEK LNA TNIELATVQPGQNFHMFTEKEELEEVKDI
5621	3	819	VVEFVEYTATDANVKNESLSSVQQLGKIMTVRYGKFLSLKLDGA ENDLTWVLKHCERFLKQOQTSIKSSLLCLQGNVAGHDWVSSLF MIMLGDKETFPQLHQFSRLLTSAFLWLPRLHISSYLPNDTVES GIHPVYFCSTHYIEMLLKAEPLVFSAFHMSGFAPSQICLQWIT QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQDDILQ HTQTQDLQVFLKEALHGFRVSDYFEYMEILEQNYRTVLLRDMR NIRLQST
5622	1122	456	AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNPMKAMY PGTFYFQFKNLWEANDRNETWLCFTVEGIRRSVVSWKTGVFRN QVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA GEVAEFLARHSNVNLTIFTARLYYFYQYFCYQEGRLSLSQEGVAV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EIMDYEDFKYCWENFVYNDNEFFKPKWGLKTNFRLKRRRLRESLQ
5623	3	954	FLPFFIRAPKISRNGQLFTFTTFFPPFANKALPGWEGIVPACFW RKKILTPTSTGTMELLQVTILFLLPSICSSNSTGVLEAANNLSLV TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST ATFLTSDKDEGLKATTTDVRKNDISIISNVTVTSVTLFNAVSTLQS SKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENT SQSQVIGTEGGKNASTSATSRSYSSIIILPVVIALIVITLSVFVL VGLYRMCWKADPGTPENGNDQPPQSDKESVKLLTVKTISHESGEH SAQGKTKN
5624	159	898	PGVAAAAGALPQYHGPAPALVSCRRELSLSAGSLQLERKRDRFT SSGSRKLYFDTHALVCLLEDNGFATQQAEEIIVSALVKILEANMD IVYKDMVTMKMQEITFQQVMSQIANVKKDMIILEKSEFSALRAE NEKIKLELHQLKQQVMDEVIKVRTDTKLDNFLEKSRVKELYSLN EKKLLELRTEIVALHAQODRALTQDRKIETEVAGLKTMLSHK LDNIKYLGSIFTCLTVALGFYRLWI
5625	1	1180	TIPSSAAAQCRAGPPAGALEALS PGARAHAEERRGEMRATPLAAP AGSLSRKKRLELDDNLDTERPVQKRARGSPQPRLPCLPLSP TAPDRATAVATASRLGPYVLEPEEGGRAYQALHCPTGTETTCR VYPVQEAALAVLEPYARLP PHKHVARPTEVLAGTQLLYAFFTRTH GDMHSLVRSRHRIPPEAAVLFRQMATALAHCHQHGLVLRDLKL CRFVFADRERKKLVLENLEDS CVLTGPDDSLWDKHACPAYVGPE ILSSRASYSKGAADVWSLGVLFITMLAGHYPFQDSEPVLLFGKI RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQ DPMPLAPTRSHLWEEAQVVPDGLGLDEAREEEDREVLYG
5626	3123	2011	PPRALGSAVAMENQVLT PHVYWAQRHRELYLRVELSDVQNP AISI TENVLHFAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWVERLTQKEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTNLKGYLFMYNLVQFLGFSWIFVN LTVRFILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAUVFVFWLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSSFLQIYILIMIFLGLYINF RHLXKQRRRRYGQKKKKIH
5627	3123	2011	PPRALGSAVAMENQVLT PHVYWAQRHRELYLRVELSDVQNP AISI TENVLHFAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWVERLTQKEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTNLKGYLFMYNLVQFLGFSWIFVN LTVRFILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAUVFVFWLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSSFLQIYILIMIFLGLYINF RHLXKQRRRRYGQKKKKIH
5628	75	1455	VAGAMASKCLKAGFSSGSLKS PGGASGGSTRVSAMYS SSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMPDYQSYFRTEELQKKTLCSKAENARLVVEI DNAKLAADDFTKYETEVSRLQLVESDINGLRRILDLTCLCKSD LEAQVESLKEELLCLKKNHEEEVNSLRQGLGDRLNVEVDAAPPV DLNRVLEBMRQYETLVENNRDAEDWLDTQSEELNQVVSSE QLQSQCAEIIELRRTVNALEIELQAQHSMDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNEQYQVLLDVRARLEC EINTYRGLLESEDSKLP CNPCAPDYS PSKSLCPLPAASCGPSA ARTNCSARPICVPCPGGRF
5629	2287	938	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV PAPALPRGRPGTEGSTLSAPAVLVAVAVVVVVSAVANAMA NYIHVPPGSPVPPKLVNTVQDQEEHRCREGALSLLQHLRPHWDP QEVTLQLFTDGIITNKLIGCYVGNTEMDVVLVRIYGNKTELLVDR DEEVKSFRLVQAHCAPQLYCTFNNGLCYEFIQGEALDPKHVCN PAIFRLIARQLAKITHAHNGWIPKSNLWLMKGKYFSLIPTGF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>ADEDINKRFLSDIPSSQILQEEMTWKKEILSNLGSPPVVLCHNDL</p> <p>LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNFEFAGVSDV</p> <p>DYSLYPPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV</p> <p>NQFALASHFWGLWALIQAKYSTIEFDLGLYAIVRFNQYFKMKP</p> <p>EVTALKVPE</p>
5630	1194	278	<p>GFWAIAQTCAHHLPPGSPWLPVSPWRLPEMSSFGYRRTLTVALF</p> <p>TLICCPGSDEKVFVHVRPKKLAVEPKGSLEVNCSTTCNQPEVG</p> <p>GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM</p> <p>NSNVSYQPPRQVILTLPQTLVAVGKSFTIECRVPTVEPLDSLT</p> <p>LFLFRGNETLHYETFGKAAPAPQEAATFNSTADREDGHRNFSC</p> <p>LAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIIVTVSVL</p> <p>LSLFTSVLLCFIFGQHLRQQRMGTYGVRAAWRLPQAFRP</p>
5631	1053	290	<p>SRVDDFVRPEPSRAEPSSRGRRRPARRAATMSVFGKLFAGGGGK</p> <p>AGKGGPTPQEAIQRLRDEEMLSKKQEFLEKKIEQELTAACKHG</p> <p>TKNRAALQALKRKKRYEKQLAQIDGTLSTIEFQREALENANTN</p> <p>TEVLKNMGYAAKAMKAADNMDIDKVDLMQDIADQQLAEIEIS</p> <p>TAISKPVGGEFDEDELMAELEELQEELEDKNLEISGPETVP</p> <p>LENPVPSIALPSKPAKKKEEDDDMKELNWAWSM</p>
5632	3	952	<p>VVLGWSPPRRLWWSGLGAAQRPVPSGLARSLHVETRRPHRA</p> <p>SVRVARGRLGVMAQPPQLLPVPSRREMPPGPPPAYAPTNGD</p> <p>FTFVSSADAEDLSGSIASPDVKLNLGDFIKESTATFLRQRGY</p> <p>GWLLEVEDDDPEDNKPLEELDIDLDIYKIRCVLMPMPSLGF</p> <p>NRQVVRDNPDFWGPLAVLVFFSMISLYGQFRVSVIITWIFGS</p> <p>LTIFLLARVLGGEVAYGOVLGVIGYSLPLIVIAVLLVVGSEFE</p> <p>VVSTLIKLPGVFAAAYSAASLLVGEEFETKKPPLLIYPIFLLYIY</p> <p>FLSLYTGTV</p>
5633	771	460	<p>QCSKTMVGRPFYRSSEFMEQLLSSHLHQVPPFCCFTVVCLCN</p> <p>CLFENSVSPLYMLCFNFFMSIFFYSLSITKLNLIYWLGLSYQSL</p> <p>LLLLLSGHRPWGSSMV</p>
5634	1446	855	<p>PRATGRIRSRRAASRPAGAGASGAEPSSGRERSRLSGRRAPAM</p> <p>ARNTLSSRRFVDIDEFDENKFVDEQBEAAAAAEPGDPDPSEVD</p> <p>GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK</p> <p>SSEIEQAVQSLDRNGVDLLMKYIYKGFEXPTENSSAVLLQWHEK</p> <p>ALAVGGLSGSIIRVLTARKTV</p>
5635	3	943	<p>DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL</p> <p>RSLFHPFPVTRSGAPRAVLVGSSWPAMVAPAVKVARGWVGLAL</p> <p>GVRRAVLQPLGLTQVRWSRYSPEFKDPLIDKEYYRKPVEELTEE</p> <p>EKYVRELKKTOLIKAAPAGKTSSVFEDPVISKFTNMMIGGNKV</p> <p>LARSLMIQTLKAVKRKQFEKYHAASAEQATIERNPYTIHQAL</p> <p>KNCEPMIGLVPILKGRFYQVPVPLPDRRRRFLAMKWMITECRD</p> <p>KKHQRTLMPKLSHKLLEAFHNQGPVIRKXKDLHKMAEANRALA</p> <p>HYRWW</p>
5636	2253	1143	<p>LEDTCIQHPPEAKKLYLYHRKLEVERNGIPRLPKDVFMDTHQG</p> <p>LTDVRAKVTGFSQGVVDSVKGFFSSFSQATHSAGAVVSKPREI</p> <p>ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK</p> <p>YGSEEDCSSATSGSVGANSTGGIAGVASSSKTNTLDMQSSGFD</p> <p>ALLHEIQEIRETQARLEESFETLKEHYQRDYSIMQTLQEERYR</p> <p>CERLEEQLNDLTELHQNELNLKQELASMEEKIAYQSYERARDI</p> <p>QEALACOTRISKMELQQQQQVQVQLEGLNATARNLLGKLINI</p> <p>LLAVMAVLLVFVSTVANCVVPLMKTRNRTFTSLFLVVFIAFLWK</p> <p>HWDALFSYVERFFSSPR</p>
5637	948	2532	<p>MSFCGARANAKMAAYNGGTSAAAAGHHHHHHHPLPLPPPHLH</p> <p>HHHPQHHLHPGSAAVHPVOQHTSSAAAAAAMNLNPG</p> <p>QQQPYFSPAPGQAPGPAAPAAQVQAAAAATVKAHHHQHSHHP</p> <p>QQQLDIEPDRPIGYGAFGVVSVTDPRDGKRVALKKMPNVFQNL</p> <p>VSCKRVFRELKMLCFKHNDVLSALDILQPPHIDYFEBIYVUTE</p> <p>LMQSDLHKIIVSQPLSSDHVKVFLYQILRGLKYLHSAGILHRD</p> <p>IKPGNLLVNSNCVLKICDFGLARVEELDESRLMTQEVVTVQYRA</p> <p>PEILMGSRRHYSNAIDIWSVGCIFAELLGRILFQAQSPQQQLDL</p> <p>ITDLLGTFSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			THEAVHLLCRMLVFDPPYKRISAKDALAHFYLDEGRRLRYHTCMCK CCFSTSTGRVYTSDFEPVTNPKFDDTFEKNLSSVRQVKEIIHQF ILEQQKGNRVPLCINPQSAAFKSFISSTVAQPSSEMPSPPLVWE
5638	125	1155	DRKMSELDQLRQAEQLKNQIRDARKACADATLSQITNNIDPVG RIQMRTRRTLGRHLAKIYAMHWGTD SRLLSASQDGKLIWDSY TTNKVHAIPLRSSWVMTCAVAPSGNYVACGGLDNICSIYNLKTR EGNVRSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET GQQTTFITGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM CRQTFTHGESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL MTYSHDNII CGITSVSFSKSGRLLLAGYDDFN CNVWDALKADRA GVLAGHDNRVSC LGVTDDGMAVATGSWDSFLKIWN
5639	125	1155	DRKMSELDQLRQAEQLKNQIRDARKACADATLSQITNNIDPVG RIQMRTRRTLGRHLAKIYAMHWGTD SRLLSASQDGKLIWDSY TTNKVHAIPLRSSWVMTCAVAPSGNYVACGGLDNICSIYNLKTR EGNVRSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET GQQTTFITGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM CRQTFTHGESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL MTYSHDNII CGITSVSFSKSGRLLLAGYDDFN CNVWDALKADRA GVLAGHDNRVSC LGVTDDGMAVATGSWDSFLKIWN
5640	280	1092	QQGNKKTMLSHNTMMKQKQKQATAIMKEVHGNDVGM DLGKKVS IPRIMLEELSHLSNRGARLFKMRQRSDKYTFENFQYQSRAQI NHSIAMQNGKVDGSNLEGGSQAPLTPPNTPDPRSPNPDNIAP GYSGLPEKIPPEKFNTTAVPKYQSPWEQAI SNDPLEALYPK LFKPEGKAE LPDYRSFN RVATPF GGF EKASRMVKFKVPDFELL LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT VESEDL
5641	27	332	CRHNCNGDVKLLSNQMDKLF AFHLFTFHGLLHFLDGSIQKLIQA EII LSDNSILVLENNFLFKVKSQFIHLIAKKFYISITIVSAS NGESFVLSMIVTG
5642	199	1247	ITPCRMDFLVFLFYLASVLMGLVLICVCSKTHSLKGLARGGAQ IFSCIIPECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTEY TWEVFGYCOELELSLHYLLPYLLGVNLFPPFLTTCGTNPGIIT KANELLFLHVVYEFDEVMEFPKNVRCSTCDLRKPARSKHCSVCNWC VHRFDHHCWVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTF LVHLVMSDLYQETYIDDLGHLHVMOTVFLIQYLF LTFPRIVFM LGFVVVLSFLGGYLLFVLYLAATNQTTNEWYRGDWAWCQRCPL VAVPPSAEPQVHRNIHSHGLRSNLQEI FLPAFPCHERKKQB
5643	1	847	PSGGVRDVETRGPGSRAARGPRVVMHRRGVGAGAIKKKLAEAK YKERGTVLAEDQLAQMSKQLDMFKTNLEEFASKHKQEIRKNPEF RVQFQDMCATIGVDPLASGKGFWSSEMLGVGDFYELGVQIIIEVC LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKLK ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVVLQAEKNGYVTVS EIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPA LF TDLYSQEITABEAREALP
5644	83	1138	PRRMGSWVQLITSVGQQNHGWTVAGQFQEKRFTEEVIEYFQ KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP YVAIEDKDMQQKEQQFREWFLKEFPQIRWKIQESIERLRVIANE IEKVHRGCVIANVVS GSTGILSVIGVMLAPFTAGLSL SITAAGV GLGIASATAGIASSIVENTYTRS AELTASRLTATSTDQLEALRD ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW RYVPINVETLRTRGAPTRIVRKVARNLGKATSGVLVVDVNNL VQDSL DLHKGEKSESABLLRQWAQEELENNELTHIQSLKAG
5645	537	799	VQSVRD LKRLSPTDPPGDSGNRDVTREDPVTGPNLSASSQVPTL YLCLQNSLGHSSVEDARATMELYQISQIRARRGLPRLAVSD
5646	3745	3328	AEQVGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTADP AGKPAPCRVTLTLRLRASIPATKRASFLSSFI KMFFBELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ
5647	288	800	GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH EEDTQRHETYHQGCQCVLVQSRSPWLMRMGILGRGLQEQYQLPY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QRVLPLPIFTPAKMGATKEEREDTPIQLQELLALLETALGGQCVD RQEVAEITKQLPPVVPVSKPGALRRSLSRMSQEAQRG
5648	7	1518	VLSELGRHEALREVGAEWPPPTCSNICSGLQQAGNTDWSLTM APQSLPSSRMAPLGMILLGMLAACFTFCLSHQNLKEFALTNPEK SSTKETRKETKAEELDAEVLEVFHPHTEWQALQPGQAVPAGS HVRNLNLTGEREAKLQYEDKFRNNLKGKRLDINTNTYTSQDLKS ALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVV IETDMQIMVRLINKFNSSSSSLEEKIAALFDLEYVYVHQMNAQD LLSFGGLQVVINGLNSTEPLVKEYAFAFVLGAFFSNPKVQVEAI EGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYACRQFLK LGGLQVLRRLVQEKGEVLAVRVVTLVLDLVTEKMFEEAEELT QEMSPKLLQYRQVHLLPGLWEQGWCEITVHLLALPEHDAREKV LQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLASLELQDGE DEGYFQELGVSNSLLKELR
5649	1172	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL KQLRRKRSIPTSLTDLASLASAPPLSGRSTPKLTSRAAQDLDR MGVMTLPDDLKRRKLLSPVSRREENREDKATIKCETSPSSPR TLRLEKLGHLPALSQEEGKSALEDQGSNPSSSSSSQSLHKGAKR KGIKSSIGRLFGKKEKGRLLIQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTAQEKDRRLKKKHQLLEDARRKGMPPFAQWDGPTVVSWL ELWVGMPAWYVAACRANVKSAGIMSALSDEIQREIGISNALHR LKLRLAIQEMVSLTSPSAPPTSRSTSSGNVWVTHEMETLETSTK TDSEEGSWAQTAYGDMNHEWIGNEWLPGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGINCLKRLNYDRKE LEKRREESQHEIKDVLVWNTDQVHVWVQSIGLRDYAGNLHESGV HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNLLALG TDRKLDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAEITLPA GFRVSTLGTLLQPPPPAPPKIMPEAHSHYLYGHMLSAFRD
5650	1172	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL KQLRRKRSIPTSLTDLASLASAPPLSGRSTPKLTSRAAQDLDR MGVMTLPDDLKRRKLLSPVSRREENREDKATIKCETSPSSPR TLRLEKLGHLPALSQEEGKSALEDQGSNPSSSSSSQSLHKGAKR KGIKSSIGRLFGKKEKGRLLIQLSRDGATGHVLLTDSEFSMQEPM VPAKLGTAQEKDRRLKKKHQLLEDARRKGMPPFAQWDGPTVVSWL ELWVGMPAWYVAACRANVKSAGIMSALSDEIQREIGISNALHR LKLRLAIQEMVSLTSPSAPPTSRSTSSGNVWVTHEMETLETSTK TDSEEGSWAQTAYGDMNHEWIGNEWLPGLPQYRSYFMECLV DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGINCLKRLNYDRKE LEKRREESQHEIKDVLVWNTDQVHVWVQSIGLRDYAGNLHESGV HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNLLALG TDRKLDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAEITLPA GFRVSTLGTLLQPPPPAPPKIMPEAHSHYLYGHMLSAFRD
5651	646	1869	ARQGQRQPGW*EARAKGPASEPRV*EGSGWEGPASP*TPGSTL AWGEGAGIR*ASGLTAAGAASAAA/PPPTRGGPAPAGCGRAPP WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAALSPASPAGP ADP*LPGHSSQSPPRG*RWGRSRSAAPAPAHPEHPAPAGSASASQ QTPGWFGSCCLAQGWQAEPLGAPGAEDG\VPVPPQRGFPLGTLS PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA PALHRAPAAADPGSPLOAPPRAWASPAAGPGLSSSDYCGGLGA GWRAGISPPELLGAAGLSDNWARCPGPGPAB*GGQPGCRTI PASA CMPSPPVEGSLGLSRKGGHGLPSQAR*GWHECRRAHVLPLPRL LGPRGRGTGRPSSPS
5652	735	343	HHKKYQHIHQKFSFCPEPACGKSFNFKKHLKEHMKLHSDTRDYI CEFCARSFRTSSNLVIHRRITGEKPLQCEICGFTCRQKASLW HQRKHAETVAALRFPCFECGRFEKPDVAAHRSKSHPALLLA
5653	66	1401	RGRLQSRGRLLTLGLVLLLLDILGARQHGQRVSHGWGGFLTAPL CFPQPCQPGTRRRRRSLKEATEPQLAMAEFVTLKDVGMDFTL GDWQLGLEQGDTFWDALDNCQDLFLLDPPRPNLTSHPDGSSED LEPLAGGSPEATSPDVTETKNSPLMEDFFEFGFSQEI/SRDVIQ GWLLELQFRRLYRGHLVR*FARRSRKSSEV*YCHQRGKSHGMO

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ES*IKERTQSCVHRFHGRFRHG\DNVSEKTLTPAKSKEYRGEFF SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK PTVHQECEQGFDKASHSGYPKTHGTGYKFFVCNEYGTPFSQSTY LWHQKTHAGEKPKSQSDSHPPSHDTQSGEHQKTHDTSKSYNCN ECGKAFTRIFHLTRHQKIHTRKRYECSKCOATFNLKHLIQHQK THAANV
5654	3	598	TLPLFPGRFRGWRRCGAAVARNSTGGNVSINQRDSVRMSAL NWKPFVYVGLASITABCGTFPIDLTTRFQIQGGTNDKFKKEII YRGMHLALVRIGREGLKALYSG*VGLHAFCHCSLFHMGIDFR PRLHRSQVKSRLCV*KEQIA**/MFSLLISTLISKYIYYAADVL EKLFYYIQVQTDNNKKICLFKNI
5655	2	867	RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP PLSYPSVFFPAVARVLPQRSQDYRAAGMPQLSGGGGGGGGDPCLC ATDEMI PFKDEGDPQ\REKIFAEIVNPEEGDLADIKSSLVNES EII PASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGLYNKG PSYSSYSGYIMPMNMNDPYSNGSLSPPIRPTSNKVPVQPSH AVHPLTPLITYSDEHSPGSHPSHIPSDVNSKQMSRHPAPDI PTFYPLSPGGGGQITPPLGWQQQP
5656	228	1066	PRRVPLPEFASGPGAFFHSGRLQRLTKDSAGCFSQCRSRAM LVLRSGLTALASRTLAPQVCSSFATGPRQYDGTFFYERTYYLK PSNMNAFMENLKNHILRTSYSELVGFWSVEFGGRTNKVFHIWK YDNFPHRAEVRKALANCKEWQEQSIIPNLARIDKQETEITYLIP WSKLQKPPKEGVYELAVFQMKPGGPAWGDAPERAINAHVNLGY TKVVGVFHTEYGELNVRVHLWWNESADSRAAVRHKSHEDPISWG GVRESVNYL\VSQQNM
5657	105	1052	GQRLQSPRVQMPVQPPSKDTEEMEAEAGDSAAEMNGEEEESEER SGSQTESEEEEESEMDDEDYERRRSECVSEMLDLKQFSELKEKL FRERLSQLRLLEEVEGAERAPETTEPLGGQLRSLKIRIQVAGIY KGFCLDVIRNKYECLELQGAQHLESEKLLLYDTLQGELOERIQR LEEDRQSLDLSEWDDKLHARGSSRSWDSLPPSKRKKAPLVSG PYIVYMLQEIDILEDWTAIKKARAASVPQKRKSD\DLDPVHVSQ GDPQSSWHCTQDSRLPPADRRTHRLRVCPARLLWCCWALPLHL ALVWTPPL
5658	2346	3541	TERRVYNPWPEPDPD\CIQEDPWNLFNSIKTLVDNIQRYVEDGK NQLLALLKCTDTLQLRRDAIFCQALVAAVCTFSEQLLAALGY RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLSPATVKEE RTMLEDIWVTLSELNVTFSEFKQLDENYVANTNVFYHIEGSRQA LKVIFYLDSYHFSKLPRLREGGASLRHTALFTKVLENVEGLPS PGSQAEDLQODINAQSLKQVQYRKLRAFYLERSNLPTDAST TAVKIDQLIRPINALDELCLRMKSPVHPKPGAAGSVGAGLIPIS SELCYRLGACQMVCMGTGMQRSTLSVLEQAAILARSHGLLPKC IMQATDIMRKQGPVEILAKNLRVKDQMPQGAFLYRLCQPKMN GDL
5659	2	696	WKRSGEVSPKGEFGAWRGNSGRPKIIGRAAEANEDRTLGRLLP GNERSQPRSPRLRLAPQLKAEAAADKGLAPVPPFSSGHSGPC\ EREGERQGRGRSRRAHLELKPSGLRAGAPTDRGRGGPAEVA AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPVWMEQRKEL FRRLQKWELNTYL
5660	229	853	PVTMAFSELPMLLINLIVSLLGFVATVTLIPAFRGHFTIARL CGQDLNKTSRQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE QRKAFPHHEFVALIGALLAICMI FLGFADDVINLRWRHKL LLP TAASLPLLVMVYFTNFGNTIIVVPKPRPILGLHLDLGR*SYHCC PYGTYFREPFVLVHILLQVFLFCLCVFPDPFW
5661	2	473	LNLYPSPCGGIPKLPGLPREAAALGASFLAEAPLPVTVRSGGL AGMAVTCDPKAFSLICFVTLVFLQLPLASICQN*GTDSCASRGK ADFVDTGPHAPILAMAGGHVELQCQLFPNISAEDEMLRWYRCQP SLAVHMHGMDMDGEQKWYRGRT
5662	2	1318	LRKEGRCRRGSRNGVWAAPAEGLGGRGMLGVRCLLRSVRCSSA PFFKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LHVNDGSSLESLOVVADSGLDSELTFGSSVEVQGLIKSPSKR QNVELKAEKIKVIGNCDKDFPIKYKERHPLYLRQYPHFRCRT NVLGSILRIRSEATAAHSFFKDSGFIHTPIITSNDSEGAGE LFQLEPSGKLVPEENFFNVPAFLTVSGQLHLEVMSGAPTQVFT FGPTFRAENSQSRRLAEFVMIABEISFVDSLQDLMQVIEELFK ATTMVLSKCPEDVELCHKFIAPGQKDRLLHMLKNNFLIISYTE AVEILKQASQNFPTFEWGADLRTEHEKYLKHCNIPVFIYNY PLTLKPFYMRDNEGDFQLEGSVA*HSLGLMILLSIVVIGQP
5663	119	698	PADIGRSTAKTPGPPRSLEMDPRYGMCPKLGASGCPGAERSLL VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQGLYRKVMLENYR NLVFLGIALTKPDLITCLEQKGPWNKRHEMVAKPPVICSHFP QDLWAEQDIKDSFQEAAILKKYKYGHANFQIQKCKSVDECKVH KEHDNKLNQCLIPKTKK
5664	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG GPPPGWDAAPPERGCEIFIGKLPDLFEDELIPLCEKIGKIYEM RMMMDFNNGNRGYAFVFTSNKVEAKNAIKQLNNYEIRNGRLGV CASVDNCRFLVGGIPKTKK
5665	347	702	VVQHLIILLHCERTSPAMITSELVQDSTNETTAHSDAGSELE ETEVKGKRRKRGPRPPSTNKKPRKSPGEKSRIEAGIRGAGRGR ANGHPPQNGEGEPVTLFEVVKLGKSAMQRC
5666	213	540	VSCLPSTCKMITLNNQDPVPFNSSHPDEYKIAALVPYSCIFI GLFVNITALWVFSCTTKRTTVTIYMMNVALVDLIFIMTLFRM FYYAKDEWPFGGEYFCQILGA
5667	1	695	HPLPSASISLGPLSVSLGVSALCVRSALLEAVVPMKRRRARVGSF SGAASSTPPSTRPFGVAIYLVPRMGRSRRAPLTGLARSKGFR VLDACSSEATHVMEETSAAEAVSWQERRMAAAPGCTPPALLD ISWLTESLGAQVPVVECRHRLEVAGPSKGPLSPAWMPAYACOR PTPLTHTHTGLSEALEILAEAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQ
5668	691	894	CSFLFCIPDLFLQFLGRKEEAEVLVGGEWSPSLDGLDPQADPQ VLVRTAIRCAQAQTGIDLSGCTKW
5669	407	1	DSGAPEGLSFLMSTQEGLSMHAHPQAYTFPIYLHARKRRGEIGD ADSRFNDRYAHKSAQLYFLYFVCWIFQDVVYFTIKEKNHFFPK ARGAPTKYSGSPIGSPTTTPTRPSPFNLPAPHLASMLQKL NSQ
5670	3	373	SSECLTMAWIFLLLPLLLILCTVSVASYELAQPSSSVSPSQTAI ITCSGDVLAKKYARWFOQKPGQAPVLVIYKTERPSGIPERFSG STSGTIVTLTISGAQVEDRADYFCYSATDNFLWVF
5671	280	524	KFPFKKTPPHLGMEASITLWQFLQLLLDQKHEHLICWTSNDGE FKLLKAKKVAKLWGLRKNKNTNMNDKLSRALRLFLMT
5672	2	557	FVPATPDGVLPPSRDPAMAKRSSLYIRIVEGKNLPKADITGS SDPYCIVKVDNEPIIRTATVWKTLCFPWGEYQVHLPPTFHAVA FYVMDEDALSRDDVIGKVLTRDTIASHPKGKFLPSHTGLPSP WPPSHSETSPSGSVWSPAQKPFLLSPEAGATPCTPGLCSAACS QAWLLPLP
5673	327	696	ITVADQISHWSAGRIKRNTRIPECIHSSAATTLAGPHTMEGESV KLSSQTLIAGDDEKNQRTITVNPAMHGKAFKVMNELRSKQLLC DVMIVAEDVEIEAHRVVLAAACSPYFCAMFTGDMS
5674	17	984	GGSGMEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLEVKGE AKNSITDSQMDDEVVYITIDIQYIPCYQLFSFYNSSGEVNEQA LKKILSNVKNVVGWYKFRHSDQIMTFRRERLLHKNLQEHFNSQ DLVFLLLTPSIITESCSTHRLHSYKPKGLFHRVPLVVANLG MSEQLGYKTVSGSCMTGFSRAVQTHSSKFEEEDGSLKEVHKIN EMYASLQEEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID MFLKVAVTTTTISM
5675	80	753	EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFGRVSECRPPG KSGVPVSPAGSDGKWEERPGMFSLMACCGWFKRWREPVRKVT LLMVGLDNAGKTATAKGIQGYPEDVAPTGVGSKINLRQKFEV TIFDLGGGIRIRGIWKNYABSYGVIFVVDSSDEERMEETKEAM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SEMLRHPRISGKPIVLANKQDKEGALGEADVIECLSLKLVNE HKCL
5676	2	930	FVSSPPPRPVQPARPGGFLSGRRSLCQVASTPAHVGMRS PV RD LARNDGEESTDRTPLLPGAPRAEAPVCCSARYNLAILAFFG FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACEHSAPIKVH HNQTGKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGGKM LLGFGILGTAVLTFTPTAADLGVGPLIVLRALEGLGEGVTFPA MHAMWSSWAPPLERSKLLSISYAGQLGTVISLPLSGIICYMN WTYVYFFGTIGIFWLLWIWLVSDTPQKHKRISHYEKEYILSS L
5677	1	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA VTAETHPLPLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP GRSLPGLTAATMSSFSALEKKLSELSNSQSVQTLNLWLIHH RKHAGPIVSVHRELKAKSNRKLTFYLANDVIQNSKRKGPEF TREFESVLDAFHVAREADEGCKKPLERLLNIWQERSVYGGEF IQQLKLSMEDSKSPPKATEEKSLKRTFQIQEEDDDYPGSY SPQDPSAGPLLTELIKALQDLENAASGDATVRQKIASLPQEVQ DVSLEKITDKEAERLSKTVDEACLRNRPGETS
5678	3	593	SSSPFSTPSLPLPFYLLGQLRLQLLWGTALHSGAGEAAPCPG GSGRTAAPRTRADPAAQSLMIMNMKNFKRRFSLVPRTEIEB SLAEFTQFNQLHNRNENLQGLPLGRDPPQECSTFSPDTSGER PQQLSPGVQFORRQNRFRSMEVASGALPRQVAGCTHKGVHR AALQPDFDVSKRLSLPMDI
5679	2	623	LNSRVDDFVAVPGAIMDEYVGSAAEWGDEADGGQEDDSGEGE DDAEVQOECLHKFSTRDYIMEPSIFNTLKRYFQAGGSPENVIQ L LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLIKH FDPKADSIFTEGETPAWLEQMIATTTWRDLFYKLAAHPDCL MLNFTVKVGRVLELRRKVFMMVYFWLLVCFI
5680	258	592	RRITSTSEKLQNRNHSHTPLESLIHPQPSYKGFIMFGKKKKIE ISGSPNFEHRVHTGDPQEQKFTGLPQQWHSLLADTANRPKPMV DPSCITPIQLAPMKTIVRGNKPC
5681	45	869	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA RCTRPRQLRKAEAREPPTPGSCPGGTGMDGKKCSVMFLPLVFTL FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAGDDP PASCVFSSQVMNMAFLALVAVLRFIQLKPKVLNPNLNLISGLVA LCLASFGMTLLGNFQLTNDDEIHNVTSLTPGFGTLTCWIAQAL TLKVNINKEGRRVGIPRVILSASITLCVGPLLHPGPKHPPHVC S QGPVGPGLHVL
5682	39	622	PSRSLGLTMRKWRHREVNLPVETQQDAVCAPAPISPGLSAQTL QKIWGTIHCQVCPGAPAWPGSPWHEEMGLLLVPLLLPGSYGL PFYNGFYYSNSANDQNLNGHGXDLLNGVKLVVETPEETLFTYQ GASVILPCRYRYEPALVSPRRVRVKKWKLSENGAPEKDVLAIG LRHRSFGDYQGRVHLRQD
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRADMORA HYKTDWHRYNLRKVASMAPVTAEGFQERVRAQRAVAEESKGS ATYCTVCSKKFASFAYENHLKSRHVELEKAVQAVNRKVVEM NEKNLEKGLGVDSDKDAMNAIQAIKAQPSMSFKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAQKLAHSEDD SEDEEHLDC
5684	195	677	TWCFRGLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QEAVINKLTDASWYTVVFDGDEKTLRRSSLCLKGERHFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE
5685	779	1262	LLLOQPVVHCFLFFPPFRFSHMIIPGPPGPHTTGIPHAIPTPQ VQEQHPHTSDLMHVKPKQEQKEQEPKRPHIKKPLNAFMLYMK EMRANVVAECTLKESAAINQILGRRWHALSREEQAKYELARKE RQLHMQLYPGWSARDNYVSPSSIPVALHS
5686	128	1181	CTWWQVNTITLTDINDNHPTWKDAPYYINLVEMTPPDSVTTTVA VDPDLGENTLVYSIQPPNKFYSLNSTTGKIRTTAMLDRNPD PHEAELMRKIVSVTDCGRPFLKATSSATVFVNLLDLNDNDPTF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QNLFFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVGM RMDFLINSSSGVVVTTTELDREERIAEYQLRVVASDAGTPTKSST STLTIHVLDVNDETPTFFPAVYNVSSEDVPR\GSGWSG*AARN NDVGLNAELSYFITGGNVGDKFSGYRDAVVRTVGLDRETTAA YMLILEAIDNGPVGKRHTGTATVFTVLDVNDKRPILQSSYV
5687	17	917	AAPPAPPDG/PPP/PPPAPPT/PGPAA/APASSCQPRLSAGRAA QGDOGAAAVGHVLPVAVGPVVRVNPGLQTPVPRPELLPGP\SSS LHSDSSYPDAGLSDDEEPDASLPDPPLTVP/ADA/PMPVT SGCRMPSTSASE/AAGGQGACTHAKGSETPPPASPTSEPA LPHLTGGPGMYSSEAKLPNSFSCGLAGTGAGI*GTASAHGTG PPVLPHVCTPSLANPQP\AVGPEASSLPGLVSGIGMSA/SAPIS SSPFAIGSCWLRGIPPPGSGFLCPGRAPGPVPIITHGQEGQGP VLDI
5688	1	420	LTKWDLFGNCRYRLKGTIEHGAMPEQGVVWYS/CLYDSRKLFF *SHMIIRSL*KVIDSLGQLPLRELL*LNVIDRCIILAYV LRVEKTFAITYLKNFTVKVDFSLGELPLISMAAILKWMIMKID DGYIPAVF
5689	1504	3	HELSGKHISMVSGNTCNWHPGGHSPGGGGQGEITSKDRGEIPAL IWA/RKPIGTWTATKPTHRAG*GGAEEYQPPQPCGPRSTSRG GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCQRAFEAGAH GSTARKPAPATPGTRHPTMETREVAQGWAPGPRSQFWDQHPHS PGEHRPSG\SLPACPPRAWPKAGAVASATGTG\POLPGSRGKQ KLPRTRPPLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\ PQTPGGRGSLEWGLPLYLGPHHVVK*RSDDL*PP*GGGGGGH GAPSTPGPGGEAW*LPQQTSRPKPGQAY*GE\GSPGLQCPCSK EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF GQELKGPLDAGRLWPGAPSASSHR*GG*ERARAGAGHRGST*A SSKIEQGRPRPGPTSDALADVEGGAES/GPHPWPLPGTLPNR/P GSPPPA*ASAGRKGTSTLGGGLL
5690	1424	58	PSPFAGVCAAPAPLPLALARRDRRCPSPGAEAAPWQTGGPAID GAWRTSVSALRRGATG/APCSPGAEAAPWQTGGPAIDG\DGELP *VRSEEAPRGCGAEGGGPGSGPVRPAGAGAHAGQGRQDDPEP DGLRHRQHGAASHARHLRQLRPGHHQNRHVRDPQAPPGGPAP GHAAALPERTRGVAEPFAWAHAGSDAWRAGR*SQRT*ERARPRH PTFGGRAGS\GQPGYQPPNPHPGSPSPAAP\GPRGA*GNPQLE KAPRSRDNPSQGLRTRIRRPETPDGFPSPAGSSASASTFRCTS SLSLGPG/PGAHNLDTAPQDR*HGP*GDKRGAPGVAGEDPRPP* GNFVR*LLLMP/GVA*RHGTSPLGLPSLGENGQWDSGNLFGTP KG*SHPAFTKST*SMEAESYWNHPR\DRGRQGVRIINCLRVGE SEMWGPYSAPRPGTVFLSSFLSPASEEH\PEGSSSFNT?FPPAG PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGYNIQMAKRGKKLVLPYTVKGMDFSGILSFIED VAHRMLATGECTPEDLCFSLQVMQ*KTGTESWG*RFYIVEQN*S GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG GVGVYVLESVPLSYS
5692	1193	548	TQAWTRAEKDRKGSVRALRLHLERGPPPT*RGSHPL/QSVPCIQK PSIFSSYP/ILPQSGGEPGPVGEQPPVRRPEQPSGCPASRMPL TSRSVPPGRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQ RLNLPMGATRSNLQPPRKVAVPGPTR*RDQDSQDFSSKPLQS VPGLASTQQLTPADSGPGTGGRDATRAGLPGVETMGNGVD
5693	1258	1330	ALTVPVVRKGTWTAQPHGCSNLVSRARLDLSSRPSQNTPEQAP *QAGPPSSLRPP\SRRR*APEWPKRATGSRRCGLSAPPWPWPA RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSLPRNS PEAIVWRSSRFPLWFLRCCFWVSGFKDPNPVLRFF
5694	3	1338	GSKEPARSLHRRGSGHKSSAGKWSVTLSAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSLSLNPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEKAPKKLEYDSGLKMEPGTSKWRRRPES CDDSSKGGELKKPISLGHGSLKKGKTPFVAVTSPITHAQSA KVAGKPEGKATDKGLAVKNTGLQRSSSDAGRDLSDAKKPPSG IARPSTSGSFGYKKPPATGTATVMQTGGSATLSKIQSSGIPV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
			KPVNGRKTSLDVSNSEAPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLEPTKVASGRRT PAPVNTDREKEKAKAKAVALDSDNISLKSIGSPSTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNNSLDLPSSS DTTQCI
5695	3	1338	GSKEPARSLHRRGSGHKSSAGKWSVTLSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEKAPKKLEYDSGSLKMEPGTSKWRERPES CDDSSKGGELKKPISLGHGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG IARPSTSGSGYKPPATGTATVMQTGGSATLSKIQSSGIPV KPVNGRKTSLDVSNSEAPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLEPTKVASGRRT PAPVNTDREKEKAKAKAVALDSDNISLKSIGSPSTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNNSLDLPSSS DTTQCI
5696	3	1338	GSKEPARSLHRRGSGHKSSAGKWSVTLSTAGALG*KQLHQ*WT QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR SLAESGLSWFSESEKAPKKLEYDSGSLKMEPGTSKWRERPES CDDSSKGGELKKPISLGHGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG IARPSTSGSGYKPPATGTATVMQTGGSATLSKIQSSGIPV KPVNGRKTSLDVSNSEAPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLEPTKVASGRRT PAPVNTDREKEKAKAKAVALDSDNISLKSIGSPSTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNNSLDLPSSS DTTQCI
5697	1147	47	PSEALSPACPSAPAPRRSIISRLFGTSPATEAAPPPPEVPVAA QGPAIVQSVDFVPDDRDLDRSFLEDTTPARDEKKVGAQAAQDS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGFVPSQDITL SSEEEAEVAAPT KGPAPAPQCCEPETKWSSIPASKPRRGTAFT RTAAPPPWGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDPDFESEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPKPLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKKEEEKAKKSKHKKSKDKEEGKEERR RRQRRPPRSRRTAA
5698	2	666	GAEAAEPOEDLPPLSQSSRFQEQQKMNKSLGPVSFKDVAVDFT QEEWQQLDPEQKIT YRDVLENYSNLVSVGYHIIKPDVISKLEQ GEEFPIVEGEFLQSYDVEWQTDLLIERIQEENKPSRQTVFI ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLHLIKLEKTHPGDQAYE FNQ
5699	2	1448	RVRQPPGLWVRRTPVAMQCPAGLSRVPGVAG/DFSLPSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKELA RPS/GRTNAPPQGGKPAKAAAGPAAAGRVAMR\PGHPGLLAS DSQRSSSKSGSWETVPWWS*AQPGWVSGLLLLGDPSGPGSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS*HLDPNT WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN VPILFQNPFGALRSRTEFAGWVPTRHE*DDG*TAAPASGGAP VSTPTWAGTP/LNASLGPTDPQKPGCRPPCALPKPAGPERSA* GGS LGCR/SMLPASSGPPAPGPRRLAAGAHTSASARCPAAAA GWQPRRPGFAGRAALPGPPHPPSS*RELGLPGPGW*TLDELPA HPAHPFGSAPPWALGGWAAARASLPWSPSLCLSFPAVTPVAGL FPPGRG
5700	923	597	NGHKGVWEINIIY*RRSNHKNKSSESHLNQDHSFPPTPNSARS KLHSTGTAKNTGLPLSGAPRQRAVFSGRITICQEFSSCLQCAAYLD E*CSIASSLIKAILRVSVLSE
5701	59	410	IFEKICSDTQEFISPEINPQICSWLIFDKGAK/NHATGKDSLFPN KNSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIRCETVKL LEENTGENLHDTGLGNVFLDMTPKTQPTKQK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5702	3	1517	ETFVDPSCGGIPSDSPHPVITPSRASESSASSDGGPHPVITPSRASESSASSDGLHPVITPSRASESSASSDGLHPVITPSRASESSASSDGGPHPVITPSRASESSASSDGLH P V I T P S R A S E S S A S S D G P H P V I T P S W S P G S D V T L L A E A L V T V T N I E V I N C S I T E I E I T T S S I P G A S D T D L I P T E G V K A S S T S D P P A L P D S T E A K P H I T E V T A S A E T L S T A G T T E S A A P H A T V G T P L P T N S A T E R E V T A P G A T T L S G A L V T V S R N P L E E T S A L S V E T P S Y V K V S G A A P V S I E A G S A V G K T T S F A G S S A S S Y S P S E A A L K N F T P S E T L M D I T T K G P F P T S R D P L P S V P P T T T N S S R G T N S T L A K I T T S A K T T M K P T A T P T T A R T R P T \ A * V Q V K M E V S S S C G * V W L P R K T S L T P E W Q K G * C S S T G N S T P T R L T S R S P Y C V S G E A N G / P S A A R H V P Y A K R G C C P * P G P P P T D C S C V T V L R G T Q K V P M K G S M S K P L T P D V A T G P S L T S T G Y V V W G A S P V P R G V L G L T L A H V L C F S K E K T
5703	14	1117	HHKDSRSQGLPRTQECARPELRPLLCPRALWPVTRLSYRCPWQA PKAGIGTKAKPSESHKLHPGWPSLDRQGEPA TLGTGTGHCSDS R I L R W H P * H T A A R * P R W R L P S S H R W T R H L G V L R V Q D K S * * V S L D P S C R P R F L R T C * * Y G M R S V A S S S N P P G W S G P G A S V F P A R P V S A L P T G P R C W * A P R G R T R Q P C G W P R L S S P H A T A D W G P C P L S P S R G S W E T A P G S * W C P W L * A A R W T G W R T A S G A S A G L G R A A D R P S A W A R R V A G L L P Q Q G L T V R R * H * T A G A P A S V R S S Q G A T R S P A P G G D Q C A C G R G P G S C * H P P F W P V S P S S P V P C P S G R * H L R G P L L S A A R P R A A G W P R H S P H D T Q T P E P
5704	23	562	GDYFDSFVWDDISQAADLVTRLMEVEQDQRTAEAEISHEWI SGNAASDKN I K D G V C A Q I E K N F A R A K W K A V R V T T L M K R L R A P E Q S S T A A A Q S A S A T D T A T P G A A G G A T A A A S G A T S A P E G D A A R A A K S D N V A P R R P * L P P Q P Q M E V P P Q P L M A V S P Q P P M E A S L Q P L M G E S F Q P
5705	23	562	GDYFDSFVWDDISQAADLVTRLMEVEQDQRTAEAEISHEWI SGNAASDKN I K D G V C A Q I E K N F A R A K W K A V R V T T L M K R L R A P E Q S S T A A A Q S A S A T D T A T P G A A G G A T A A A S G A T S A P E G D A A R A A K S D N V A P R R P * L P P Q P Q M E V P P Q P L M A V S P Q P P M E A S L Q P L M G E S F Q P
5706	1161	610	QLGRFXAQDTVAIRKVKVEVFGTGAMRHVVILFTHKED*GGQALD DYVANTDNCSLKDLVRECERRYCAFNWNGSVVEEQRQQAEALLAV I E R L G R E R E G S F H S N D L F D A Q L L Q R T G A G A C Q E D Y R Q Y Q A K V E W Q V E K H K Q E L R E N E S N W A Y K A L L R V K H L M L L H Y E I F V F L L L C S I L F F I I F L F
5707	28	609	GSPAPT PGFRRR PGRGT P S P G T R H H Q G R A E P E P D A P E R A P L R R * M F A I Q P G L A E G G Q F L G D P P P G L C Q P E L Q P D S N S N F M A S A K D A N E N W H G M P G R V E P I L R R S S S E S P S D N Q A F Q A P G S P E E G V R S P P E G A E I P G A E P E K M G G A G T V C S P L E D N G Y A S S S L S I D S R S S S F E P A C G T P R G P G P D P L L P S V A Q A
5708	44	1925	SFSWEETISPCFPKMAEPWWLSFVSLGAAGWPGQPRPYLDLPA QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQAKPKP PRCFPPTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLASALLPPSFSLGAPGAPSP L R V S P A S G G P R K E G R Q G S G G * A G G G G P \ A R T H A D L P C V G F V C S P P L L K * S D S P V K Q L P A \ S G Q G S G A G M P P V G S S D I L R P R P T S V S G T G R A A G * C S W Q P A A C C T P R S Q * W A V A R S P S R C S R W * R Q S G R * R Q * S S R R R R G P * A A G R S T P A V P * P C S * G G A G R R A Y A C R T G W G Y A P S R * L E P S G P T S G S A L * T W A S H T G A * * S R L C G T A G T G P L C S Q S S R S * A G * R C C C T A A S P C G G S G P S H P G S P A H C L S W S G G R T Q P R A P S A H G R G R A M G S R C V C T C T G L P C P G I P L S G A S P G G S G E T G A G R S H T L K A A R S R L S P R P G S G S R G S Y * S H N D N W G T W P A P P S A G H L L V G G * N S Q R T S S D H * Y T G T R R P W A G P G T R C S T A P S R A A P P V S R C R P P P P P P P R P R P R L P A A A S / S G G A S G S P A A S C S C S C R A P A K P A S S / G E A P A P P P R P E P P P P P A R R P
5709	2	2031	ITLCLPLQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG LHQIVVRNGAUVVMRAGMGRCRCWGVMAPPAPR/NALSFLVNDCE LIHNVCMAAVFVDRAGENKLGGLDYMYSAGNGGGGPRKGIPE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LEQYDPELADSSGRVREKRSADMWRLGCLWVEFNGPLPRAA ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLQNCRAPGGFI SNRFVETNLFLEEIQIKEPAEKQKFFQELS KSLDAFEDFCRHK VLPQLLTAFEFGNAGAVVLTPLFKVKGKFLSAEYQQKIIPVVV MFSSTDRAIRIRLLQQMEQFIQYLDEPTVTNTQIFPHVHGLD NPAIREQTVKSMILLAPKLNANLNVELMKHFARLQAKDEQGP RCNTTVCGLKIGSYLSASTRHRVLTSAFSRATRDPPAFSRVAG LGFAATHNLYSMNDCAQKILPVLVCLGLTVDPBKSVRDQAFKAIRS FLSKLESVSEDPTQLEEVKDVHAASSPGMGGAASWAGWAVTG VSSLTSKLIRSHPTTAPTETNIPQRPPTPEGVPAPATPVPATPT TSGHWETQEDKDTAEDSSATDRWDEDDWGSLEQEAESVLAQD DWSTGGQVSRASQVS\TPTTNPNNPQSPTGAAGK\RGLLGTGLA GAKLPGATS*RYTAGQRV
5710	1	562	IPGSTISCEVELMARMAKTIDSFTQNTRLVVIDGLDACEQDK VLQMLDTRVRLFSKGPPIAIFASDPHI IKAQNQLNSVPSGFK \LNGHDMYRNIVHLPVFLNSRGL/RQ/LOENFS*LQQQMETFHA QILQGYRKMLT EEFHRTALGR*QNLVARQPSIDG*DAIGFELYV CIAIQFNTNKDDAT
5711	1526	1130	RRHPFQWTTVTQEAFSHHDVAFTSTPVLFFYDPSAQPFIVKSESS SQIAKAVLSQQRPSLFFHECAFHFFS*SLQRHTINLDQGI*LLM LSEBRQHLFESS/IWTTPHNLK*/FEIHEHLSGHEGHWTLLFFLL QIL
5712	3	1391	GRKLFQSLDISERLKLTLTDCVDDTLVLAEHBGCLDIKELP ETVIDLNLKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPPTKPA SLFSSSLRCADLTLPEDISQLCKDINNLYLAERSIEEVYVLWC AGGDLEKELVNKEIIRSKPPICTLPNFLPEDGESFGQGRDRSS/ TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN NELSAAATLPLIIREKDT EYQLNRIILFDRLLKAYPYKKNQIW EARVDIPPLMRGLTWAALLGVEGAIAHAKYDAIDKDTPIPTDRQI EVDIPRCHQYDELLSSPEGHAKFRVLKAWVVSHPDLVYWGGLD SLCAPFLYLNNFNEALVYACMSAFIPKYLYNFFLKDNNSHVIQ EY LTVFSQMIAPHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFL HKIFHLW\DTLLLGEFLFPILYWE
5713	634	284	PVCAPVVDWRPVLPREQEGGQL*AKLPRDFRR*FQILGPMEGH TACRCSRRGAQVQHLPREDIRAAE*DPLHREVWPGLP TSSATSP *RAVLTPCSHLGSADAASSHWLGCVSFH
5714	212	613	WGLGLGPTMSSSLGGGSGDAGGSSSSSTNGSGGSGSSGPKAGAAD KSAVVAAAAPASVADDTPPPERNRKSGII SEPLNKS LRRSRPLS HYSSFGSGSGSGGSGMMGESADKATAAAAAASLLANGHDLAAA MA
5715	131	1979	ESASQQRKSKCLITLTKLELSGSAPKKT SARPGSSLWLPHPSQE QTPPASKLQGGGGLQTRGWLHPVPVTAASPLPRWCLFGAVAK/ GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSPMVENN DSTCHEHHEGILAAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS PRPPGS/SDLGPRPQMHLRAFFAAHGGPVNTPHGGEKFTFMS QIRRKETKPL*RTKPAG\NNYQNSIPVSQSPQLTVDLLPSAGR TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL YPKTPKQRRWRRL/LLGPSQ*GSRQSTC*EV\GALGEPVRI L*PDLSCILSNGSKHRRREGLSFPRSLGPGRRGPAQLQSLGCSPT PKNTACHSSGHVALQAGHDSARDVSGSHVALQAGHDSTQDVGRF VWRWIFLE*LGLSRETGOATRRLVWISPGRAAAACVACAQALE EGPLRLPGQDRGAQPCSHCPGRAAGQBPBGAGAPCRE/GG*DP TGLT/GVPGTDPRKGRKPGQSGQETQGTPTVWSGPESPLQPKP*E RQE/VGAGASSGVGLSRGRAGGPSSAW EVAAMLLLLRHGSHSEL TDLTAQTSQH
5716	1711	1370	RVFSLLCEGPHGYCQGA VCREACAASPLDLSAAEFHRLCEHTD *LPK*GPGYIQHFHCDNSNLCILYNISFNLSYSF*GVARYAC* RCPLVL*SGFFTIIIVGGYS CCMPLKT
5717	44	1489	LPTEALRESEWVSEYKCGKPRGLVPEGESTSPLPSSVDTEDSL BGPGALVLESDLLLGDLLEFEFEFEFEFEEDGNSDQLMGFERDSE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GDSLGRPGLPYGLSDDES GGRALSAESEVEEPARGPGGEARGE RPGPACQLCGGPTGEGPCCGAGGPGGGLLPRLLYSCRLCTFV SHYSSHLKRHMQTHSGEKPFRCGRCPYASQVLNLRHTRTHGT EKPYRCPHCPFACSSGLNLRHQRTHAGPPTPPCPTCGFRCTP RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPVPGGASFLPDCG Q\CGVKGASAGLDQNHQS/SLPFWTCRGCGQEELEEGESRLG AAMCGRCMRGEAGGASGGPQGPSDKGFACSLCPFATHYPNHLA RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGKPKYCPL CPYACGNLANLKRHGRHSGDKPFRCCLNYSCNQSMNLIRHM
5718	120	284	VAHALSLPAESYGNVSMTHPQLPPTQLAWDLCTCLPLSYNFT S**STADPLHL
5719	48	428	ELNNGPFPQMLCNGGNLAVTGSWADRSPLHEAASQGRLLALRTL LSQYVNAVTLDHVTPLEHACLDGHVACARTLLEAGANVNAIT IDGVTPLFNACSQGPSCAELLLEYGAKAQP\ESCLPSP
5720	1	1051	LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK \RCT\YYE\TCGGTYGLQMWVSVDQVAKVVAL\RKKQQ\LAI GPCK\SLPN\SPSH\SAVSAASIPARAPINQGE/SGGSAFSD Y\SSSVPTSPISQRELRIETIAASSTPTPIRKQSKRRSNIFTS RKGADP\DREKKAAGCKVDSIGSGRAIPKQKILLKRSKSLNK EWKKKYVTLCDNGLLTYHPSLHDYMQNIHKEIDLRTTVKVP KRLPRATPATPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS LHSEPLSSAWAGPRPEGLHQRSCSVSSADQWSEATSLPPGM QHPASG
5721	97	492	RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA VFYAIAGGLFLERAYYYFAAHHTGIDTTRVGIILSRGTAASI SFMFSYILLTMCRNLITFLRETFLNRYVPPDAAVDFHRLIASTA
5722	88	1043	VALDVLGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP GSLGVSHAAAPPARPQGAASPHRGRRHGGGAGLPPPRSPRFP QESVPASTSTARGPRRVSRRLPPQHGPGRGRRRRPGAGVGAPRR GRARGQAGLLGRQQGGRGAERERAAQARRGRPPGPEPDQSCG GRPRRAAAPGRAPADPQPPAPRPAPADVRFPADAPAPAPAPA PPPPHLAGALTAGSGEERQSOPRAETLRLGRGAPLP\PRERGG RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT KSSTREIPEMI
5723	88	1043	VALDVLGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP GSLGVSHAAAPPARPQGAASPHRGRRHGGGAGLPPPRSPRFP QESVPASTSTARGPRRVSRRLPPQHGPGRGRRRRPGAGVGAPRR GRARGQAGLLGRQQGGRGAERERAAQARRGRPPGPEPDQSCG GRPRRAAAPGRAPADPQPPAPRPAPADVRFPADAPAPAPAPA PPPPHLAGALTAGSGEERQSOPRAETLRLGRGAPLP\PRERGG RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT KSSTREIPEMI
5724	3	1841	FTNEAPPAPLPDASAPLSPHRRAKSLDRRSTEPSVTPDLLNFK KGWLTQYEDGQWKXHFALADQSLRYRDSVABEADLDGBID LSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRTBKQAEELGEP DPEQKRSRARE\RRREGRSKTFDWAEPRIQALAQERVGGVGP ADTH\DPWRPEAEHGELEERARRRERERRKRFGLMDATDGPTE DAALRMEVDRSPGLPMSDLKTHNVHVEIEQRWQHVTETPLREEK QVPIAPVHLSSDGGDRSLSTHETLSLEKELEQSQKEASDLLEQ NRLQDQLRVALGREQSAREGYVLQATCERGFAMEETHQKKIE DLQRQHORELEKLRKDRLLAEETAATISAIEMKNAREEME RELEKSQRSQISSVNSDVEALRRQYLEELQSVQRELEVLSQYS QKCLENAHLAQALEAERQALRQCQRENQELNAHNQELNNRLAAE ITRLRILLTGDDGGEATGSPLAGKDAYELEVPSSGARPCLTQLC TQEPQGSAAWPLSYRVVGGTDLRQESQGPGRSKSPGEGEEQ
5725	3	1049	VNGHSEETSQSPNRTEPHSDSCSVDLGISKSTEDLSPOKSGPVG SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLOPLK/FTSAVDG KNIVRSKAATLLYDQPLQVFTGSSSSSDLSGTAKAIFKFDNNHN PE/GAKYNKRPHKWAHNLHLYMVLHSIISNTVAV\RSQRHFVA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LQTKSPNRPQCFSSSAPS/VDQRAQ/INQSYAKHSANMNFNSHN NVRANTAYHLHQLRGLPARHGEMWAISPNDRLIPAVTRSTIQRQS SVSSASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMMPG SQRPLSARTYSIDGPNASRPQARSINEIPERTMSVSDFNYSR TSP
5726	2	486	SRSLSMWNSGLPASSHSSKLPVTVGFGSCVKRLRLHGRPLGAP TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG QSGPGSGEGPPLSSPSQPLPADLPGLATLPDVGLELEVRPLAVT GLIFHLGQARTPPYLQVTEKQVLLRADDG
5727	21	221	RPILILKETRRLPWTGYAEVINAGKSTHNEQASCEVLTVKKK AGAVTSTPNRNSKRRSSLPNGE
5728	2	877	GTRNGQFEPRRGRAWEGSAGGLRAPGAAAGGPGVQPRGSG/LPG NAIRAGVNPGRGPASPFWDLSPWDLWPPPTDHAPGAPDPFAVE GR/PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ GGPAGAGGDAG/LPGRCPSPAPWRAGSRPAASCPDWIPGPQGLWL HRNPTS/GPPSQIGEGAEQGDGVDAPQIQCKN/GAEDPPAED EPPQVPEAGEEDAVPABEGPGGT PETQADQVREPERAHLAEGGA KGSRRLLADPQDLFAGQMSLAPFPFVAVIRSNK
5729	1	1525	AGGAREVLTLLQLGHFAGFVGAHWNQDAAALGRATDSKEPPGEL CPDVLYRTGRTLHGQETYPRLILMDLKGSLSSKEGGLYRDK QLDAAIAWQGLTTHKEELYPKNPYLQDFLSAEGLSSDGVVWRV KSI PNGKSSPLPTATT PKPLIPTASIRVWSDFLRVHLHPRSI CMIQKYNHDGEAGRLAFAFGGESVLKEPKYQEELEDRLHFYVEE CDYLQGFQILCDLHDGFSVGAKAAELLQDEYSGRGIITWGLLP GPYHRGEAQRNIYRLNTAFGLVHLTAHSSLVCPLSLGGSLGLR PEPPVSFPYLHYDATLFFHCSAILATALDTVTCS\YRLCSSPVS MVHL\ADMLSFCGKKVVTAGAIIFFLAPGQSLPDSLMQFGGAT PWTPLSACGEPSTRCFAQSVVLRGIDRACHTSQLTPTGTPPPSA LHACTTGEEILAQYLQQQPGVMSSSHLLLTPCRVAAPPYPHLFS SCSPPGMVLGDSPKGAIVESVPVFG
5730	1258	1713	KKFQAPARETCVEQKTVYPMERLLANQQVFHISCFRCSYCNK LSLGTYSALHGRICYCKPHFNQLFKSKGNYDEGFGRPHKDLWAT KIETEGFWERPRNFENQGRPLKSPGGEDCPSC*GGCPGSNY*AQ GSSSREKGGQASWNPKLRLVA
5731	122	443	RSHRGELIPKDS CYMRKPPRRPKRRQG/CALPQGCCLTFKDVAI EFSLEENKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK KPGRGRGKQRRQEWFFLRVY
5732	226	772	PPSRSCQSPRRKSRRAHVTVTLVCGFTSFSFSLFLYLCGCCLRF PERTCSQLQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N LLGTKEQAHRIALNLEQGRGKDQPGRLKKVQGIWYLDENLA QVSTNLLDFEVTALHTVYBETCREAQELSFPVVGSQLVGLVPLK ALLDAA
5733	1	460	PALQEVNANALAWGQYENDARTLFEFTSGVNDTESPIIYRDES MRTACSPDGLCSDGNGLKCPFTSRDFMKFRLGGFEAIKSAYM AQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYM\AS FDEI\VP\EFIGKMDEVLSRDPM
5734	3	968	RCNSPESLTSLLVLLTTANNLFVLI PAYSKNRAYAIFFI VFTVI GSLFLMNLTAI IYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS SMVGEGGAFPPQAVGVKPNLLQVLQVQLDSSHKQAMMEKVRSY GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYFYDYLGNLIALANLVSI CVFLVLDADVLPAERDDFILGILNC VFIVYLLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS TL\CTDCHTQAGGRWW/RLLSLWDMTRMLNLIVFRFLRIIP SMKPMVAVVASTVLGL
5735	2	540	FFTPCVARAFNFPDQATVKKAAYS LPRVGGGTSCGLPQARRISL ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNO YPVFPWVLTNYESELDTLPQGNFRDLSKPIGALNP KRAVFYAE RYETWBDQSPPHYNTHYSTATSLSWLVIRVISIFIELACLWY LKILT
5736	1	382	GTRPSTKSKSGYSPQQVAVIHCKGHQKENTAVAHNSQKADSAQV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TARLSVTPPNLLPTVSFPQDLDPNPNVYSTTEKLASDLRANKN QES**ILPDGIPIP*T*TSYLQSTTHLRRAKLPQLLR
5737	290	1041	KACLHLLSSFLTNSFLNPLLPDSLYSVEARSQRANLGPCCRKR LQTLMLAAGFYSSHKDPSLSAKEKHTDYHNEARGPWPGWVG* RTADGSCGRGPDGAHHPGPKSSSWRASRLPLGLGGSHHLDAYVG RDLECGTPAPLQLEIPPQPRGHPAPIPTGQAGPRDSGPGASP*V ETRPLTDGRR*PGVRPVGWTPAHAGTTLRPRGAVEPSVSACGKW APSPTSQGCCEGRCDVAPKHAWRTPLCSEQ
5738	8	460	DTLSLNLCTLPETLPMTPSF*LSFL*FPGLARAKSIPTKTSYNEV VTLWYRPPDILLGSTDYSTQIDMW*GQVEVWQGPCGKGGGLVTT ATQPAAPLFTVPSLPRGVGCIFYEMATGRPLFPSTVEEQLHFI FRILSEEAWALCAVETHR
5739	1	1222	SFQRRGIRWNVHTLHPHPRAVWAGIGRGHGS*ALLGRARAPALC FPTLLEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEV SAEVDGVPVGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKI LQCCGFYQLCGVHQEDVIYALPLHYMSGSLGIVGCMGIGATV VLKSKFSAGQFWECCQHRVTVFQYIGELCRYLVNQPPSKAERG HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY TGQRGAVGRASWLYKHIFPFSLLIRYDVTGEPIRDPOGHCMATS PGEPGLLVAPVSQQSPFLGYAGGPPELAQGLKLDVFRPGDVFFN TRDLLVCDDQGLRFRHRTGDPFRWKGENVATTEVAEVFEALDF LQEVNVYGVTV
5740	265	231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A YVYERVYN*NISRMVHALEQKRHPAGLSSSMALQLNPLCLGMLMA LQSELHLKYDEETQSWVSGSACGGYP
5741	1	650	PRKTMRRGVMLTLLQQSAMTLPWLWIGKPGDRPPLCGAIPASGD YVARPGDKVAARVKAVDGDEQWILAEEVVSYSYSHATNKYEVDIDE EGKERHTLSRRRVIPLPQWKANPRTDPEALFQKEQLVLALYPQT TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPPLNVAQRYV ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPLKKK
5742	2	362	TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTETVQDLDAG TYVNIIPDRSGDVTLVIGAVRGHVEIVRALLQKYADIDIRGQDNK TALYWAWEKGNATMVRDILQCNPDEICTKG
5743	2	415	GKTPEGIDAIEEIEIDLEETEREISPOENGLEEVKPLGEMQTDL KATGREISPREKTPEVIDATEEIDKLEETGRREISPEENGPEE VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPQE
5744	3	703	TRRTTTTSPTTTQMTTTPAALPTTVVTTTPTDITGTFLQMTTIA VFTTANTCLSLTPSTLPEBATGLLTPEPSKEGPILTAESETVLP SDSWSSAESTSADTVLLTSKESKVNDLPSTSHVSMWKTSDSVSS PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMI IAP SLGFVLFAFLFVAFLLRGKLMETCYCSQKHTRLDYIGDSKNVLDV QHGREDEDGLFTL
5745	1400	599	GKSFRVNLMKHSKKTYSDFQDELEDYIKVQKARGLEPKTCFRKM KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPSCNIPQT VENRLPQWLPAHDSRLRLDSLSCQFTRDCFSEKPVPLNFNQOE YICSGHGEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPKEGR EKSEERSKHKKKSCEEIDLDKHKSIIQRKKTEVEIETVHVSTE KLKNRKEKSRDVVSKEERKRTKKKKEQGQERTEEEMLDQSI LGF
5746	3	821	SFASGRLLTPSSPAFDGELDLQRYSNPGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRRFNSILALHLRTHQPERPRSPAARLLE LEERALLREARLGRARSSGGMQATPATEGLARPOAPSSSAFRCP YCKGKFR TSAERERHLHLRHPWKGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPPQPPQPPQPEPRSVPPQPEPEPQPER EATPTPAPAAPPEPPAPPEFRCCVCGQSFTQSWFLKGHMRKHA SFDHACPV
5747	2	1328	DRHVETLCIHFLGPSTGSTAKTGGRNWLKTNCLYGNTCRFVHG PPRGKGYSSNYRRSPERPTGDLRERIKNRQDVTETPQKRNT ESSSPVRKESSRGRHREKEDIKITKERTPESEENVEWETNRDD

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SDNGDINYDYVHLSLEMKRQKIQRELMKLEQENMEKREETIIK KEVSPVVRSKLSPPSLRKSSKSPKRKSSPKSSSASKKDRKTS AVSSPLDQQRNSKTNQSKKKGPRTSPPPPIPEDIALGKKYKE KYKVKDRIEKTDRGKDRGRDFERQREKRDKPRSTSPAGQHHS ISSRHSSSSSQSGSSIQRHSPPRRKRTSPSPYQRTLTPLRRS ASPYPHSLSSPQRKQSPPRHSPMREKGRHDHERTSQSHDRRH ERRDTRGKRDEKDSREEREYEQDQSSSRDHRDDREPRDGRDR RE
5748	934	473	SEGPQVIFYKGLAPTLIAIFPYAGLQFSCYSSSLKHLVKWAI PAEG KKNENLQNLGSGAGVISKLTLYPLDLFKRLQVGGFEHARAA FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLKKAALSTGFM FFSYEFFCNVFMNRTASQR
5749	552	1	GFPVDPVRVGSSTLSLAERP KGMIRSGSFRDPTDDVHGSVLSLAS SASSTYSSAEERMQSEQIRKLRRLESSQEKVATLTSQLSANAN LVAAFEQSLVNMTSRLRLHAETAEEKDTELLDLRETIDFLKKN SEAQAVIQGALNASETTPKELRIKRONSSDSISSLSITSHSSI GSSKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLNLFVDDSGRYLAIQF HLEWAYVFLYYEYRKAKDQLDIADISQLQIDLTGALGKRTF QENYVAQLILDVRREGDVLNCEFTPAPTQBEHLTKNLELNDT ILNDIKLADCEQFQMPDLCAEEIAIILGICTNFQKNPVHTLTE VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRQ TQALADQPEDKTTSVLERLKI FYCCQVPPHWAIRQLASLLFEL GCTSSALQIFEXLEMME
5751	3	751	SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA FAAGETPLVLRSSAHWWLAARARSGETGYVPPAYLRRLQGLEQ DVLQAIIDRAIEAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS RRGPSASSVAVMTSSTSDHLDAAAARQPNGVCRAGFERQHSLS SSEHLGADGGLFQIPLPSSQIPQPRRAAPTTPPPPVKRRDRREA LMASGSGGHNTMPSSGNSVSSGSSVSSCI
5752	3	471	GPVCGVGLSVAWAGPWRGPVHVSVGGGGRALHGAELPCLSGAAT VEREMELRHKNEMLRVETEARARAKAERENADIIREQIRLKASE HRQTVLESIRTAGTLFGEGRFAFVTDKVTATVNIFIKQGWQV AERQHVGSASWSPRSCPCRLCTAL
5753	34	483	DDXSAIPGGVQAPFGAVRNITYTPTGHRIRKLDQIQSGGNYVAG GQEAFFKKNLYLDIGEIKKRPMVEVNTVKPVIHSRINVSARFRK PLQEPCTIFLIANGDLINPASRLIIPKRTLNQWDHVLQMVTEKI TLRSGAVHRLYTLLEGRLV
5754	14	331	TLVHVVEPAGEHAEAIASREQEVLQGWKELLSACEDARLHVST ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLFPSPW WPTPATPSPLTAPFSME
5755	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI WMEKRHRGPGGLAPGQLYTPARCWRKRRRLHPPDPKLRLLLEIK PEVELPLKKGFTSESTTLEALLRGEVGEKKVDAREEESIQEIQ RVLENDENVEEGNEEDLEEDI PKRKNRTRGRARGSAGRRRRD AASQEDHDKPYVCDICGKRYKNRPGLSYHYATHLASEEGDEAQ DQETRSPPNHRNENHRPQKGPDTGTVIPNNYCDPCLGGSNMNKK GRPEELVSCADCGRSAHLGGEGRKEKEAAA
5756	3	621	SSKLQALFAHPLYNVPEEPPLIGAEDSLLASQEAALRYRRKVAR WNRHRKMYREQMNLTSLDPPQLRLLEASWVQFHLGINRHGLYSR SSPVVSKLLQDMRHFTISADYSQDEKALLGACDCTQIVKPSGV HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFYFIDFQRHNAEI AAFLDRILDFFRRVPPTVGRIVNVTKIIL
5757	3	473	YKDALLPDNHRQVVFENGTLKLTVDQKGMDEGEYLCSVLTIQPO LSISQSVHVAVKVPPLIQPFEPFPAISIGQLLYIPCVVSSGDMPI RITWRKDGQVVISGSGVTIESKEFMSSLISSVSLKHNGNYTCI ASNAATVSRERQLIVRVPFV
5758	1	474	FRRGAGAERGEHREGGAAGMGEPKVHRVRRFFNYVPSGIRCV YNNQSNRLAVSRDTGTVEIYNLSANYFQEKFFPGHESRATEALC WAEQQLRFSAGLNGEIMEYDLQALNIKYAMDAFGGPIWSMAASP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SGSQLLVGCEDGSKLQITPDKIPV
5759	2	1240	GNAAFAGQGVVYETFFHMSDLPSYTTNGTVHVVNNQIGFTTDP MARSSPYPTDVARVNNAPIFHVNADDPRAVIYVCSVAEWRNTF NKDVGADLVYRRRGHNEMDBPMFTQPLMYKQIHRQVPVLKKYA DKLIAEGTVTLQEFEEIAYDRICEEAYGRSKDKILHIKHWL DSPWPGFFNVDPGPKSMTCPATGIPEDMLTHIGSVASSVPLEDF KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIVHVL NGQDVERGTFSHRHVHLHDQEVDRRTCPMNLHWPDAQPYTCN SSLSEYGVLFELGYAMASPNALVLEAQFGDFHNTAQCIIDQF ISTGQAKWVRHNGIVLLPHGMEGMGPEHSSARPERFLQMSNDD SDAYPAFTKDFEVSQ
5760	1	1221	VRDITSDLSLSWTVPEGQFDHFLVQFKNGDGQPKAVRVPGHED GVTISGLEPDHKKMNLGYGFGGQVRGVPVSAVGLTAPGKDEEMA PASTEPTPEPPIKRLEELTVTDATPDSLSLSWTVPEGQFDHFL LVQYKNGDGQPKATRVPGHEDRVTVISGLEPDNKKMNLGYGFGG QVRGVPVSAIGVTAEEETPTPTPEPSMEAPPEPPELLGELTVTG SSPDSLSLSWTVPGQRFDSFTVQYKDRDGRPVVRVGGEESEVT VGGLEPGRKYMHLVGLHEGRRVGPVSTVGVTAPQEDVDETPSP TEPGTEAPEPPEPPELLGELTVTGSSPDSLSLSWTVPGQRFDSFT VQYKDRDGRPQAVRVGQESKVTVRGLEPGRKYMHLVGLHEGR RLGPVSAIGVT
5761	3	1275	SCDMAEAAALVWIRGFGFGCKAVRCASGRCTVRDFIHRHCQDN VPVENFFVKCNGALINTSDTVQHGAIVSLEPRLCGGKGGFGSML RALGAQIEKTTNREACRDLSGRRRLRDVNHKAMAEWVKQAERE AEKEQKRLERLQRKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK GMQAASSKMVSAEISENRKRQWPTKSQTDREGASAGKRRCFWLG EGLETAEGSNSSESDDDSEEAPSTSGMGFHPKIGSNGVMAAK FPSGSQARVVNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK EHMESRMVTETEETQEKKAESKEPIEEPTGAGLNKDKETEERT DGERVAEVAPEERENVAVAKLQESQFGNAVIDKETIDLLAFTSV AELEKLGLEKLCCELMLGLKCGGTLQ
5762	2	344	GSTGQTPLHSQGGGGSGGGRRTPRGMPKEKYEPDPDRMYTI MSSEBAANGKKSHWAELEISGKVRSLASLWSLTHLTALHLSDN SLSRIPSDIAKLHNLVYLDLSSNKIR
5763	3	429	LDKDTGLIMLIARLDYELIQRTLTIIARDGGGEETTGVRVINV LDVNDNVPTFKDAYVGALENEPSVTQLVRLRATDEDSPPNNQ ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYBQISNGLIYL TVMAMDAGN
5764	19	441	VCARACGEMRQLLRPIDRQRYDENEDLSVVEITVSVRGFSLBEK LRSQLYQGDFFVHAMEGKDFNYEYVQREALRVPLIFREKDLGLIK MPDPDFTVRDVKLLVGSRRLLVDVMDVNTQKGTSMMSQFVRYE TPEAQDKL
5765	3	825	QKILRLNNSHQPTSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETS KSKVKRSKTSKDANKSLPSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGSGGNPNSTSTSTS AATAGAGSCGSKKEKPGKSQSSRGAKRDKDAGKSRKDKHDLQ GHQNGSGSQAPSGGHLVGFAGKSNGGGASPFHCGGTSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEEESHRIKKLKTEKVDPLF TVPAPPPHV
5766	1608	663	SGLFSVDPASSQAMELSDVTLEIGVGNEMVAVGVVLLILALVL AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTLPHPSGNDKAEAGEGRGDSTGEAGAGGGVEPSLEHLLD IQGLPKRQAGAGSSPEAPLRSSESTCLPSPGLITVRLKPLND TEELAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL RSLNITDNCVICHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVVVFVLLGVVWYFRINRYQFTAPATVSLVGVTVFVSFLV FGMYGR
5767	2	892	NFRATPRPPTRPELRTGTGVILWYLDWRALMKRKRKMKANIKLVG SGFPLPSSDLDDSLTEEIDEKIGFRNDANFDWQNVADFRDAGGS LTEVKEVEEERDPQSPEFEIEEEEMLSVPIPSRRENELPDFP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			HIDEFTLNSTPSRSAYDEPHLLVNIEKQKLEKRRLDIEAER LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKLRLQIV NSEKPSLRNELGQGEKSMQPDIEKLEKLERERLQLEKDRLO FLKFSEKLEKIEKERLQVEKDRLEKQEGHLO
5768	3	476	SSRSRLSVSVSPPPGIVELGPPFAWEFCRSLGSVTSQRAGPA AMVAKDYPFYLTVKRANCSLELPPASGPAKDAEPPSNKRVKPL SRVTSANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP WSRNAAPSSTKRRDSKLSWSETFDVC
5769	38	667	TKTKKGKVEKATDQSVKFAEHCPQLQYVGMGCSVTSKGVHIL TKLRNLSSLDLRHITELDNETAMEIVKRCNKLISLNLCLNWIIN DRCVEVIAKEGQNLKELYLVSKITDYALIAIGRYSMTIETVDV GWCKEITDQATLIAQSSKSLRYLGLMRCDKNEVTVQVLVQY PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
5770	1	484	DSRRYDVTRKWSFLLLEHSLIAKVRCLPQVQLDPLPTTLTLA FASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFQRAGVNF AKGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVPSSVRFT WEQAFRLRWLPSLSPDCINVVVTGKDRLLTA
5771	168	741	GLLPSACLRRARSWEASEGPPSSRACSNQSDTFEACYSGTSTPS FHGSHCSGSDHSSGLGLEQLQDYMVTLRSKLGPLEIQFAMLLRE YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF LEGVIGREGGILTDSFGRIKRSMSSTSASAVRSYDGAQRPEAQ AFHRLADITHDIE
5772	148	383	EFNLALVSPSHPIKAEDDQPLFGVLLSLSGGLFRSNLLTQDNG ILTFSNLVTCSAIYHLPVFPEREPCGSMRDLRA
5773	2	723	PRVRSKHNFCEMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE KIPLSQEEITLQGHAFBARIYAEDPSNNFMPVAGPLVHLSTPRA DPSTRIETGVRQGEDEVVHYDPMIAKLVVMAADRQAALTCLRYS LROYNIVGLHTNIDFLNLSGHPEFEAGNVHTDFIPQHHKQLLL SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHQDQSPFSSSSG RRLNISYTRNMTLKDGKNSK
5774	2	592	FVEENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST VTECBVHILHGHRLNLTGQLNPNHLLQLYSCSLDGTIKLWDYI DGILIKTFIVGCKLHALFTLAQARDSVFVIVNKEKPDIFQLVSV KLPKSSSQEVEAKELSFVLDYINQSPKCIAGNEGVIYVAAREF YLSVYFFKKETTSRVTLSSS
5775	3	538	SSGCCDPAAPSSLAEEATMPVSKCPKKSSELWKGWDRKAQRNGL RSQYVAVNGDYVVGWKNVKGKGTQVWKKKGAIYEGDNKFGK RDGYGTLSLPDQQTGKCRVYSGWVKDKKSGYGIQFFGPKYY EGDWCGSQRSQSGWGRMYYSNGDIYEGQWENDKPNEGMRLRLSQNP RP
5776	2	484	RLPQDCVQCNLSESLGTLCPSKGLLFVPPIDIRRTVELRLGGNF IIHISRQDFANMTGLVDLTLSRNTISHIQPFSLDLESRLSLHL DSNRLPSLGEDTLRGLVNLQHLIVNNQLGGIADEAFEDFLTL EDLDLSYNNLHGPVGLRGDAWVQFSTS
5777	2	949	QDPEPGQDLFQPEREVDPSWGRGREPRLGKLRQNDHLSVLKQ VKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSRRPWDRSLENV YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKGKPGIGFRKEKR NLPLPLSLPPPLPSSPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRDWYAQTKLGLTRTLSEENVYEDILDPMKENP YEDIELHGRCLGKKCVLNFASPTSSIPDTLTQSLSKPAFFRQ NSERRNV
5778	1	1210	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEGGEPAGVAEPPGS GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSP WAPLGAPERPEHLLNRVLERLAGGATRDSASDILLDDIVLTHS LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE TVELKIPEENQPPSKQVKPLFRHFRIDSCLQTRVAFRGSDEIF CRVYMPDHSYVTIRSRLSASVQDILGSVTEKLQYSEEPAGREDS LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYEALV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLPEEIQVSPGDTEIHRVEPEDVANHLTAFHNELPRCVHELEFV DYVFHGE
5779	138	1671	EAVQVLIKHSADVNRDKNWQTPLVHAAANKAVKCAEVIIPLLS SVNVSDRGRTALHHAALNGHVEMVNLALLAKGANINAFDKKDRR ALHWAAYMGHLDVVALINHGAEVTCDDKKGYTPLHAAASNGQI NVVKHLNLNGVEIDEINVYNTALHIACYNQGDVAVNELIDYGA NVNQPNNGFTPLHFAAASHTGALCLELVNNGADVNIQSKDYGK SPLHMTAVHGRFTRSQTLIQNGGEIDCVDKDNTPLHVAARYGH ELLINTLTISGADTAKCGIHSMPFLHLAALNAHSDCCRLLSSG QKYSIVSLFSNEHVLSAGFEIDTPDKFGRTCLHAAAGGNVECI KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN ETDDWGRALTALHYAAASMDRNTILGNAHDNSEELERARELKEK EATLCLEFLQNDANPSIRDKEGYNSIHYAAAYGHRQCLELLE RTNSGFESDSGATKSPHLAVSEMP
5780	154	624	QFFRVITCLPFKGPDRYLYKSEPELTTVAEVDSENGEEKSEPVSEIETSVVKGSHFPVGVPPRAKSPTEPESSTIASYVTLRKTCKMM DLRTERPRSAVEQLCLAESTRPRMTVEEQMERIRRHQACLEK KKLNVIGASDQSPSQSPNLDRNP
5781	19	941	RGSLGGHPWRPFMRASQGLPVSVFTGPHQERAYGGRPGGAF PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAHRDGE QAPCRAGPTRKVAVAPRPPSCP*GPE\ PGEPRRPLDRSPPLGQ VQPHFTSQDAKSAEDEAPSRHLGKHQPRSAQVGSRLDALQGPKT QHSIHTVTCSPQKEDRSPPQAPKHPEHGRQS\QAPPPLP VAPSRTCGGC*TWDPAALLVSP/PQGDSTPELPAP\QQPTGGPSR CRQALPPQG*ROQPRQRP/PTGASRSHPAKAGCQGPPIRNY NIMD
5782	5176	1237	DRSMMSMAADSYTDSYTDITYEAYMVPPLPPEEPPTMPPLPPEE PMPTPLPPEEPPEGPALPTEQSALTAENTWPTVEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPPEP PPESSITLTPVESAVVABEHEVVPBPVTCMVSETPAMSAEPT VLASEPPVMSETAETFDMSRASGHVASEVSTSLVPAVTTPLVLA ESILEPPAMAAPESAMAVLESAVTVLESSTTVLESSTTVL EPSVVTVPPEPPVAEPDYVTIPVPVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVITEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPFIMGQEIALHSGEEPFAE EHLKGDFFESEHGINIDLNNHLLIAKEMEHNVTCAAGTSPVGE IGEKILPTSETKQRTVLDTPGVSEADAGETLSSTGPFALPEPD ATG\TSKGIEFTTASTLSLVNKYDVLSTLTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVPRVSSPRTWNLPSPRAG\EGP\LLASDFGPVQNLVSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVDTHEKSKKNKNDKG EKEKKRDSSLRSRKRKSSSEHKSRKLTSSESRRARKRSKSKS HRS\QTRSRRS/RDRRRRSRSRKSRRGRRSVSKEKRRSPKH RSKSRERKRKRSSSRDNKTVRARSRTPSRRSRSHTPSRRRSR SVGRRRSFISISRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRRRSRVVRRRSFISISPVLRRSRTPLRRRFS RSPIRRRSRSSERGRSPKRLTDLDKAQLEIAKANAAAMCAKA GVPLPNLKPAPPTIEEKVAKSGGATIEELTEKCKQIAQSKE DDDVIVNKPVHSEDEEEPPFYHHPFKLSEPKPIFFNLNIAAK PTPKQSQTLTKEFPVSSGSQHRKKEADSVYGEWVPEKNGEEN KDDNVFSSNLPSEPVDISTAMSERALAQKRLSENADLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQALANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSNGFSAAAMKDLGKHPVSALMEICN KRRQPPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y
5783	1693	698	DSGLRVAFTMEGINSFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGESL NDLIEE/PI*SQ/PKILFQQP/LILKVALNMARGLYLHQEKKL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LHGDIKSSNVVVIKGFETIKICDVGVSPLDENMTVTDPEACYI GTEPWKPKAVEENGVIITDKADIFAPGLTLWEMMTLSIPHINLS NDDDEDKTFDESDFDEAYYAALGTRPFINMEELDES YQKVIE LFSVCTNEDPKDRPSAAHIVEALETDV
5784	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLDWVNDQMEKDKVKIH GILSNTHRQAARVNLSFDFFPYGHFLREITVATGGFIYTGEVH RMLTATQYIAPLMANFDPVSVRNSTVRYFDNGTALVVQWDHVL QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV GLSDAFVVHRIQQIPNVRRRTIYEHVRELQMSKITNISAVEM TPLPTCLQFNRCGPCVSSQIGFNCSSWCKLQRCSSGDFDRHQDW VDSGCPBESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP E/DAVTSQFPTSLPTEDDTKIALHLKDNASTDDSAEKKGGTL HAGLIVGILILVLIVATAILVTVMYHHPTSAAISFFIERPSR WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQ
5785	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLDWVNDQMEKDKVKIH GILSNTHRQAARVNLSFDFFPYGHFLREITVATGGFIYTGEVH RMLTATQYIAPLMANFDPVSVRNSTVRYFDNGTALVVQWDHVL QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV GLSDAFVVHRIQQIPNVRRRTIYEHVRELQMSKITNISAVEM TPLPTCLQFNRCGPCVSSQIGFNCSSWCKLQRCSSGDFDRHQDW VDSGCPBESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP E/DAVTSQFPTSLPTEDDTKIALHLKDNASTDDSAEKKGGTL HAGLIVGILILVLIVATAILVTVMYHHPTSAAISFFIERPSR WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQ
5786	2532	1674	SYKLPAEERRASSCSQPPTPTRRRWAPGRTSRGHRFQM*SGTP APRPPARSTVSPASPLPKPRAGRCGRPSACSTFRPC*SLN*M S*H*KRNLSQRSSSMSRRPLSCARPHR**RQGLTVAARLPTWAK SPPLACSFQAAQKSQSLSSGRSTR*PERMSFRP/SPPGNPAIP SLAPSSRF/PKGRPQCTWI PSRWASPTAPPTT*APTSSPGST GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA TGGSTATAPPKFRPNWNPMAE
5787	2	1460	MASAAVSITSLADEVNCP\ICQGTLEAGSLNCG/HKNFCRACL T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP/GSFRPNWQLANV VENIERLQLVSTLGLGEEDVCOEHGEKIYFFCEDDEMQLCVVCR EAGEHATHIMRFLDAA\APYREQIHKCLKLIKEREIEIQEIQS RENKRMQVLLTQVSTKRQVISEFAHLRKFLFEEQQSILLAQLES QDGDILRQRDEFDLLVAGEICRFSALIEELEBKNERPARELLTD IRSTLIRCETRKCRKPVAVSPQLGRIROFPQALPLQREMKMF LEKLCFELDYPAHISLDPQTSHPKLLSLEDHQRAQFSYKWQNS PDNPQRFDRTATVLAHTGITGRHTWVVSIDLAHGGSCITGVVVS EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP RQVRVSLDYEVGWVTFTNAVTRPIYTTASFTRKVIPFFGLWG RGSSFSLS
5788	2	6860	EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG SEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPLQRLNVGGVR AIFYMQVILMLTTDLGDEKDKGALDNLSQLIAELGMDKDV SKKNERSALNEVHLVVMRLLSVFMSTKSGSKSSICESSLISS ATAAALLSSGAVDYCLHVLKSLLEYWKSQONDEEPVATSQLLKP HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRPLPYQI KKITDINSRIPPPVFDHSWFYFLSEYLMIQPTPFVRRQVRKLL FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEBQGI FLRASVVT SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY FLLQVSFLVDEGVSPVLLQLLSLALCGSKVLRALASSGSSSS SSPAPVAASSGQATTQSKSTKSKKKEKEKEKDGSTSGSQBDQ LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH IYRNSKSKQELLDLDMWSIWPELPAYGRKAAQFVDLLGYFSLK TPQTEKKLKEYSQKAVEILRTONHILTNHPNSNIYNTLSGLVEF DGYLES DPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQOVVKLI GSHTISKVTVKIGDLKRTKMVRTINLYNNRTVQAIVELKNKPA RWHKAKKVQLTPGQTEVKIDPLPIVASNLMI EFADFYENYQAS TETLQCPRCASVPANPGVCGNCGENVYQCHKCRSINYDEKDPF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LCNACGFCYARDFDMLYAKPCCAVDPIENEEDRKKAVSNINTL LDKADRVYHQLMGHRPQLENLLCKVNEAAPEKPODDSGTAGGIS STSASVNRYYILQLAQEYCGDCKNSFDELSKIIQKVPASRKELLE YDLQQREAATKSSRTSVQPTFTASQYRALSVLGCGHTSSTKCYG CASAVTEHCITLLRALATNPALRHILVSQGLIRELFDYNLRGA AAMREEVRQLMCLLTRDNPEATQQMNDLIIGKVSTALKGHWANP DLASSLQYEMLLLTDSISKEDSCWELRLRCALSLFLMAVNIXTP VVVENITLMCLRILOKLIKPPAPTSKKNDVPVEALTTVKPYCN EIHQAQQLWLKRDPKASYDAWKCLPIRGIDGNGKAPSKSELRH LYLTEKYVWRWKQFLSRRGKRTSPLDLKLGHNWLRQVLFPTPAT QAARQAACTIVEALATIPSRKQVLDLLTSYLDLSIAGECAAE YLALYQKLITSAHWKVYLAARGVLPYVGNLITKEIARLLALEEA TLSTDQLQQYALKSLTGLSSFEVESIKRHFKSRIVGTVLNGY LCLRLVVQRTKLIDETQDMLEMLDMTTGTSETKAFMAVCI ETAKRYNLDDYRTPVFIIFERLCSIIYPEENEVTEFFVTLEKDPQ QEDFLQGRMPGNPYSSNEPGIGPLMRDIKNKICQDCDLVALLED DSGMELLVNNKIIISLDLPVAEYKVKVWCTTNEGEMRIYVRMRG LLGDATTEEFIESLDSTTDEEEDDEEVYKMGVMAQCGGLECMNL RLAGIRDQKGRHLLTVLLKLFSCYKVKVNRQQLVKLEMTLN VMLGTLNLALVAEQESKDSGGAVAEQVLSIMEI\IQAEPNVEP LSEDKGNLLLTGDKDQLVMLLDQINSTFVRNPSVLQGLLRIIP YLSFGEVEKMQILVERFKPYCNFDKYDEHSGDDKVFL\DCPCK IAAGIK\NNSNGHL\KDL\ILQKGTONALD\YMKKHIP\SA RIWDADI\WKSFCRLPALPFILRLRLGLAIQHPGTQVLIGTDSI PNLHKLEQVS\SDEGIGTLA\ENL\LESREHPDVNKKIDA\AR RETRAEEKRMAMAMRQKALGTG\MTTNEKGQVVD\TRTALLEA DWEELIEEP\GLTCCICREGYKFPQPTKVLGIYTFTRVVLGGVW ENKPRETSRATSTVSHFNIVHYDC\HLA\AVSLARGREEWESAA LQANATKCNGLLPVWGPVHPESAFATCLARHNTYLQECTGQREP TYQLNIHDIKLLPLRFAMEQSFADTGGGGRESNIIHLIPYIHT GLYVLNTRATRSREKNLQGFLEQPKWKVESAFVDPGPYYFTV LALHILPPEQWRATRVEILRRLLVTSQARAVAPGGATRLTDKAV KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGWSSCLAEYIR HNDMPYIEAADKALKTFQEEFMPVETVSEFLDVAGLLSEITDPE SFLKDLLNSVP
5789	1	2407	LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ TEEEKKKEPKSKDTEEIAEEETVFPKAKQVKKKAEPSEVDMN SPKSKKAKK\KEEPSQNDISPKTKSLRKKKEPIEKKVSSKTKK VTKNEEPSEEEIDAPKPKMKKEKEMNGETREKSPKLKNGFPHP EPDCNPSEAASESNSIEIQEIPVEQKEG\AFSNFPISEETIKL LKGRGVTFLLPIQAKTFHHVYSGKDIIAQARTGTGKTFSFAIPL IEKLHG\ELQDRKGRAPQVLVLAPTRELANQVSKDFSIDITKKL SVACFYGGTPYGGQFERMRNGIDILVGTGRIKDHQNGKLDLT KLNHVVLDEVDQMLDMGFADQVEEILSVAYKDSSEDPQTLLFS ATCPHWVFNVAKKYMKSTYBQVDLIGKKTOKTATVEHLAICH WTQRAAVIGDVIRVYSGHQGRITIFCETKKEAQELSONSAIKQD AQSLHGDIPQKOREITLKGFRNGSFGVLVATNVAARGLDIPEVD LVIOSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIISKASKDAIRLLDSVPPTAISHF QSAEKLEEKGAVALAAALAHISGATSDQRLSINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSVKGMVFLKGLGVCF DVPTASVTEIQEKWHSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGRGQRDGNRRFRGQREGSRGPRGQRSGGKNKSNRSQNK GQKRSFSKAFGQ
5790	3786	1585	ARRQRDPLQALRRRNQELKQQVDSLLSESQLEALEPNKRQHIY QRCIQLKQAIKENKNALQKLSKADESAPVANYNQRKEEHTLLD KLTTQQLQGLAVTISRENITEVGAPTEEESESEDSGSGGEE DAEEEEEEKEENESHKWTGEEYIAVGDPFTAQQVGDITFKKGEI LLVIEKKPDGWWIAKDAKNEGLVPRTYLEPYSEEEBQGESSE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN HVSFCYLIVLMNRNMTVEDTNGSETGFRAWNVQSRGRIFLVSK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PVLQQTINTVDVLTMTGAIPAGFRPSTLSQLLEEGNQFRANYFLQ PELMPSQLAFRDLMDATEGTIRSRPSRISLILTLWSCKMIPLP GMSIQVLSRHVRLCLFDGKNVLSNIHTVRATWQPKPKTWTSP QVTRILPCLLDGDCFIRSNSASPDGLIFELGISYIRNSTGERG ELSCGWVFLKLFDAAGVPIPAKTYELFLNGGTFYEKIEVDPSI SRAHGSVFYQIMTMRQPQLLVKLSLNRRSRNVLSLLPETLI GNMCSIHLLIFYRQILGDVLLKDRMSLQSTDLISHPMLATFPM LEQPDVMDALRSSWAGQES\TLKRSEKRPKEFLKVPFRLLVYH \GCVLPL/HTPTRLPPFRWAEETETARWKVITDFLKQNGENQ GALQALLSPDGVHHPFDLSEQTYDFLGEMRKNAV
5791	3	1636	LRVAEFAGTSR/IGAGLIQPLHRAPARDHGLLRGGAAPALSVSH GN/GKQL/AMSSQGSDEQIKRENIRSLTMSGHVGFESLPDQLV NRSIQQGFCCNILCVGETGIGKSTLIDTLFNTNFEDYESHFCP NVKLKAQTYELQESNVQLKLTIVNTVGFGDQINKEESYQPIVDY IDAQFEAYLQEEELKIKRSLFTYHDSRIHVCLYFISPTGHSKLT DLTLMKNLDSKVYIIPVIKADTVSKTELQKFKIKLMSSELVSN VQIYQFPTDDDTIAKVNAAMNGQLPFAVVGSMDEVKVGKMKVKA RQYPWGVVQVENENHCDVFKLREMLICTNMDLREQTHTRHYEL YRRCKLEEMGFTDVGPEKPVSVQETYEAKRHEFHGERQRKEEE MKQMVFQVRVKEKAILKEAERELQAKFEHLKRLHQEERMKLEEK RRLLEEEIIAFSKKKATSEIFHSQSFLATGSLNRKDKDRKNSQF FVKQKVPHEHRSSSQANFIKKKLEVCDFFAVICFTSIFGEQPO LLIFMEKYFQVQGGVYSQSE
5792	2263	653	AAAAPSAPWCGVVFVYVHTCWVMYGIIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPILT YMPKPEEINLLTGESDTQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRRLRFWIHQDAVYSLQQ FGFSEKDADEVKGI FVDTNLYFLALTFFVAAFHLLFDPLAFKND ISFWKKKSMIGMSTKAVLWRCFSTVVI FLFLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYESERKTEY DTQAMKYL SYLLYPLCVGGAVYSLN IKYKSWYSLINSFVNGV YAPGFLEMLPQLFVNYKLKSV AHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVFLVLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD
5793	2263	653	AAAAPSAPWCGVVFVYVHTCWVMYGIIVYTRPCSGDASCIQPY LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPILT YMPKPEEINLLTGESDTQIEADKKPTSALDEPVSHWRPRLAL NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN RVKDLMVINRSTTELPLTVSYDKVSLGRRLRFWIHQDAVYSLQQ FGFSEKDADEVKGI FVDTNLYFLALTFFVAAFHLLFDPLAFKND ISFWKKKSMIGMSTKAVLWRCFSTVVI FLFLDEQTSLLVLVP AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYESERKTEY DTQAMKYL SYLLYPLCVGGAVYSLN IKYKSWYSLINSFVNGV YAPGFLEMLPQLFVNYKLKSV AHLPWKAFTYKAFNTFIDDVFAF IITMPTSHRLACFRDDVFLVLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD
5794	1	5016	MGPRLSVWLLLLPAALLLHEHSRAAKGCGAGSGCGKDCCHGV KGQKGERGLPGLQGVIGFGPMQGPQGPQGPQKGTGEPGLPG TKGTRGPPGASGYPGNPGLPPIPGQDGPQGPPIPGCNGTKGER GPGPPGLPGFAGNPGPPGLPGMKDGPGEILGHVPGMLLKGERG FPGIPGTPGPPGLPGLQGVGPPGFTGPPGPPGPPGPPGKGM GLSFQGPQKDGQGVSGPPGVPQQAQVQEKGFATKGEKQKQK EPGFQGMPPGVGEKGPKEGPKGPRGKPKGDKGDKGKSGSPGPEP YPGLIGRQGP\QGEKGEAGPPPPGIVIGTGPLGEKGERGYPGT PGPRGEPGPKGFPGLPGQGPPLPVPQAGAPGPPGERGEKGD RGFPGTSLPGPSGRDGLPGPPGSPGPPGPGYTNGIVECQPGFP GQGGPPGIPGQPGFIGEIGEKQKGESCLICDIDYRGPPGPGQ PPGEIGFPGQPGAKGDRGLPGRDGVAGVPGPQGTPLIGQPGAK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>GEPPGEFYFDLRLKGDKCDPGFPGQPGMPGRAGSPGRDGHPLPG PKGSPGSGVLKGERGPPGGVGFPGSRGDTGPPGPPGYGPAPIG DKQAGFPGGPGSPGLPGPKGEPGKIVPLPGPPGAEGLPGSPGF PGPGQDRGPPGTGPR\PG\PGEGKAVG\QPGIGFPGPPGPKGV DGLPGDMGPPGTGPRPGFNGLPGNPGVQGOKEPVGVLPLGLKGL PGLPGIPGTGPEKGSIGVPGVPGHGAIGPPGLQGIIRGPPGPPG LPGSVGSPGVPGIGPPGARGPPGGQGGPGLSGPPGKGEKGFPG FPGLDMPGPKGDKGAQGLPGITGQSGPLPGQQGAPGIPGFP SKGEMGVMTGTPGPGSPGPGWAPGLPGEKGD\HGFPSSSGPRGD PGLKGDKGDVGLPGKPGSMDKVYMSMKGQKGDQGEKQIGPIG EKSGRGDPGTGVPKGKDGQAGQPGQPGKGDPGISGTPGAPGLP GPKGSGVGMGLPGTPGEGKGVPGIPGPGQSGPLPGDKGAKGEKQ AGPPGIGIPGLRGEKGDQGIAGFPGSPGEGKEKGSIGIPGMPGS PGLKSPGSGVYPGSPGLPGEKGDKGLPGLDGI PGVKEAGLPG TPGPTGPAGQKGEPGSDGIPGSAGEKGEPLPGRGFPFGPAKG DKGSKGEVGFPGLAGSPGIPGSKGEGQFMGPPGQGGPGLPGSP GHATEGPKGDRGPQGGPGLPGLPGMPGPPGLPGIDGVKGDKNP GWPGAPGVPGKGDGPGFQGMPIGGSPGITGSKGDMGPPGVPFG QGPKGLPGLQGIKGDQGDQGVPGAKGLPGPPGPPGYDIKGE GLPGEPGPPGLKGLQGLPGPKGQGVTLVGI PGPPGIPGFDGA PGQKGE MPAGPTGPRGFPGPDPGLPGSMGPPGTSPVDHGL VTRHSQTIDDPQCPGSGTKILYHGYSLLYVQGNRAHQDLGTAG SCLRKFSTMPFLFCNINNVNCFASRNDYSYWLSTPEPMPMSMAP ITGENIRPFISRCVCEAPAMVMAVHSQTIQIPCPGSGWSSLWI GYSFVMHTSAGAEGSGQALASPGSCLEEFPSAPPTECHGRGTCTN YYANAYSFWLATIERSEMFKKTPSTLKAGELRTHVSRQVCMR RT</p>
5795	1192	61	<p>STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECI RHE PLAKIILFSNQFRDFFKYVELSTFDIASDAFATPKDLLTRHKVL VADFLEQNYDTIFEDYKELLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH KTQPIVEILLKNQPKLIEFLSSPQKERTDDEQFADEKNYLIKQI RDLKKTAP*RALRDSKR</p>
5796	2	1078	<p>GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVRNKF FGEIGLLDPGMDVYGGENIELGIKVLCCGSMELVPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSCLKCNPQWYLDHVYPEMRRYNNVTAYGE LRNNKAKDVCLDQGPENHTAILYPCHGWGPQLARYTKEGFLHL GALGTITLLPDTRCLVDNSKSRLPQLLDCDKVSSLYKRWNFIO NGAIMNKGTRCLENENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTS CPGETTARGQVLDGPPRASPG QHRDPG</p>
5797	2	891	<p>PRVRQKTLVDVTLSENSIKDQIRNLQOTYEASMDKLEKQRQLE VAQVENQLLKMKESSQANAEVMREMTKKLYSQYEEKLQEEQR KHSAEKEALLEETNSFLKAIEBANKMQAAEISLEEKDQRIEGL DRLIERMEKERHQLQLLLEHETEMSGELTDSKERYQQLEEAS ASLRERIRHLNDMVHCQKKVKQMVVEEIESLKKKLQKQLLILQ LLEKISFLEGNNELQSRDLDTETQAKTEVETREIGVGCDDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTILT</p>
5798	644	115	<p>KILGSRWKSMSNQEKQPYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKLRIGYKQLMRSRRQEMRQFTVGGQPPQIPITGTG VVYPGAITMATTTPSPQMTSDCSSTASPEPSLPVQISTYGMKT DGGSLAGNEMINGEDEMYYDDYEDDPKSDYSSENEAPAVSAN</p>
5799	2679	1435	<p>LLSTYIKFINLPETKATIQGVLRAGSQLRNADVELQORAVEYL TLSSVASTDVLATVLEMPFFPERESSILAKLKRKKGPGAGSAL DDGRDPSSNDINGMEPTSTVSTPSPSADLLGLRAAPPAPAP PASAGAGNLLVDVDFGPAAPSLGPTPEEAFSPGPDIGPPPI EADLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPTVVHPGDLQTLAVQTKRVAQVDGGAQVQVQL NIECLRDFLTPLLSVRFRYGGAPQALTCLKPVTINKFFQPTM AAQDFFRQWKQLSLPQCEAKIFKANHPMDAEVTKAKLLQFGSA</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LLDNVDPNPENFVGAGIIQTALQVGCCLLRLEPNAQAQMYRLTL RTSKEPVSRLHCELLAQFF
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVLOQRAVEYL TLSSVASTDVLATVLEEMPPFFPERESSILAKLKRKPGAGSAL DDGRRDPSSNDINGGMEPTPTSTVSTPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAPQPSLGPPTBEAFLSPGPEDIGPPIP EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN KTSVQFQNFSPITVVHPGDLQTLAVQTKRVAQVDGGAQVQQVL NIECLRDFLTPLLSVRFRYGGAPQALTLKLPVTINKFFQPTM AAQDFFQRWKQLSLPQQAQKIFKANHPMDAEVTKAKLLGFGSA LLDNVDPNPENFVGAGIIQTALQVGCCLLRLEPNAQAQMYRLTL RTSKEPVSRLHCELLAQFF
5801	3	1413	FPRLYHLIPDGEITSIKINRVDPSSELSIRLVGGSETPLVHIII QHYYRDGVIAARDGRLLPGDIIILKVGMDISNVPHNYAVRLLRQP CQVLWLTVMREQKPRSRNNGQAPDAYRPRDDSFHVLNKSSPEE QLGIKLVKQVDEPGVIFINVLDDGGVAYRHGQLEENDRVLAINGH DLRYGSPESAHLIQASERRVHLVSRQVRQSPDIFQEAQWNS NGSWSPGPGERSNTPKPLHPTITCHEKVNNIQKDPGESLGMTVA GGASHREWDLPYIVISVEPGGVI SRDGRITGDILLNVGVELT EVSRSSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH NMAPPSPDWSPSWVMWLELPRCLYNCKDIVLRRTAGSLGFCIVG GYEYNGNKPFPIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG MIHACLARLLKELKGRITLTIWSPGTFPL
5802	3	290	CFSLYQIMERIMDLPTLLRHAFREMFSGVGLFWMFRIIILCLM GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLLIYISIMYREV ITQRLTR
5803	2234	1299	EAQFGTTAEIYAYREEQDFGIEIVKVAIGRQRFKVLELRTQSD GIQQAQVQILPECVLPSTMSAVQLESNLKQCIFPSKPVSRQDQC SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQRE WDENLKDDSLSPNPI DFSYRVAACLPIDDLVLRQLLKGSAIQIR LRCELDIMNKCTSLCKQCQETETTKNEIFSLSLCGPMAAYVN PHGYVHETLTVYKACNLNIGRPSTEHSWFPGYANTVAQCKICA SHIGWKFTATKKDMS PQKFWGLTR SALLPTIPDTEDEISPKVI LCL
5804	2	1707	EMEKQRQEEQRKRTTEERKRRIEQDMLEKRIQRELAKRAEQIE DINNTGTESASEGDDSLITVVPVKS YKTSKMKKNFEDLEKE RBEKERIKYEEDKRIRYEEQRP SLKEAKCLSLVMDDEIESEAKK ESLSPGKLKLTFEELERQRQENRKKQAESEARKRLEEEKRAFEE ARRQMVNEDEENQDTAKIFKGYRPGKLKLSFEEMERQRREDEKR KAESEARRRIEEKKAFAEARRNMVDDDSPEMYKTISQEFLLTP GKLEINFEELLKQKMBEEKRRTBEERKHKLEMEKQEFQELRQEM GEEENETFGLSREYEELIKLRSGSIQAKNLKSKFBIQGLS EKRIQKKIEERARRRAIDLEIKEREAENFHEEDVDVDRPARKS EAPFTHKVNMKARFEQMAKAREEEQRRIEBQKLLRMQPEQREI DAALQKKREEEEEEGSIMGSTAEDDEEQTRSGAPWFKPLKNT SVVDSEPVRFVTKVTGEPKPEITWWFEGEILQDGEDYQYIERGE TYCLYLPETFPEDGGEYMKAVNNKGSAASTCILITIESKN
5805	3	776	YISDTLGQVYKSKIRWWIEENGNGNISVDDLIALLDLAEHASS APKESQQQSEDRYEYVKERLYPKSKRRYDTYNIAGYQGEIEVGL YTIQILQLIPFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLA LKNYIPLYTLKLFSLKKSDFDFDEYFVLLKPRNNIKQNEEAKTR RKVAGYFKKYVDIFCLLEESQNTGLGSKFSEPLQVERCRRNLV ALKADKFSGLLEYLIKSDAISTMKCIVNEYTFLK
5806	1257	877	AVFTFHNHGRRTANLYSLHSWLGITTVFLFACQRFGLFAVFLLPW ASMWLSLLKPIHVFFGAAILSLSIASVISIGINEKLFSLKNTT RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRF
5807	2267	1302	RFSKKTFRPMAVDIQPACGLYCGKTLFLKNGSTEIYGECCGVC PRQRTNAQKYCQCTESPELYDWLYLGFMAMLPVLHWFIEW YSGKSSSALFQHITALFECSSMAAIIITLLVSDPVGVLVYRSCR LMLSDWYTMLYNPSPDYVTVHCTHEAVYPLYTIVFIYAFCLV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LMMLLRPLLKVIACGLGKSDRFKSIYAALYFFPILTVLQAVGG GLLYYAFPIILVLSLVTAVYMSASEIENCYDLLVRKRLIVL FSHLLHAYGIISIRVDKLEQDLPLLALVPTPALFYLFYFTAKFT EPSRILSEGANGH
5808	2	433	SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKNGSS EGRITHGFQKLSAYENNLMPYTYNTFDKGVIDYIFYSKTHMNV LGVLPDLPQWLVENNITGCPHPHPSDHFSLLTQLELHPPLLP LVNGVHLPNRR
5809	464	2422	ILVPGFQGIHHPGVYCALQSQHQAEVLADIDECEVSLGRHGG RCVNTHGSFECYCMDGYLPRNGPEPFHPTTDTATCTBIDCGTPP EVPDGYIIGNYTSSLGQVRYACREGFFSVPEDTVSSCTGLGTW ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE SPGGKITSVCTEKGTTWRESTLTCTEILTAKINDVSLFNDTCVRWQ INSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPEVC LALYPGTNYTVNISTAPPRSRMPAVIGFQTAEDLLEDGGSFNI SIFNETCLKLNRRSRKVGSEHMYQFTVLGQRWYLANFSHATSFN FTTREQVPVCLDLYPTDYTVNVTLLRSQKRHSVQITATPPA VKQTIISNIGFNETCLRWSIKTADMEEMYLFIHWQRWYQKEF AQEMTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSSELVVISL TTQITEPPLPEVEFPTVHRGFLRLRLKAKEKNGPISSYQVLV LPLALQSTFSCDSEGASSFFSNASDADGYVAEELLAQDVDDAM EIPIDRLYYGEYNAPLKRGSDYCIILRITSEWNKVRHSCAV WAQVKDSSLLMLQAGVGLSLAVVILTLFLSFSFAV
5810	3	1641	KVPGTHKDEHVSITLDTAISAVKVLAEFLENLQEKSLRIEAFVS BIESFFNTIENCCKNEKRLEBQNEEMMKVLAQYDEKAQSFEF VKKKKMEFLHEQMVFHLSQMDTAKDTLETIVREAEELDEAVFLT SFEEINERLLSAMESTASLEKMPAAFSLEHYDDSSARSQDMLK QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCMC EPQDDQEVNLEVEEYRLTVKESYCIFEDLEPDRCYQVWMAVNF TGCSLPSERAFRTAPSTPVIRAEDCTVCWNTATIRWRPTPEA TETYTLEYCRQHSPEGEGLRSFSGIKGLQKLVNLQPNDFYFFV RAINAFGTSEQSEALISTRGTRFLLRETAHPALHISSSGTVI SFGERRRLTEIPSVLGEELPSCQGHYWETTVTDCPAYRLGICSS SAVQAGALGQGETSWYMHCSPEQRYTFFYSIGIVSDVHVTERPAR VGLLDYNNQRLIFINAESQELFIIRHRENEGVHPAPALEKPG KCTLHLGIBPPDSVRHK
5811	1918	851	AAALADPLPEDKWSAEKRRPLKSSSLGYEITFSLNPDPKSHDVI WDIEGAVRRYVQPFNLALGAAGNFSVDSQILYYAMLGVNPRFDS ASSSYLDHMSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA HSPLYIQDKGAPVATNAPHSRWWGIMVYNVDSKTYNASVLPV RVEVDVVRVMEVFLAQLRLFLGIAQPLPKCLLSGPTSEGLMT WELDRLLWARSVENLATATTTLSLAQLLGKISNIVIKDDVASE VYKAAVAVQSAEELASGHLASAFVASQEAVTSSSELAFFDPSLL HLLYFPDDQKFAIYIPLFLPMVAVPILLSLVKIFLETRKSWRKPE KTD
5812	5204	2744	GGRCRCGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPOPLQSGSQ DMVSILQLVQNLHMGDEDEEPQSPRIQNIQEGQHMALLGHSLGA YISTLDKEKLRKLTRILSDTTLWLCRIFRYENGCAFYHBEERE GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAARPGLGQ YLCNQGLPFPCLCRVPCNTVFGSQHQMDFVAFLEKLIKDDIERG RLPPLLAVANAGTAAVGHDTKIGRLKELCEQYGIWLHVGEVNLAT LALGYVSSSVLAAKCDSTMTPGWGLPAVPAVTLYKHDDPA LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS QRLQESLKKVNYIKILVEDELSSPVVVFREFQELPGSDPVFKAV PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDELA EGTCLRFSPMLTAAVLGTGEDVDQLVACIESKLPVLCCTQLQR EEFKQVEATAGLLYVDDPNWSGIGVVRVYEHANDDKSSLSYPQ GENIHAGLLKKLNELESDLTFKIGPEYKSMKSLYVGMASDNVH AELVETIAATAREIEDNSRLLENMTEVVRKGIQEAQVELQKAS EERLLEGVLRQIPVVGSVLWNFSPVQALQKGRTFNLTAGSLES

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TEPIYVYKAQGAGVTLPTPSGSRTKQRLPGQKPKRSLRGSDA LSETSSVSHIEDLEKVERLSSGPEQITILEASSTEGHPGAPSPQH TDQTEAFQKGVPHPEDDHDSQVEGPESLR
5813	2936	699	HRDGVSGSLERPLTDRSRTGAFQAQGRGKMATAGGGSGADPGSRG LLRLLSFVLLAGLCRGNVERKIYIPLNKTAPCVRLNATHQI GCQSSISGDTGVIHVVEKEEDLQWVLTGDPNPPYVLLSKHFT RDLMEKLGKRTSRIAGLAVSLTKPSPASGFSVQCPNDGFGVY SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLDENETKVI KQCYQDHNLSQNGSAPTFFLCAMQLFSHMAWLSFSTAT\CMRRS SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLPDDRUVVA ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL PRNVMFVFPQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL GQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP AVILRRPNQSQPLPPSSLRQFLRARNISGVVLADHSGAFHNKY QSIYDTAENINVSYPEWLEPLKE/ETWNFG*QDTAKALADVATV LGRALYELAGGTNFSFDTVQADPQTVTRLLYG\FLIKANNWFSQ ILQGRDLRSYLG*RLGFQ\YIAV\SPNTNTIYV/VLQYALANL TGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLP RCVRSTARLARALSPAPELSQWSSTEYSTWTESRWKDIRARIFL IASKELELITLTVGFGILFSLIVTYCINAKADVLFIAPREPGA VSY
5814	8500	432	ALKCRPRRVLAILVGPVQDRMAEEGAVAVCVVRPLNSREESL GETAQVYWKTHNNVIYPVDSKSFNDRVLHGNETPKNVYEA\I AAPIIDSAIQGYNGTIFA\YQQT\ASGKTYTMMGSEDLGVIPQ GQFHGHFSQKI*EVFLDREFLLRVSYMEIYNETITDLLCGTQKM KPLIREDVNRNVVADLTEEVVYTSEMALKWITKGEKSRHYGE TKMNQSSRSHTIFRMILESREKGEPSNCEGSVKVSHLNLVDLA GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSGQVGGFI NYRDSKLTRILQNSLGGNPKTRIICTITPVSFDETLTALQFAST AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLTRAQ AMEKDQLAQLLEEKDLLQKVQNEKIEINLTRLVTSSSLTLQOEL KAKRRRRTWCLGKINKMKNSNYADQFNIPNTITTKTHKLSINL LREIDESVCSSEDSVFSNTLDTLSEIENWNPATKLLNQENIESELN SLRADYDNLVLDYEQLRTEKEEMELKLEKNLDDEFEALERTK KDQEMQLIHEISNLKNLVKHREVNQDLENELSSKVLELREKED QIKKLQEYIDSQKLENIKMDLSYSLESTIEDPKQMKQTLFDAETV ALDAKRESAFLRSNLELKEKMKELATTYKQMENDIQLYQSOLE AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK ITDLQKELNKEVEENEALREEVILLSBLKSLPSEVERLRKEIQD KSEELHIITSEKDKLFSEVHVKESEVQGLLEEIGTKDDLATTQ SNYKSTDQEFQNFKTLHMDFEQYKMYVLEENRMNQEIIVNLSKE AQKFDSSLGALKTELSYKTQELQEKTRVQERLNEMEQLKEQLE NRDSPLOTVEREKLITELQQTLEEVKTLTQEKDDLQLOESL QIERDQLKSDIHDVTNMNIDTQEQRLNALESKQHQETINTLKS KISEEVSRLHMEENTGETKDEFQCKMVGIDKKQDLEAKNTQTL TADVKNDEIEEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL KENIEMTIENQELRLGDELKKQQTETVAQEKHAIKKEGELSR TCDLAEVEEKLKEKSQQLQKQQLLNQVEEMSEMOKKINBIE NLKNELKNKELTLEHMETERLELAQKLNNYEEVKSITKERKVL KELQKSPETERDHLRGYIREIEATGLQTKELKIAHILKEHQE TIDELRRSVSEKTAQINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMEKEDNETKIVSEMEQFKPKDSALLRIEIMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLSQESDQLKENIKEIV AKHLETEELKVAHCCLEKEQERTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIEKEEQNLKQISEVQEKVNLKQFKEHR KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEEEMKRVQEA LQIERDQLKENTKEIVAKMESQEQEYQFLKMTAVNETQEKME IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD DLRSVEETLKVERDQLKENLRETITRDLRKEELKIVMHMLKEH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QETIDKLRGIVSEKTNESNMOKDLEHSNDALKAQDLKIQEELR IAHMLKEQQETIDKLRGIVSEKTDKLSNMOKDLENSNAKLQEK IQELKANEHQILITLKKDVNETQKKVSEMEQLKKQIKDQSLTSLK LEIENLNLAQKLHENLEBMSVSKERDNLRRVEETLKLRLDQLK ESLQETKARDLEIQOELKTARMLSKHEKKTVDKLRKISEKTIQ ISDIQKDLKSKDBLQKKIQBLQKKELQLLRVKEDVNMSSHKKIN EMEQLKKQFEPNYLCKCEMDNFQTLKKLHESLEIRIVAKERDE LRRIKESLKMEDQFIATLREMIARDRONHQVKEPKRLSLSDGQQ HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH RIMKKLYVLSYVTIKIEEQHCINKFEMDFIDEVBQKQELLIK IQHLQQDCDVPSELRLDLKLNQNMDLHIEILKDFSESEFSPK TEFQQVLSNRKEMTQPLEEWLNTFRDIEKLKNGIQKENDRIQV NNFFPNRIIAIMNESTEFERSATISKWEQDLKSLKEKNEKLF KNYQTLKTSLASGAQVNPPTQDNKNPHVTSRATQLTTEKIRELE NSLHEAKESAMHKESKIKMQKELEVTNDIAKLQAKVHESNKC LEKTKETIQVLQDKVALGAKPYKEEIEDLKMMLGKIDLEKMKNA KEFEKEISATKATVEYQKEVIRLLRENLRSSQQAQDTSVISEHT DPQPSNKPLTCGGGSGIVQNTKALILKSEHIREKEISKLKQON EQLIKQKNELLSNNQHLSENVKTKERTLKREAHKQVTCENSPK SPKVTGTASKKKQITPSQCKERNLQDPVPKESPKSCFFDSRSKS LPSPHPVRYFDNSLGLCPEVQNAEVSQSP\GPWARLFQGGK DVP\ECKTQ
5815	23	1460	SELVMTVQNRESLGLLSFPVMITMVCCAHSSTNEPSNMSYVET VDRLKGYDIRLRPDPFGPPVDVGMRIDVASIDMVSEVNMDDL TMYFQQSWDKRLSYSGIPLNLTLDNRVADQLWVPDITYFLNKK SFVHGVTVKNRMIRLHPDGTLYGLRITTTAACMDLRRYPIDE QNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSIVDY KMVSKKVEPTTGAYPRLSLPRLKRNIGYFILQTYMPTSLITIL SVVSFWINYDASARVALGITVLTMTTISTHLRETLPKIPYVK AIDIYLMGCFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSA NEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSTVSDPKA TMYSDSASIQYRKPLSSRE\A*GRAPDRHGVPKGRIRRRAS\ QLKVKIPDLTDVNSIDKWSRMFFPITPSLFNVVYWLYYVH
5816	861	191	TSSRSRAAAEGDAETPGSVERRRAGAEAGMSQAPGAQSPSP TVYHERQRLELCAVHALNNVLQQQLFSQEAADBIKRLAPDSRL NPHRSLLGTGNYDVNVIMAAQLGLAAVWDRRRPLSQLALPO VLGLIILNLPSPVSLGLLSLPLRRRLRWPCARL/VTVSYNLDL K\LRAPGPGGLRTE*GPFLAAALAQGLCEVLLVVTKEVEKGS SWLRD
5817	851	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCP*PPSPPAAD VMSNTTVPNAPQANSDSMVGYYLGPFFLITLVGVVAVVMYVOK KKRVDRRLRHLLPMYSYDPAEELHEAEQELLSMDGDPKVV\QAG RVATSTSGCHCWMSRRDLTPLPHPEPGVLDCLGFCHELLPLSP GSPCWVLGLHPSLHPPSAASASHALTITSLPPGLLPFVGVELTA HPQALMGRGFPFGMAAAGRHLCLF
5818	3	3918	QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQKIQAAAFDKGD DRRLGKKPIFSSSQQRKQVSDSGDIKISWRGNKKCEWSYLS NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDKTKIASKI TKELKTGGKNVSGPKPTVTKSTENGDKARLENMSPRQVVERSA TAAAAATGQKNLLNGKGVNRQEGQISGARPKVLTGNLNVQAKAK PLKKATGKDSPLSLIAGPSSRSTDSSMEFSISTECLDEPKENG TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRT NGTSNKKSIHEQDTNVNNSVLKVKSGKGCSEPVPAAILKKRGTS NGCTAAQQRKTSTPSNLTKTQSGQGESPNVSVSSVSRQSDNV AKLDHNTTTEKQAPKRKMVQVHTALPKVNAKIVAMPKNLQSK KGETLNNKDSKQKMPGQVISTQPSQRPLKHETSTVQKSMFH DVRDNNKDSVSEQPKHPLINLASEISDAEALQSSCRP\DPQK PLNDQEKELALECQNI SKLDKSLKHELESKQICLDKSETKFPN HKETDDCDAANICCHSVGSDNVNSKFYSTALKYMVSNPNENSL NSNPVCDLSDTSAGQIHLISDRENQVGRKDTNKQSSI KCVEDVS LCNPRTNGTLNSAQEDKSKVPVEGLTIPSKLSDESAMDEKDH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH</p> <p>WNLSTGVLHQRESPESDTGSATTSDDIKPRSEDYDAGGSQDD</p> <p>GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK</p> <p>MKKQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIPR</p> <p>GSVQFAQEIDQVSSADETERSEAEVNAENFSISNPAPQFQ</p> <p>GIINLAFEDATENECEFRSANKKFKRSVLLSVDECEELGSDEGE</p> <p>VHTPFQASVDSFSPSDVDFDGISHEHHGRTCYSRFSRESEDNILE</p> <p>CKQNKGSVCKNESTVLDDLSSIDSRKNKQSVSATEKKNTIDVL</p> <p>SSRSRQLLREDKKNNGSNVENDIQORSKFLDSVDVKSQERPCHL</p> <p>DLHQREPNSDI PKNSSTKSLDSFRSQVLPQEGPVKESHSTTEK</p> <p>ANIALSAGDIDDDCTLAQTRMYDHRPSKTLSPYEMDVIEAFEQ</p> <p>KVESETHVTDMDF*DDQHFAQDWTLLKQLLSEQDSNLDVTNSV</p> <p>PEDLSLAQYLIQNTLLARDSSKPGGITHIDTLNRWSELTSPLD</p> <p>SSASITMASFSSDCSPQGEWTILELETQH</p>
5819	1	5557	<p>AAAGLLGALHLVMTLVVAAARAEEAFVQSESIIEVLRFDGGL</p> <p>LQETTLGLSSVQQKSISLYRGNCRPIRPEPMLDFHEQPVGM</p> <p>KMEVYLHNPSSE*ITILVSI FATTSHFASFPQNRKILPGGNT</p> <p>SFDVS/VFLARVGVNVENTLFINTSNHGVFTY\QVFGVGVNPNY</p> <p>RLRPFLGARVTVNSSFPIIINHNPHSEPLQVVMYSSGGDLHL</p> <p>ELPTGQQGGTRKLWEIPPYETKGMVRSFSSREADNHTAFIRIK</p> <p>TNASDSTEFILPVEVEVTTAPGIYSSTEMLDGTLRTQDLKPV</p> <p>LNLHLLNSGT KDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK</p> <p>YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV</p> <p>LDGVLGFDHAATLFIHDSPADPVERPIYLTNTFSFALLIHDVL</p> <p>LPBEAKIMFKVHNFSKPVLLPNESGYITLLFMPSTSSMHIDN</p> <p>NILLITNASKFHLPRVYTGFLDYFVLPPKIEERFIDFGVLSAT</p> <p>EASNILFAIINSNPIELAIKSWHIGDG\LSIELVAVDRGNRTT</p> <p>IISLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH</p> <p>DGAIQITTDYEILTIPVK\AVIAGSLTCSPKHVVLPPSPFGKI</p> <p>VHQSILNIMNSFSQKVIQQIRSLSEBDRFYKRLRGNKEDLEPG</p> <p>KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPGVAMQEDM</p> <p>WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI</p> <p>TAEISWSPILSSPRHLKFPLTNTNCSS\EEEITLENP/SQDVPV</p> <p>YVQFIPALALYSNPSVFVDKLVSFRNLSKVAKIDLRTLEFQVFRN</p> <p>SAHPLQSSSTGFMEG\LSPLHILNLILKPEGKSVKVK\FTPVHN</p> <p>RTVSSLIIVRNNTVMDAVMVQGGTTENLRVAGKLPGPGSSLR</p> <p>FKITEALLKDCTDSLKLREPNTLKRFTKVENTGQLQIHIETIE</p> <p>ISGYSCEGYGFKVNCQEFTLSANASRDIIILFTPDFTASRVIR</p> <p>ELKFITTSSEGFVFI LNASLPYHMLATCAEALPRPNWELALYII</p> <p>ISGIMSALFLLVIGTA\YLEAQGIWEP\FRRRLS\FEASNPPFD</p> <p>VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA</p> <p>GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA</p> <p>SSQFANKTRPLVLDSNTGAQGSAGRKS KGAKQS QHGSQHHAHS</p> <p>PLEQHPOPPPLFPVPVQPQEPQPERLS PAPLAHPSPHERASSARH</p> <p>SSESDSITSLIRAMDKDFDHDSPALEVFTEQPPSPLPKSKGKG</p> <p>KPLQRKVKPPKKQEEKEKKGKGPQDELDKSLADDDSSSTTTE</p> <p>TSNPDETEPLLEDTEKQKQKQAMPEKHESEMSQVKQKSKLLNI</p> <p>KKEIPTDVKPSSELEPYTPPLESKQRRNLPSKIPLPTAMTSGSK</p> <p>SRNAQKTGTSKLVNRPALAKFLPNSQELGNTSSSEGEKDS</p> <p>PPEWDSVPVHKPGSSTDLSYKLSLQTLNADIFLKQRQTSPTPAS</p> <p>PSPPAAPCPFPVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA</p> <p>SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS</p> <p>HAPVDSGSDSSGLWSPVSNPSSPDFTPLNSFSAPGNSFNLTGE</p> <p>VFSKLGLSRSCNQASQSRWNEFNSGPSYLWESPATDPSPSWPAS</p> <p>SGSPHTATSVLGNTSGLWSTTFSSSIWSSNLSALPFTTTPAN</p> <p>TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPITGR</p> <p>RSSDPWNSNSHFPHEN</p>
5820	310	1270	<p>RVSLSGPVSGLVLLCARSSMTGKRDNRAVYMNPIAMARSRGPIQ</p> <p>SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFEKMN</p> <p>ENWKKELEKHREKLLSGSESSSKRQRKKKKKKSW*\DSSSS\</p> <p>SSSSDSSSSSSDSEDEKQKRRKKKKNRSHKSSSSSMSETES</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DSKDSLKKKKKSKDGTETEKEKDIKGLSKKRMYSSEDKPLSSESLS ESEYIEEVRAKKKSSSEEREKATEKTKKKKKKKHKKKKKKKAA SSSPDSP*H*EKSGFPYKESAMSEISTVKTTTYLLKCMNPLVF GIIPGLFSSSHSDATV
5821	179	915	KWRNQSQRWPKPGTNWMLSCSVCWRRVTWTGVSVMRKLKGHPQT PT/IKDCSIAATGKRPSARFPHQRRKKRREMDGLAEGGPQRSN TYVIKLFDRSVDLAQSENTPLYPICRAWMRNSPSVRERECSPS SPLPLPEDEEG\SEVINSKSR*CVQACPTHTPGGQPKNACR\ SRIPSPALALRMQGT*P*RWSPFEPEPSPSTLIYRNMQRWKRIRQ RWKEASHRNQLRYSESMKILREMYEQ
5822	464	4379	QTLKEMPIVMARDLEETASSEDEEVISQEDHPCIMWTGGCRRRI PVLVPHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA HGFHEVHPSSTDYNLMWTGSHLKPFLRLTLSEAQKVNHFPRSYE LTRKDRLYKNIIRMQHTHGFKAFHILPQTFLPAEYAEFCNSYS KDRGPWIVKPVASSRGRG\YVLINPNQISLEENILVSRYINNP LLIDDFKFDVRLVYLVTSYDPLVIYLYEGLARFATVRYDQGA NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLR LKQEGRDTTALMAHVEDLIIKTIISAEALAIATACTFVPHRSSC FELYGFDVLIDSTLKPWLLEVNLSPLACDAPLDLKLKASMISD MFTVGVFVCQDPAQRASTRPIYPTFESSRRNPFQKQRCRPLSA SDAEMKNLVGSAREKGPGLGGSVLGLSMEEIKVLRVKEENDR RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFPQDRMTADG APELKI*SLNSKAKLHAALYERKLSLEVRKRRRRSSRLRAMRP KYPVITQPAEMNVKTETSEEEEEVALDNEDEEQEASQEEESAGF LRENQAKYTPSLTALVENTPKENSMKVREWNKGGHCKKLETOE LEPKFNLMLQIDQNGNLSKMQARIAFSAYLOHVQI\RLMKDSGG QTFASWAAKEDQEMELVVRFLKRASNNLQHSRLMVLPSSRLAL LERTRILAHQLGDFIIVYNKETEQAEEKSKKKVEEEEDGVNM ENFQEFIRQASEAELEEVLTFTYQKNKSASVFLGTHSKISQNN NYSDSGAKGDHPETIMEEVKIKPPKQQQTTEIHSCLKSRFTTSA EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPPGCHHSS LSQIPSAIPSPHQPTILLNTVSASAPCLHPGAQNIPTPTGLP RCRSGSHTIGPFSFQSAAHYISQKLSRPPSSAKAGSCYLNKHHS GIAKTQKEGEDASLYSKRYNQSMVTAEQLRLAEKQAAQYSPSS HINLLTQQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ SDPQAPENHSSSPGSRSLQTGGFAWEGEVNNVYSQATGVVPQH KYHPTAGSYQLQFALQQLQQLQSRQLLDQSRARHQAFSGST LPNSNLWTMNGAGCRISSATASGQKPTTLPQKVVPPSSCASL VPKPPPNHEQVLRRTSQAASKGSSAEGQLNGLQSSLNPAAFVP ITSSDPAHTKIMNHKHTKQPVHHSWVHD
5823	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLADEKFDF DLSSLSSSSANEDDEVFFGPPGHKERCIAASLELNNPVPEQPPLP TSESPFAWSPLAGEKFVEVYKEAHLALHIESSRNQAAQAAP EDPRSQGVVERFIQESKF\KINLFEKEKMKKSPTSLKRETYYS DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPFHSAHALP RESCATAHAASQAATQKPGTKLLPRAASVRGRGIPGAEEKPKK EIPASPSRTKIPEKESHARDVLPDKPAPGAVNPAAGSHLQGGK RAIPVP\NKLGLKKTLLKAPGSYN\LQRKSSSGA\VWSSGASSA CTPQPVAKSSSEFASIPAN*LPGLCPNISK\GRMGPAMLRPA L\PAGEVG\ASSWQAKRVDVSELAEEQLTAPP\SASPTQPTPE GGG\QWLNSSCAWSESSQLNKTRSIIRRDSCLSKTKVMPTFTN QFKIPKFSIGDS\PDSSSTPKLSRAQRPQSVGRVTVHSTFVR RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPTKMPRAVGS PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDNR\LVDVSPDR GSPPSRVPQALNFSPEESDSTFSKSTATBVAREEAKPGGDAAPS EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPADK ENVDSPLLKF
5824	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLADEKFDF DLSSLSSSSANEDDEVFFGPPGHKERCIAASLELNNPVPEQPPLP TSESPFAWSPLAGEKFVEVYKEAHLALHIESSRNQAAQAAP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EDPRSQGVVERFIQESKF\KINLFEKEKEMKKSPTSLSKRETYLLS DSPLLGPPVGPRLASSPALPSSGAQARLTRAPGPPHSAHALP RESCATAHAASQAATQRKPGTKLLLPRAASVVRGIPGAEEKPKK EIPASPSRTKI PAEKESHDRDVLDPKPAAGAVNPAAGSHLGQK RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA CTPQPVAKAKSSEFASIPAN*LPGLCPNISK\GRMGFAMLRPA L\PAGFVG\ASSWQAKRVDVSELAEEQLTAPP\SASPTQPQTPE GGG\QWLNSSCAWSESSQLNKTRSIIRRDSCLSNKTVMPTPTN QFKIPKFSIGDS\PDSTPKLSRAQRPSCTSVGRVTVHSTPVR RSSGPAPQSLLSAWRVSALEPTASRRCSGLPMPPTKMPRAVGS PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDNR\LVDVSPDR GSPPSRVPAALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSPLIQLSPADK ENVDSPLKLF
5825	2	4210	FLQTESASPAPSSGFLAAHPHSPGGLATKGRSRLSAPGMLHL SAAPPAPPPPEVTATARPCLCSVGRRGDGGKMAAGALERSFVEL SGAERERPRHFREFTVCSIGTANAVAGAVKYESAGGFYVESG KLFSVTRNRFIHWKTSODTLELMEESLDINLLNNAIRLKFNCS VLPGGVYVSETQNRVILMLTNQTVHRLLLPHPSRMYRSELVD SQMQSIFTDIGKVDFTPCNYQLIPAVGISPNSTASTAWLSSD GEALFALPCASGGIFVLKLPFYDIPGMVSVVELKQSSVMQRLLT GWMPTAIRGDQSPSDRPLSLAVHCVHEDAFIFALCQDHKLKRMWS YKEQMCLMVAADMLEYVPVKDLRLTAGTGHKLRLAYSPTMGLYL GIF\MHAFKRGQFCIFQLVSTESNRYSLDHISSLFTSQETLIDF ALTSTDIWALWHAENQTVVKYINFEHNVAGQWNPVFMQPLPEE EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL DLSWSELKKEVTLAVENELQGSVTEYEFSSQEEFRNLQQEFWCKF YACCLQYQEALSHPLALHLNPHNTNMVCLLKKGYLSFLIPSSLVD HLVLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTV DMSVIMEMSCYNLOSPEKAAEQILEDMITIDVENVMEDICSKLQ EIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRNMLTQLY GSNTAGYIVCRGVHKIASTRFLICRDLILQQLMRLGDVAVIWG TGQLFQAQDILLHRTAPLLSYLIKWSECLATDVPLDTLESN LQHLVLELTDGALMANRFVSSPQTIVELFFQEVARKHII SHL FSQPKAPLSQTLGNWPEMITAITSYLLQLLWPSNPGCLFLECLM GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAL ECFQAASEVGKEEFLDRILRSEDGEIVSTPRLQYYDKVLRLLD VIGLPELVIQLATSITBASDDW\KSQATL\RTCIFKHH\DLG \HNSQAYGSL*PQIPDSSRQLDCLRLVVLCCERSQLQDLVEFS YVNLHNEVVGIIESRARAVDLMTHNYELL YAFHIYRHNRYKAG TVMFEYGMRLGREVRTLRLGLEKQGNCYLAALNCLRLIREYANI VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE CSLARIRLTLAQHDPASAVAVAGSSSAEEMVTLVQAGLEDTAIS LCQTFKLPLTPVFEGLAPKCIKLQPGGEAAQAEAWLAANQLS SVITTKESSATDEAWRLLSYTLERYKVQNNLYHHCVINLLSHG VPLENWLINSYKKVDAEELLRLVLYDLDLTPYQVIRICGC
5826	3	871	KSQLLRDHSAPPPKPTSVGAMGC*PRQ/SPKEQQRQLKKQKNR AAQSRQKHTDKADALHQOESLEKDNLALRKEIQSLQAEALW WSRTLHVHERLCPMDCASCSAPGLLGCWDQAEGLLGPFGQGHG CRQLELFQTPGSCYPAQFLSPGPQPHDSPSLLQCPLPSLSLGP AVVAEPPVQLSPSPLLFASHTGSSSLQSSSKLSALQPSLTAQTA PPQLELEHPTRGKLGSSFDNPSSALGLARLQSRHEKPAASAAT WQGLVVDPSPHPLLAFLPLSSAQVHF
5827	194	2287	GMGSENSALKSYTLREPPTFLPSGLAVYPAVLQDGKFASVIFYK RENEDKVNKAAPV**HLKTLRHPCLLRLFLSCTVEADGIHLVTE RVQPLEVALETLSAEVCAGIYDILLALI FLHDRGHLTHNNVCL SSVVFSEGDHWWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP EEMSPFTTLLPECHGHARDAFSFGTLVESLLTILNEQVSADVLS SFQTLHSTLLNPIPKWRPALCTLLSHDFFRNDLFLEVNFLLKSL TLKSEEEKTEFFKFLLDVSVCLSEELIASRLVPLLLNQLVFAEP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VAV\KSFLPYLLGPKKDHQAQGETPCLLSPALFQSRVIVPVLQLF EVHEEHVRMVLSSHIEAYVGALSLEQLKKV\IL\PQVLLG\LR D\TSDSIVAITLHSLAVLVSLGPEVVVGGERTKIFKRTP\SF TK\NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSNFSSSKK SEEPDWSGPE\EPENQTVNI\QIWP\REP\CDDVKSQCTTLDV EESSWDDCEPSSLDTKVNPGGGITATKPVTSGEQKPIPALLSLT EESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSEL GLGEEFTIQVKKKPVKDPEDMDFADMIPEIKPSAAFLILPELRT EMVPKKDDVSPVMQFSSKFAAAEITEGEAEGWEEEGELNWDNN W
5828	2	257	AREGGSLGAVAACGELS YSCDFCPARPHTSWLTRFVKMEFQAVV MAVGGSRMTDLTSSIPKPLL PVGNKFLIWIPLNLLERVGFEEV IVVTTTRDVQKALCAEFKMKMKPDIVCIPDDADMGATDSLRIYYP KLKTDVLVLSCDLITDVALHEVVDLFRAYDASLAMLMRKGQDSI BPVPGQKGGKKAQORDFIGVDSTGKRLLFMANEADLDEELVIG GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS BL\IPYLV/RGKQFSSASSQGTREKEGEGSGKGRGLKSFRISY SFY*KEANYTGTGAPY\DACWI
5829	260	1259	PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFNPS GTCIASAGSDQTVKVDVRVNKLLQHYQVHSGGVNCSIFHPSGN YLITASSDGTLLKILDLKGRLIYTLQGHGTGPVFTVSFSKGGELF ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSPHLLDIY PRTPHPEBKVETVEDFFLHLLRLIQSLR*SIKRSLLPLLWISF LLILPQQQKPVVGLCQTRVKRPVDIS*TL*CHQNVCCQPRKRR KQT*VTSVPKVK/VSIPLAVTDALEHIMEQLNVLQTVSILEQR LTLTEDKLDCLLENQQLFSAVQQKS
5830	4496	3139	GGKMAAPEERDLTQEQTLLQFQDLTGIESMDQCRHTEQHNW NIEAAVQDRLENEQGVPSVFNPPSRPLQVNTADHRIYSYVVS PPRGLLGWGYLLIMLPFRFTYITLIDIFRALRIFIRDPRSRV TDPVGDIVSFMHSFEEKYGRAHPVYFQGTYSQALNDAKRELRL FLVYLHGDDHQDSDEFRCNTLCAPEVISLINTRMLFWACSTNKPE GYRVSQALRENTYPPFLAMIMLKDRRE*PV\VGRLEGLI\QPDLL INQLTFIMDANQTYLVSERLEREERNQTVLRQQQDEAYLASLR ADQEKERKKREERERKRRKKEEVQQQLAEERRRQNLQEEKERK LECLPPEPSPDDPESVKIIFKLPNDSRVERRRFHSQSLSLTVIHDF LFSLKESP\EFQIEA\NPPRR\VLPCIPSEE\WPNPPTLQEA GLSHTEVLFVQDLTDE
5831	71	2897	FCSDKCCLYLPDSINRSKCTAKPGAHSQDRHAVMDSEKQVKD TDDIESPKRSIRDSGYIDCWDSERSDSLSPRHRGRDSDSFLDS FGSRSRQTPSPDVVLRGSSDGRGSDSEDLPHRKLDPVKDDMS ARRTSHGEPKSAVPFNQYLPNKSNTAYVPAPLRKKKAREEYR KSWSTATSPAGLGKALQDYGPRT\PVS\DDAESTSMFDMRCEE EAAVQPHSRARQEQQLINNQLREDDKWQDDLARWKSRRKRSVS QDLIKKEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKERRE RELHEAYKNARSQEEAEGILQOYIERFTISEAVLERLEMPKILE RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSPQKNSQDVLKTFK VDGKVS VNGETVHREEEKERECPVAPAHSLTKSQMPEGVARVH GSPLELKQDNGSIEINIKPNVSPQELAAATTEKTEPNSEQBDKN DGKSRKGNIELASSEPHFTTTVTTRCSPTVAFVEFPSSPQLKND VSEKQKQKPNEMSGKVELVLSQKVVKPKSPPEATLTFFFLD KMPEANQLHLPLNLSQVDSPESEKSPVTTFFKFWAWDPEEERRR QEKWQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEBRRY YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL GNCQDEKQDRRWKSFQGDSDLLKTRSDRLEEKGSLEBEGAL AHSQNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNOQTSN PTHSSBDVKPKTLPLDKSINHQIESPSERRKSIKGLKLCSSCGL PLGKGAAMIETLNLVFIHQCFROG\ICKGQLGDAVSGTDVIR NGLLNCNDCYMRSRAGQPTTL
5832	2454	829	PGRRRFRHSGCAFOKQCTIMLHICQYFLOGECKFGTSCKRSHDFSN SENLEKLEKLGMSDDLVSRLPTIYRNAHDIKNSSAPSRVPPLF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VPOGTSEKDDSSGSSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH RVHFHLPYRWQFLDRGKWEDLDNMELIEEAYCNPKIERILCSES ASTFHSCLNFMNTYGTATQARRLSTASSVTKPPHILTTDWIW YWSEDFGSWQYGRQGTVPVTTVSSSDVEKAYLAY/WYTGVR PGSHLEVPRKAQLRVRFQSLRSEKPLWHN*KGLPQTQIR\AP QDVTMTQTCNTKFPKPSIPDYWDSSALPDGPFQKITLSSSSEE YQVWNLFNRTLPPFYVQKIERYQNLALWEVYQWQGMQKQNG GKAVDERQLFHGTS AIFVDAICQNFQDWRVCGVHGTSYKGSYF ARDAAYSHHYSKSDTQTHMTFLARVLVGEFVRGNASFVRPPAKE GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV TPSILLALGSLFSSRQ
5833	170	3289	SILCLLSPCVVQFGKPVVSISSSRHSRSPCTKKGWEGMRKHLHT RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR GRDWNVKWEENLLHAAVAKNYTLLQTIPEFERPFKDHQVCLEWNM GYIWNLRANRIPQCPLNDVVALLGFPYASSGENTGIVKKFPRF RNRLEATRQRMDDYPVFTVSLWLYLLHYCKANLCGILYFVDSN EMYGTPSVFLTEEGYLHIQMHVKGEDLAVTKFIIPLEKWFRL DISFNGGQIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII GGSRYVAGIEGFFGPKYRLRSLHPAQIFNPLEKQLAEQIKL YYERCAEVQEI VSVYASAAKHGGERQEACHLHNSYLDLQRRYGR PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNQNESVSEIG GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYLAV FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYYQGDIN YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRLKDDIIL KVQTKEDGDVFMWLKHEATRGNAQAQRLAQMLFWGQGGVAKNP EAAIEWYAKGALETEDPALIYDYAIVLFKGGQGVKNRRLALELM KKAASKGLHQA VNGLGWYHKKKNYA\KAAKYWLKA\BE\MGN PDASYNLGVHLHDGIPPGVPGRNQTLAGEYFHKAQGGHMEGTI WCLSYIITGNLETFRDPEKAVVWAKHVAEKNGYLGHVIRKGLN AYLEGSWHEALLYVLAETGIEVSQTNLAHICEERPDLARLYL GUNCVWRYYNFSVFQIDAPSFAYLKMGDLYYGHQNSQDLELS VQMYAQAALDGDSSQGFNLALLIEGTIIPHHILDFLEIDSTLH SNNISILQELYERCWSHSEESFSPCSLAWLYLHLRLWGAITH SALIYFLGTLLSILIAWTVQYFQSVASDPPRPSQASPDAT STASPAVTPAADASDQDQPTVTNNPEPRG
5834	17	4020	RFRFGGRVFPFGAFPASPSDSLQGGNSQGFPTFKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQKADCPLELALKPRMAAQV TLEDALSNVDLLEELPLDQQPCIEPPSSLLYQPNFTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMMNFYFQRNAIERFC GEVRRILCHAEERRKDFVSEAYLITLGFIMFAVLDELKMKCSV KNDHSAYKRAAQFLRKMDPQSIQESQNLMSFLANHNKITQSLQ QQLEVISGYEELLADIVNLCVDYENRMYLTPSEKHMILLKVMGF GLYLMGDSVSNYKLDKAKRINLSKIDKYFKQLQVVPFLFGDMQI ELARYIKTSAHYEENKSRWCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTSGRQEAQKTDAYRKLFDLALQGLQLL SQWSAHVMEVYSWKL VHPTDKYSNKDCPDASAEYERATRYNYS EEKFAIVEVIAMI KGLQVLMGRMESVFNHAIKRTVYAALQDFSQ VTLMEPLRQAIKKKNVIQSVLQAIKRTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRAVGPSTQLYMVRTMLESLIADKSGSK XTLRSSLEGPTILDEKPHRESFFYTHLINFSETLQCCDLSQL WREFFLLELTMRRIQFPIEMSMPIWILTDHILETKEASMEYVL YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPFSNRYETLLKQR HVQLLGRSIDLNLITQVSAAMYKSLAIGRFESEDLTSIVE LDGELLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL HFWELNVDLFPNYCYNGSTNRFVRTVLPFSQEFQRDKQPNAP QYLHGSKALNLA YSSYIYGSYRNFVGPFPFQVICRLGLYQGIADV MEELLKVVKSLQGTILQYVKTLMVMPKICRLPRHEYGSPGIL EFFHHQLKDIVEYAEKTVCFQNLREVGNAILFCLLIEQSLSLE EVCDDLHAAPFQNILPRVHVKEGERLDAKMKRLESKYAPLHLVP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LIERLGTPQQIAIAREGDLTKERLCCGLSMFEVILTRIRSF LD DPIWRGPLPSNGVMHVDECEVEFHLWSAMQPVYCI PVGTHEFTV EQCFDGLHWAGCMIIVLLGQQRRFAVLDFCYHLLKVQKHDGKD EIIKNVPLKKMVERIRKQILNDEIITILDXYLKSGDGBGTPEV HVRCFPPIHQSLASS
5835	4209	1904	SGNIRMAQGS HQIDFQVLHDLRQKFPEVPEVVSRCLQNNNNL DACC AVL S Q E S T R Y L Y G E G D L N F S D D S G I S G L R N H M T S L N L D L Q SQNIYHHGREGSRMNGSR L T H S I S D G L Q G G Q S N S E L F Q Q E P Q TAP AQ V P Q G F N V F G M S S S S G A S N S A P H L G F H L G S K G T S S L S Q Q T P R F N P I M V T L A P N I Q T G R N T P T S L H I H G V P P F V L N S P Q G N S I Y I R P Y I T P G G T T R Q T Q Q H S G W V S Q F N P M N P Q Q V Y Q P S Q G P W T T C P A S N P L S H T S S Q Q P N Q Q G H Q T S H V Y M P I S S P T T S Q P P T I H S G S S Q S S A H S Q Y N I O N I S T G P R K N Q I E I K L E P P Q R N N S S K L R S S G P R T S T S S S V N S Q T L N R N Q P T V Y I A A S P N T D E I M S R S Q P K V Y I S A N A A T G D E Q V M R N Q P T L F I S T N S G A S A S R N M S G Q V M G P A F I H H H P P K S R A I G N S A T S P R V V V T Q P N T \ E Y T F K I T V S P N K P P A V S P G V V S P T F E L T N L L N H P D H Y V E T E N I H L T D P T L A H V D R I S E T R K L S M G S D D A A Y T Q D I * R I S N S W L G M V A H A C N S S A L G G Q D G R I I * A Q E F E T S W G N I W R L R L Y R R F * N Y A G M V A H T C S P S Y S V D * A L L V H Q K A R M E R L Q R E L B I Q K K L D K L K S E V N E M E N N L T R R R L K R S N S I S Q I P S L E E M Q Q L R S C N R Q L Q I D I D C L T K E I D L F Q A R G P H F N P S A I H N F Y D N I G F V G P V P P K P K D Q R S I K T P K T Q D T E D D E G A Q W N C T A C T F L N H P A L I R C E Q C E M P R H F
5836	361	2303	FHITMCGICCSVNFSAEHFSQDLKEDLLYNLQKRGPNSSKQLLK SDVNYQCLFSAHVLHLRGLVLTTPVEDEGRNVFLWNGEIFSGIK VEAEENDTQILFNLYLSSCKNESEILSLFSEVQGPWSFIYYQASS HYLWFGDRDFGRRSL LWHFSLNKGKSPCLSSVGTQTSGLANQWE VPAS \ D F S E L I L S L S F P D A L F Y N C I L G N I F L G R I L L K M L I A * V K P Q O T Y O H L Y Q R * Q M K P N C I L K N L L F L * I * C C H K L H W R L I A V I F P M C H L Q E R Y F K S F L L M Y T * K E V I Q Q F I D V L S V A V K K R V L C L P R D E N L T A N E V L K T C D R K A N V A I L F S G G I D S M V I A T L A D R H I P L D E P I D L L N V A F I A E E K T M P T T F N R E G N K Q K N K C E I P S E E F S K D V A A A A D S P N K H V S V P D R I T G R A G L K E L Q A V S P S R I W N F V E I N V S M E E L Q K L R R T R I C H L I R P L D T V L D D S I G C A V N F A S R G I G W L V A Q E G V K S Y Q S N A K V V L T G I G A D E Q L A G Y S R H R V R F Q S H G L E G L N K E I M M E L G R I S S R N L G R D D R V I G D H G K E A R F P F L D E N V V S F L N S L P I W E K A N L T L P R G I G E K L L L R L A A V E L G L T A S A L L P K R A M Q F G S R I A K M E K I N E K A S D K C G R L Q I M S L E N L S I E K E T K L
5837	4792	903	NGNAVAQAPVTNCCYLATGSKDQTI RIWCSRGVMI LKLPFL KRRGGGIDPTVKERLWLT LHWPSNQPTQLVSSCFGELLQWDLT QSWRRKYTLFSASSEQNHSRIVFNLCPLQTEDDKQLLLSTSM D RDVKCWDIATLECSWTLPSLGGFAYS LAFSSVDIGSLAIGVGDG MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT DDGKVGLYDTYSNKPPQISSTYHKKT VYTLAWGFPVP PMSLGGE GDRPSLALYSCGGEGIVLQHN PWKLSGEAFDINKLIRDNTSIKY KLPHVHTISWKADGKIMALGNEDGSIEIFQ \ IPNLKLICTIQQH HKL V N T I S W H H E \ H G S P A Q K L S Y L \ M P S G S Q Q C S P F T C H N L K N C P * K A A P E S P S D P L Q S P Y R T P P Q G H T A Q D Y P V W A W E P H I H * W E G L V F C F P I D G S P G C W D \ A F P G K E A P V A I F R G \ H Q R L L C V A W S P L D P D C I Y S G \ A D D F C V H K W L T S M Q D H S R P P Q G K K S I E L E K K R L S Q P K A K P K K K K P T L R T P V K L E S I D G N E E B S M K E N S G P V E N G V S D Q E G E E Q A R E P E L P C G L A P A V S R E P V I C T P V S S G F E K S K V T I N N K V I L L K K E P P K E K P E T L I K R K A R S L L P L S T S L D H R S K E L H Q D C L V L A T A K H S R E L N E D V S A D V E E R F H L G L F T D R A T L Y R M I D I E G K G H L E N G H P E L F H Q L M L W K G D L K G V L Q T A A E R G E L T D N L V A M A P A A G Y H V W L W A V E A F A K Q L C F Q D Q Y V K A A S H L L S I H K V Y B A V E L L K S N H F Y R E A I A I A K A R L R P E D P V L K D L Y L S W G T V L E R D G H Y A V A A K C Y L G A T C A Y D A A K V L A K G D A A S L R T A A E L A A I V G E D E L S A S L A L R C A Q E L L L A N N W V G A Q E A L Q L H E S L Q G Q R L V F C L L E L L S R H L E E K Q L S E G K S S S V H T W N T G T E G P F V E R V T A V W K S I F S L D T P E Q Y Q E A F Q L Q N I K Y P S A T N N T P A K Q L L H I C H D L T L A V L S Q Q M A S W

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DEAVQALLRAVVRSDSGSFTIMQEVYSAFLPDGCDHLRDKLGD HQSPATPAFKSLEAFFLYGRLYEFWWSLSRCPNSSVWVRAGHR TLSVEPSQQLDTASTEETDPETSQPEPNRPSLDLRLTEEGERM LSTFKELFSEKHASLQNSQRTVAEVQETLAEMIRQHQKSQLCKS TANGPDKNRPEVEAEQPLCSSQSQCKEKEKNEPLSLPELTKRLTE ANQRMAKFPESIKAWPPDVLECCLVLLLRSHFPGCLAQEMQQ QAEQLLQKYGNTKTYRRHCQTFCM
5838	110	98	KTMPHLLVTFRDVAIDFSQEWECLDPAQRDLRYDVMLENYSNL ISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFYNG LGDNMECKGNLEGQVSKSEGLYMCVKITCEKATESHSTSTSTFH RII/HYQGKIVKCKEQRQGFSYLSCLIQHEENHNI*KCSEVNKH RNTFSKKPSYI*HQ\KFRLGKPKYECMECGKAFGRSTDLIHQK IHTNEKPYQCNAKGAFIRGSQLTEHQRVHTGEKPYDCKKCGKA FSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSG EKPYECKECGKAFILGSHLYHQRVHTGEKPYICECKGKAFILCA SQLNEHQRIHTGEKPYECKECGKTFFRGSQLYTHLRVHSGERP YKCKEKGKAFISNSNLIHQRIHTGEKPYKCKEKGKAFICGKQLS EHQRHTGEKPFECCKEKGKAFIRVAYLTQHEKIHGEKHYECKEC GKTFFVRATQLYTHQRIHTGEKPYKCKEKGKAF/HLWLTILSEHQ RIHRGEKPYECKQCGR/LFIRGSHL/NEHLRHTGEKPYECKEC GRAFSRGSEHTLHQRIHTGEKPYTCVQCGKDFRCPSQLTQHTRL HN*EYSSHKICMHSIALASLDFAHLQEKNPEN
5839	1	2425	GRPFPRPPRALPRLPLRGRQDGRWTVDFEECLKD\SPRFRAAL EEEVGDVAEELEKL\DKLVKLCIA\MIDTGKAPCVANKQFMNGI RD\LAQNS\NDA\VVETKFAPSFLLSQEMINFHTIL/L*PNS EIN*GHSFQNFVKEDLRKFDAKKQFENSQ*KRKKIALVKNAFV PSRPASLEL*KPPNLTATRKCFRRIALDYVLOINVLQSKRRSE ILKSMLSFMYAHLAFFHQGYDLFSELGPYMKDLGAQLDRLVGDA AKEKREMEQKHSTIQCKDFSRDDSKLYNVDAANGIVMEGLFK RASNAFKTWNRRWFSIQNNQVVYQKKFDNPTVVVEDLRLCTVK HCEDIERRFCFEVVSPTSKCMLQADSEKLQAWIKAVQTSI\AT AYREKDDSEKLDKSSPSTGSLDSGNESKEKLLKGESALQVQ CIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSGLGVHFSK VRSLLTLDTWEPPELLKLMCELGNDVINRVYEANVEKMGIKKPPG QRQKEAYIRAKYVERKFVDKIPL*SLSPPEQQKK\FVSKSE EKRLSISKFGP/GDQVRASAQSSVRSNDSGIQQSSDDGRESLPS TVSANSLYEPBGERQDSSMFLDSKHLNPGQLYRASYEKNLPKM AEALAHGADVNNANSEENKATPLIQAVALGGSLVTCEFLQNGAN VNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQATDEBGDPLS IAVEAANADIVTLRLRLARMNEEMRESEGLYQGPGEDETYQDIF RDFSQMASNNPEKLNRFQQDSQKF
5840	698	3610	KHLHLPRQHLTTLWQISSPRWRSFQRAFMSALSKTQTQSAPALQ GLSSLLQSVTGNPVPASEAASQSTSASPANTTVYTIKGRNLPSS AQPFIPKSFNYPNSSTSEVSSTASAKASIGQSPGLPSTAFKLP SNTKGFTATHTNSPAAPPTVETICQSEVSKPKL\ESESTSPSL \EMKIHNFLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHPSDFQ RGPTSTSIDNIDGTFVRDERSGTPTQDEMMDKPTSSSVDTMSLL SKIISPGSSTPSSTRSPPGRDESYPRELSNSVSTYRPFGLGSE SPYKQPSDGMERPSSSLMDSSQEFYPTDSFQEDEDYRDFEYSGP PPSAMNLOKKPAKSILKSSKLSDTTEYQPIILSSYSHRAQEFV KSAFPPSVRALDSSENCRLSSSPGLFGAFSVRGNEPGSDRSP SPKNDSEFTPDNSHNLSQSTTGHLSLPQKQYPDSPHVPHRS LFPSPQNTLAAPTGHPPPTSGVEKVLASTISTSTIEFKNMLKNAS RKPSDDKHFGQAPSKGTPSDGVLSNLTPSLTATDQQQBEHY RIETRVSSSCLDLPDSTEKGAPIETLGYSASNRMSGEPIQT VESIRVPGKNGRNGHREASRVGWFDLSTSGSSFDNGPSSASELA SLGGGSGGLTGFTAPYKERAPQFQESVGSFRSNSFNSTFEHH LPPSPLEHGTFFQREPVGPSSAPPVPPKDHGGIPSRDAPTHLPS VDLNPFPTKEAALAAHAPPPPGHSGIPFPTPPPPPPGHESS SGGSGVPFSTPPPPPPVDHSGVVPFPAPPLAEHGVAGAVVFP KDSSLLQGTAEHFGVLPGRDHGGPTQRDLNGPGLSRVRESL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TLFHSLSLEHLGPPHGGGGGGSSSSSGPPLGPSHRDTISRSGIT LRSRPDPFRPREPFLSRDPFHSLSLRPRPPFARGPPFFAPKRPPF PPRY
5841	1908	762	GLRLFLVLTVWPMKPSWLSRTEFSKRLLCRTLWCQSGWSSRSY TRSMKMTTSINRRSRTSTKSTRTSAREGLTATVIGLSDSPTW RHCNMTARSCSGEKGHWAPRQGVYLLPGRVGCVSSRVSPSPFP GDGLDSGLARRGSASVALASGLVEEPLMGPFFHTPRPKAVSAK SKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFND QSTSDYLVVYLRLLTSGYLQRESKFFEHFIEGGRTVKEFCQ\QE \VEPMCKESDHIHIALAQGLQRVHPGWBYMGPRPRAATTNPHI FP*GLSPFKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPPLLARA LGHCYRGFSVVVWKS YFTFPFFLSHDPFPMFY
5842	307	1918	QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVRVRKL WSSRRPRTRRNLGLTACAIYLGFLVSQVGRASLQHQAEEKGP HRSRDTAEPSPFEIPLDGLAPPESQNGSTLQPNVYITLRSK RSKPANIRGTVPKRRKKHAVAAPGQEAALVGPQLQPEA\EG KLML*HLGTLREQTWLRLESDEGGWCGVRE/WRAGGPDFLQSS RESNIRIYESAPSWSLKDDIRRMRLADSAGVLRPVSSRSGA RLVLVEGAPGAVLRCPSPCGLLKQPLDMSEVFAFLDRILGL NRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSVKLTW GTYYQLLKQKQWQNGRVPKPESGCTEIIHHEWSKMALFDLLOI YNRLDTNCCGFRPRKEDACVQNGLRPKDDQGSAAALHI IQRK DPRHLVFIDNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSQ LRQKLLQSLFLDKGYWESQGGRGIEKLIDVIEHRAKILITYIN AHGVKVLPMNE
5843	500	1453	GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPGWGLGAGM RGSRMSPQPQLRRAQSSCCHFMVKLLDDGTPIPGKEVAHTSL DALVTFHQKQPIEPRELLTQPCRQDPAENVYEDFLYSNAVA EEAACPVSAPEEASPKVLC HQSKERKPSAEM/RQNNHQSGSHFL LPFKIPSWRDPPEETLEEQNAPRERPEGPAACKPPRHCELVVT LGCPEIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSCLCHISQKP LTAPGTQRKQKPGHGEQEVGQLH*GDPGQELAPNGSESPIPG VQARAPGLGRA
5844	202	2471	FDSAVLSSINVMVLPGLQLLGVLLTISLSSIRLIQAGAYYGI KPLPQPPIPPQMPPIQYQPLGQQVPHMPLAKDGLAMGKEMPHL QYGEYPHLPQYMKIEIQAPRPMGKEAVPKKGKEIPLASLRGEQ PRGEPGRGPPGPGPLPGHGIPGIGKPGPGQYGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPFGHGLPGIGK PGGPGLPQGPQKGRGPKGLPGPQCLRGPKGDKGPGMPGAPGV KGPMPGMHGPFGVGLPGVGPVTFPGP\QGPLGK\PGAPGEP GPQGPFGVPGVQGPPIPGIGKPGQDG\IPGQPGFGGKGEQGL PGLPFPGLPGIGKPGFPKGRMGVPGALGPRGKPGPIGA PGIGGPPGEPGLPGIPGPMGPFPAIGFPGPKGEGGIVPGQSPG PKGEPGLQGFPGKPGFLGEVPPGMRGFPPIGPKGEHGQKGV GLPGVPGLLGPKGEPGIPGDQGLQGPPIPGIGGPGSGPIGPPGI PGPKGEPGLPGPPGFPGIGKPGVAGLHGPFGKPGALGPQQPG PGPPGPPGPPGPAVMPPTPPPQGEYLPDMGLGIDGVKPHAYG AKKGKNGGPAYEMPAFTAELTAPFPVGPAPVKFNKLLYNGRQNY NPQTGIFTCEVPGVYFYAYHVHCKGGNVWVLFKNNEPVMYTYD EYKGFGLDQASGSVALLLRPGDRVFLQMPSEQAAGLYAGQYVHS SFGYLLYPM
5845	215	2061	HASNKASLQDKMANPKETAMCLVNELARFNRVQPYKLLNER GPAHSMFVSQSLGEQTWESESSIKKAQQAVGNKALTESTLP KPI*KPPKSNVNNPGCITPTVELNGLAMKRG/KPAIHRPLDPK PFPNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNEFFGEGKT RQAARHNAAMKALQALQNEPIPERSPONGESGKMDDDKDANKS EISLVFEIALKRNPVSFEVIKESGPPHMKSFVTRVSVGEFSAE GEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HFFKKRPKT IVKAGPEYGGGMNPI SRLAQIQAKKEKEDYVLLSERGMPPRRR EFVMQVKVGNVATGTGPNKKIAKNAEAMLLQLGYKASTNLQ DQLEKTGENKWSGPKPGFPPTNTPKGILHLSPDVYQEMEAS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RHKVISGTTGLYLSPKDMNQPSSTSSFFSISPTSNSSATIARELLM NGTSSTAEAGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC DROSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV*YATAILLC YGPARKWKAIMEAMCAHAALLSLIHVLLAPSARLEKSKLFAIG N.
5846	1126	456	FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLNPNCSVISQDDFF KPESEIETDKNGFLQYDVLALNMEKMSAISCMWESARHSVVS TDQESABEIPILIEGFLFNYPKPLDTIWNRSYFLTIPYEECKR RRSTRVYQPPDSPGYFDGHVWPMYLYKRYQEMODITWEVVYLDGT KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK LQGV
5847	2769	505	APEMEDLSSPDSTLLQGGHNLSSASFQESVTFKDVIVDFTOEE WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGT PWIMPSIPVGTCADWETRENSVSAPEDISEEELSPEVIVEK HKRDDSWSNLLSEWEYEGSLERQQANQQLPKKIKVTEKTIPS WEKGPVNNFEGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK KEKSCCKNECGKAFSYCSALIRHQRHTHTGKPKYKCN*/CVEKAF SRSENLIHQRIHTGDKPKYKCDQCGKGFIEGPSLTQHQRHITGE KPYKDECGKAFSQRTHLVQHQRHITGKPYTCNECGKAFSQRG HPMEHQKIHTGKPFKCDKCTFTTRSTHLLTQHQRHITGKPYK CNECGKAFNGPSTFIRHMIHTGKPYECNECGKAFSQHNSLTQ HQTHTGKPYDCAECGKSFYSWSSLAQHLKIHTGKPYKCN GKAFSYCSSLTQHRRHITREKPFCECGKAFSYLSNLNQHQT HTQEKAYECKECGKAFIRSSSLAKHERIHTGKPYQCHECGKTF SYGSSLIQHRKIHTGERPYKCNCGRAFNQNIHLTQHKRIHTGA KPYECACGKAFRHCSSLAQHQKTHTEKPYQCNKCEKTFPSQSS HLTQHQRHITGKPYKCNCDKAFSRSTHLLTQHQRHITGKPYK CNECGK\TFSQSTYLIQHQRHISGEKPFQNCDCGKSFYRSALN KHQRLHPGI
5848	22	2961	AAPRRLLRGGDGRTPRFFLPALLRPGPFAEAPERRKMPAVSK GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL DGYSKKKYVCKLLFI LLGHDI DFGHMEAVNLLSSNRYTEKQIG YLFISVLVNSNELIRLINNAIKNDLASRNPTFMGLALHCIAV GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLQCY PPDPAPVRGRLTECLETILNKAQEPKSKKVQHSNAKNAVLFEA ISLIIHHDSEPNLLVRACNLQGLQHRETNLRYLALESMTLA SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN APQIVAEMLSYLETADYSIRSEIVLKVAILAEKYAVDYTW\YVD TILNLIRIAGDYVSEEVWYRVIIQVINRDDVQGYAAKTVEALQ APACHENLVKVGYYILGEFGNLIAGDPRSSPLIQFHLHLSKPHL CSVPTRALLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVEL QORAVEYLRLLSTVASTDILATVLEEMPPFPERESSILAKLKKK GPSTVTDLEDTKDRSDVDVNGGPEPAPASTSAVSTSPSADLLG LGAAPPAPAGPPSSGGSGLLVDVFSASVVAFLAPGSEDNFA RFVCKNNGVLFFENQLLQIGLKSEFRQNLGRMFI FYGNKTSTQFL NFTPTLI CSDDLQPNLNLQTKPVDPTVEGGAQVQVNVNIECVSD FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFQ RWKQLSNPQEQVQNI FKAKHPMDTEVTAKIIGPGSALLEEVD NPANFVGAGIHTKTQIGCLLRLEPNLQQAQMYRLTLRTSKEAV SQRCELLSAQF
5849	3545	1895	KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWTSEVHNW TLEDTLQWLIIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQQLKALDVLFGPLTRPPHNWMDPILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESQTAEQSLMDLQER LEKAQENRNVAVEKQNL*RKMMDEINYAKEEACRLRELEGAE CELSRRQYAEQELEQVRMALKKAEKEFELRSSWSVPDALQKWLQ LTHEVEVQYNYIKRQNAEMQLAIAKDEAEKIKKCRSTVFGTLHV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
			AHSSSLDEVHDKILEAKKALSELTTCLRERLFRWQQIEKICGFQ IAHNSGLPSLTSSLYSDHSWVMPRVSIIPPYPIAGGVDDLDDEDT PPIVSQPPGTMAKPPGSLARSSSLCRSRRSIVPSSPQPQRAQLA PHAPHPSPHRPHHPQHTPHSLPSPDDILSVSSCPALYRNEEE EEAIYFSAEKQWEVPDTASECDLSNSSIGRKQSP/SKPRDIPN IIS/DERYQEMRCP*RIPSGGIL
5850	3	1895	KAVLNFSASGSVISLTGSNPMHDSMWHLKNGIIVYLDVPLLN LICRLKLMKTDRIVGQNSGTSMKDLLKFRQYKKWYDARVFE SGASPEEVADKVLNAIKRYQDVDETFISTRHVWPDCEQKVSA EFFIEAVIEGLASDGGFLVPAKEFPKLSCGEWKSIVGATYVERA QILLERCIPADIPARLGEMETAYGENFACSKIAPIVRHLGSGN QFIELEFHGPTGSPKDLSLQMPHIFAQCIIPSCNYMILVATSG DTGSAVLNGFSRLNKDKQRIAVVAFFPENGVSDFQAKIIGSQ RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA NSINWGRLLPQVYHASAYLDLVSQGFISFGSPVDVCIPTNGSG NILAAVYAKMMGIPIRKFCASNQNHVWTDFTKGT\HYDLRGKE N*AQTFFTVQ*IIFLPLNSLNLRLHLMANKDQQLMTELFRNLES QHHPQIEKALVEKLQDDFVADWCSEGECLAINSTYNTSGYILD PHTAVAKVVADRVQDKTCPVVISSTAHYSKFAPAIMQALKIKEI NETSSSGLYLLGSYNALPPLHEALLERTKQKEKMEYQVCAADMN VLKSHVEQLVQNQFI
5851	3120	1802	RCYLQFLALLLTSTSAARAAATAAAEAPAGSFSVMTRAGDHNRO RGCCGSLADYLTSAKFLLYLGHSLSTWGDRLMWHFAVSVFLVELY GNSLLLTAVYGLVAGSVLVLGAIIGDWVDKNARLKVAQTSVLV QNVSVILCGIILMMVFLHKHELLTMYHGWLTSCYILITIANT ANLASTATAITIQRDWIVVAGEDRSKLANMNATIRRIDQLTNI LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKT PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH ELEHEQEPTCASQMAEPFRTRDQWVSYYNQPVF/LGWHGSCFP LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNGNCSFY LATSKMWFSGSDRDLRIGTAFDLFDLVDLCIHAWKPPGLVRFSP
5852	1	422	KITTFPSSLCPLRQLEPVRYSGQPLTDPLISLCRSHKCRGKGW SSSYPSLPALLRARSAPGHCTHRSCGPEWRIDSISRLEMQGARR SGWAQAQPTILLVPLRLKSLPSIWG/SLMGPFITSGPG/WFRQ YVFFISGRH*VLFTESDFYVAMDFGGHGLSSHYSYSGVFPYLLQT FVSEIRRVVAGKKQSVYFRRCGCSRAPPLITGGGVGSRKQRWP ESGAWALAPGLPAIHGRSWES
5853	223	1346	RLGLSRVKGHLHGPAASAWISDPETRGDPGPGWGMWRGSDLRPR PVSLTGLTLVCK*AAQGPQV\HSVKLCFGLGG\PCLL\FPIFRP LLHPRRPRRLHPTGRGVAVEPHALRVVHVHAGEEAGIRAAGPGH GGVEIPQG/VGSLGARRGLRPSRPSRHRNRVPAPPPGRPLATP HRRRFPPDPALTCPLGQDQGPREQQKQSGSRHDTILGDWGESE SRWVRGNFRGTAAATLIGFSRNPTLNGSENWGLSVSIQEEGPDT GWEREKRNPAEMGNPQRWASPIHTPPLGPEILRAMPEALRAMPE ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP LSSLCITESPSONWTPCLLLLTCPRLGF
5854	86	938	KGRNTAPEKKGAAALNNRENASS*NGY/SRWKQDIRRIENHIQ LKHLCAMIKRVLLERLENTKRLRELTEGRTLDPQNRITEVSAK RQIVTEYREKGRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS GAETIKDLE/ENFPKLNELDLQMEKAHRIPLKFNEKKAASRH IRVTEL/KFQRRNILQASSQRKQVYTKGAKVRLTSDFPSAILNA RRQW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQ LGKYINQELSLKILLKDLLQLTENLN
5855	536	2391	LSRYGCKAPSRISHLHK\FLPLLLLPSLLMGYSESPPFITDSWAP FISLTHHVLSSQSPLSSNCWICLSTHTQ*FTALPADLLTWTQS NVSLHISYLAIPFLADSFLLKPV/L*PGNSAKHLSFKLSSLSMV GRAVALLHLIASGLTSIQNTASSKPPWGY\LSTQTSFISPPP LCLSRTPNPAHAMVGOVQPSLCGLIFTL/RTPCRPSILHPNY KIISTSAWKVLCFSGSPITHTSLHLTTGSSFLSFHPIPGFPAA NSALYVSSLKGPFGKNTIPSPVTGT*QPPHRSN/RLTVDKDN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FFLSPKPNLSLHQLPSQ\TPYQALTGAALAGSYPIWENENTLSWL PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFQAPTIN ILPQNQTILISVEASISSSPIRNKWLHLITLLTGLGITAALGT GIAGITTSITSYQTLFTTSLNTVEDMHTSITSLSRQLDFLVGVI LQNRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD RAEL*HQVADSWWQSSLLRWIPWVAPFLGPLIFLLLMIGP CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV*YQSLRGNH SEAPEPRP
5856	173	1137	PWLHGLGLSAVFLPYL*/YVTFHLYGGIILLLLIPISIAIGILYK FQVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL IRYTGDNPSYSPITIIYFHGNAGNIGHRLPNALLMLVNLKVNLL VDYRGYKSEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLPSFFP MRYLPWCYKKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ LYELSPSRTRKRLAIFPDGTHNDTWQCQGYF\ALEQFIKEVVKSH SPEEMAKTSSNVITII
5857	1597	563	KLIGKVLVLSVVADAMAAFAVEPQGPALGSEPMMLGSPTSPPKPG VNAQFLPGFLMGDLAPVTPQFRSISGPSVGVMMRSPLLAGGS PPQFVVAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRRQPNIS VMQSPLVGVSTSPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ GDSLTSEDH\LDSSWGDCIWGFLKASA\SYILL\QFAQYGGIS* NMWMSNTGNWMHIRYQSKLQARKALS KDGRIFGESIMIGVKPCI DKSVMESDRCALSSPSLAFTPPIKTLGTPTQPGSTPRISTMRP LATAYKASTSDYQVISDRQTPKKDES LVSKAMEYMFGE
5858	355	1419	PPHQAAAASXHQQQQPPPPQDSSKPVVAQGGPGAPGVGSAP PASSAPPATPPTS GAPP GSGPGPTPTPPPAVTSAPP GAPPPTP PSSGVPTTPPQAGGPPPPAAVPGPGPGKQGP GPGKGGKMP GGPKPGGPGGLSTPGGHPKPPHRRGGGEPRGRQHHPYHQHHQ GFPFGPGGRSEEEKISGPRRGFKANLSLLRRPGKTYTQRCRFC LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR ALA*NCPKPELG*YTP*GGRQLPSSSLFPTHACLPLSCSVIFSPF MFPQ*NCWGRKPFPRNLGPHLKGAVCNRWDDFWEGPTGKGHCLN FAS
5859	307	1503	GGSSARPRASSRRLSRKKTINEVSKPAEVQGGYVKKETSPLLR NLMFSFIRHGPTIPRRDIDCLPDSSPNAFSTSGDGVVSRNQSF RTPIORTPHEIMRRESNRLSAPSYLARSLADVPREYSSQSFTV EVSPFAVENGDSGSRYYSNDFDQQRKRPLGDRAHEDYRYEYN HDLFQRMPPQNGRHSAGIGRVAATSLGNLTNHGSEDLPLPPGWS VDWIMRGRKYYIDHNTNTTHWSHPLEREGLP GGWERVESSEFQT YYVDHTNKKAY\RHPCAPTCTSV*STTSCHI/AS/RQQTERNQ SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFQLADLDT YQGMKLKLFMEKELEQIVKMYEAYRQALLTELENRKQRQWYAQQ HGKNF
5860	2956	1270	TIRVEEFPLCPGGGKAQLSSASLLGAGLLLPPTPPPLLLLLFP LLLFSLRCGALAGPIIVEPHVTAVWGNVSLKCLIEVNETITQI SWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLPKNYSINDATI TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP NETATIIISQYKLPTRFARGRRITCVVKHPALEKDIRYSFILD QYAEVSVTGYDGNWVFGKGVNLKCNADANPPPKSVMSRLDG QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LAEP*KIA PSPLSTL\ATIKGTQLPTIIA*CSGVGALFIV\LVKCFGLGIF CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDYPYDVS KKENKNPVNNLIRKDYLEBEKTQWNNVENLNRFERPMDYIEDL KMGKMFVSEHYDENEDDLVSHVDGVSISRREYV
5861	2051	1305	EVCACVQAFWLVAASGDDSGGDKCGCEVGSWVGSMRVMMARLL SEGEQGIPTACAAFAQQPAG/BPRRGLAGVGEPPQCSWVNYRC TLEFLVSLGTDLAGRGNASGPTAPADSKQL/ML*DVHRRVI LE*RMNSGSPARDNAPSQRFCNTLSEGLRFGISPSWREALYGC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5862	1556	483	PPFQLIMGEIKVSPDYNWFRGTVPLKKIIVDDDDSKIWSLYDAG PRSIRCLPIFLPPVSGTADVFFRQILALTGWGYRVIALQYPVYW DHLEFCDFGRKLLDHLQDKVHLFGASLGGFLAQKFAEYTHKSP RVHSLILCNSFSDTSIFNQTTWTANSFWLMPAFMLKKIVLGNFSS GPVDPMMADAIDFMVDRLESIGQSELASRLTLNCQNSYVEPHKI RDIPVTIMDVFDQSALSTEAKEEMYKLYPNARRAHLKTGGNFPY LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQWSVPSRLRCRKA ALASARRSSSVSLAVNDELTRCVLV*SVASAPVSRPPPSGSSGS PVLTVSGK
5863	2714	249	PPFSRGSLLAAPREDTMGPLMVLFCLLFLYPGLADSAPSCPN VNISGGTFTLSHGWAQPSLLTYSCPQGLYPPSPASRLCKSSGQW TFGATRSLSKAVCKPVRCAPVSPFENGITYPRLGSYPVGGNVSF ECRDGFI\LRGSPVRCRPNMWDGETAVCDNAGHCNPNPGLISL GP\VRTGFRFGHGDKVRYRCSSNLVLTGSSERECCQNGVWSGTE PICRQPPSYDFPEDVAPALGTSFSHMLGATNPTQKTKEGLGRKI QIQRSGLHNLNLYLLDSCSQSVSENFDFIKESASLMVDRIFFSFEI NVSVAIIITFASEPVLMSVLNDNSRDMTEVISSLENANYKDHEN GTGTNTYAALNSVYLMNNQMRLLGMETMAW\QEIRHAIILLT DGK\SHMGSGPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV DWRELNELGSKKDGGERHAFILQDTKALHQVFEHMLDVSKLTDIT CGVGNMSANASDQERTPWHTI KFKSQET\CRGALISDQWLT AAHCFRDGNDHSLWRVNVGDPKSGWGKEFLIEKAVISPGFDVFA KKNQGI\EFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM \EANLGFLRETFCGSTCR\DHENEL/VWNKQSV\PAHF\VALN GSKLEHLTLRMGVWETSCCRGLSPKKTM\FPNT\DVRE\VVT D\QFL\CS\GPOEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC SWGL\YNP\CLGSA\DKNSPKKGPSVAKVPPPTTR/DFHIN\LFP Q*SPWLRQHPPGMS*IFLPLLANGHLSPPFACPARICRPLHFLPS EWATLRTL
5864	173	1013	PLISVPQSLISLPQPLLCCFFGGQEPSAPSCLYSFLWACSFTMG KLPPSIPSSPLACVLNKLKPLQTPDLKPKCLIFFCNTAWPQY KLNDNSK*PENGTFEFSILQVLDNSCHKMGKWEVDPVQAFF\S HWSLPSLCSQC/GLIPNLSSFSFPCSFQ/PPQVPS/P/TEFFS MDSSDLPPSPQAAPRAEPGNHSLASAPPYPNPFITSPHTWS SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSWLIWQP
5865	568	1684	CLPGPRWEGEGWRAGHTIVGCIFFKTAII SHFGKGMVLCVCMCTC LSVCVCVQVGSWICV/CVSMCAVSLCTC\ICRCISMYTREHAC ACTRV*VYMCS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC TCV*MCVCMHEHVC/MCACSVLL/CRGHICM/MCMSAYICI /CVYVCVLCVWACMRMSTCVLVYG*ACTCVMMH/CSCTCR/C VHVCCMSMHACECLCVYLHICGAGTRRWAGSARGSRSCSRP CWAPGGLSLPGPSCPSVEQGLGGPGQLQGRSGEARLGEHRGW GSPAAVCSRNTVSPRRGADCFEAPDVPKQPPGWGRASFEERG GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK
5866	98	3197	ARPEVPAPPAWLSRRGAAMGDKDDKDSPKKNKGKERRDLDDL KKEVAMTEHKMSVEEVCRYNTDCVQGLTHSKAQEILARDGPNA LTPPPPTTPEWVKFCRLFGGFSILLWIGAILCFLAYGIQAGTED DPSGDNLYLGI VLAADVITGCFSYQEAQSSKIMESFKNMVBPQ QALVIREGEMQVNAEEVVVGDVLEIKGGDRVPADLRISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNFVEGTA RGVVVATGDRITVMGRIATLASGLEVGKTPAIEIEHFIQLITGV AVFLGVSFILSLILGYTWLEAVIFLIGIIVANVEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNR TVAHMWFNDQIHEADTTEDQSGTSFDKSSHTWALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASEALLKCIELSSGVSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRLLVMKGAPERILD RCSTILLQKQPLDEEMKEAFQNAYLELGGGLGERVLFCHYYL PEEQFPKGFADCDVNFNTDNLFCVGLMSMIGPPRAAVPDAVG KCRSAGIKVIMVTGDHPITAKAIAGVGIIFEGNETVEDIARL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NIPVSVQVNPDAKACVIGHGTDLKDFTSEQIDEILQNHTEIVFAR TSPQKKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI AGSDVSKQAADMILLDDNFASIVTGVBEGRILFDNLKKSIAVTL TSNIPETIPFLFIMANIPPLPLGTITILCIDLGTDMVPAISLAY EAAESDIMKRQPRNPRTDKLVNERLISMAYGOIGMIOALGGFFS YFVILAENGFLPGNLVGI RLNWDDRTVNDLED SYGQWQTYEQRK VVEFTCHTAFFVSIVVQWADLIICKTRRNSVFQGGMKNKILIF GLFEETALAAFLSYCPGMDVALRMYP LKPSWWFCAPPYSFLIFV YDEIRKLI LRRNPGGWVEKETYY
5867	3	1485	LPGRRARGGGRGLGWPPAQAALDGSRMGKAKVPASKRAPSSPVAKP CPVKT LTRKKNKKKKR FWKSKAREVSKKPASGPGAVVRPPKAP E DFSQNWKALQEWLLKQKSQAPEKPLVISQMGSKKKPKIIQONKK ETSPQVKGEEMPAGKDQASRGSVPSGSKMDRAPVPRTKASGT EHNKKGTKERTNGDIVPERGDI EHKRRKAK\GQPPHPPR/IDI WFDVDVPADIEAAIGPEAAKIARKQLGQSEGSVLSLVKEQAFG GLTRALALDCEMVGVGPKGEESMAARVSVINQYKGCVDYKYVKP TEPVTDYRTAVSGIRPENLKQGEELVVQKEVAEMLKGRILVGH ALHNDLKVFLDHPKKKIRDTQKYKPKSKQVSKGRPSRLRLSEK ILGLVQQAQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLLT A PDHCSDDA*QSCPAAAAAPLQRQCDQSQGQITSPQSGNSGETFS BSWQRGVAWCY
5868	2122	833	LTAGASHTODASQSTS AKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPDPV TERSAFTERDAGSGLVTRLRERPALLVSTSWTEDEDFSI LLAA LES RV*T\MTLDGHNLP SLVCVITGKGPLREYYSRLIHQKH FQH IQVCTPWLEAEDYPLLGSADLGVC LHTSSSGLDLPKVVDMFG CCLPVCAVNFKCLHEL VKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDES SVVQTVLPLVMDT
5869	2122	833	LTAGASHTODASQSTS AKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPDPV TERSAFTERDAGSGLVTRLRERPALLVSTSWTEDEDFSI LLAA LES RV*T\MTLDGHNLP SLVCVITGKGPLREYYSRLIHQKH FQH IQVCTPWLEAEDYPLLGSADLGVC LHTSSSGLDLPKVVDMFG CCLPVCAVNFKCLHEL VKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDES SVVQTVLPLVMDT
5870	2122	833	LTAGASHTODASQSTS AKYPAAAQNL/CVTNAMREDLADIWYIR AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPDPV TERSAFTERDAGSGLVTRLRERPALLVSTSWTEDEDFSI LLAA LES RV*T\MTLDGHNLP SLVCVITGKGPLREYYSRLIHQKH FQH IQVCTPWLEAEDYPLLGSADLGVC LHTSSSGLDLPKVVDMFG CCLPVCAVNFKCLHEL VKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDES SVVQTVLPLVMDT
5871	3	3465	FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYIRIVKSTLLLYQSPTTGLFPPTKT CGDQKAKIQDSL YCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQFQKQDPRPTTCLHSVFNVTGDELLS YEEYGH LQINAVSLYLLYL VEMISSGLQIIYNTDEVSFIONLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFNGNQCWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLF SQTLDKVVRKLKGKYGPKR FLRDGYRTSLEDPNRCYYPKAEIKLFDGIECEFFIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNPGSQKRFP SNCGRDGKLPFWGQALYIIAKLLADELISP KDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLD DIKNAQFIKQYWKMHGRPLFLVL IREDNIRGSRFNPILDM LAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTBELPEFKS FEELEPPKHSKVKRQSSTPSAPELGQQPDVNI SEWKDKPTHEIL QKLNDCSCLASQAILLGILLKREGPNFITKEGTVDHIERVYRR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AGSQKLWSVVRRAASLLSKVVDLSLAPSTITNLVQGRQVTLGAFG HEEEVISNPLSPRVIQNIYYKCNTHDEREAVIQQELVIHIGWI ISNNPELFSGLTKIRIGWIIHAMEYELQIRGGDKPALDLYQLSP SEVKQLLLDILQPQQNGRCWLNRRQIDGSLNRTPTGPFYDRVWQI LERTPNGIIVAGKHLPPQPTLSDMTMYEMNFSLLVEDTLGNIDQ PQYRQIVVBLLMVVSIVLERNPELEFQDKVDLDRLVKEAFNEFQ KDQSRLEIEKQDDMTSFYNTPLPGKRGTCSTYTKAVMNLLEG EVKPNNDPCLIS
5872	68	665	VQGYMYRFVIKINSYSEKTSICRHRCCPELPATQPWPTPTVFF NIAIDSESLGCI\SFKLFADKV/PKRWKNFVLLNTGEKVLGDK GPCFYRIIPG/LCQGGDFTHHNGTGGKSLYSKEFDENFI/LKH TAPGVLSTANAGPTTNGSQFFICTAKTEDG*QHVVFQKVDGMS IVEALERSGSRNGKTSKKITAAACGQL
5873	2240	506	RRPPEGSGGGRTRARMPLPWSLALPLLWSVAGGFNAASAR HHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKF GECVGPKNCRCPFGYTGKTCSDVNECGMKPRPCQHRVCVNTGHS YKFCFLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCP SSGLRLAPNGRDLCDIDECASGKVICPNRRCVNTFGSYCKCK IGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKC KQGYKGNGLRCSAIPENSVEVLRAPGTIKDIRKLLAHKNSMK KKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGNSHGG\KKG NEEKMEGLEDEKREEKALKD*HRRERPFGR\DVFFPKVNEAGE FGLIL\VORKALTSKLEHKADLNI SVDCSFNHG\ICDW\KQDR\ EDPDFW\NPADR\DNAI\GFY\MAVPGWLWQGHK\KDIGRLKLL PDLPQSNFCLLDYRLAGDKVGLRVFVKNNSNALAWEKTTSE DEKWKTKGIQLYQGTDATKSIIFEAEKRGKTGEIADVGVLLVS GLCPDLSLSVDD
5874	2	3387	ACPRLARRRRRVRSLRRRRGWLRLARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAMEYDD VHSDGRYSLSGSVASRDAGRESLRSDVFGSPFRSSNPSISDD SYRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGWS EQDFGHVPSQESSWSQEYSFGPSAVLGDGFGSSRLIEKECLEKE\ SRDYDVHDSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTARGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI KQNTSPSDVTLGTNPGTEDIQFPQKIPGLDLKLNRLPRRMS FDIIDKSDVFSRFGIEIKWAGFHTIKDDIKFSOLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVTKNCFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLNPLDLALALETTNSLCRKSLLLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAPPNFEDSTLFGREYIDHLKAWL VSSGCPQVKKABPEPMREEEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSFKPAGVDISEAPQTSSPCPSADIDMDKNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDWFL\HDQNSS\AFK FY\RKKVFELCPSICTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEDEDDEDGGEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL\ALGAPALFTGLLQVTCFPFG RGFSSSKLVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQL\TDK\NLGFG\MLQKMGWKEGHLGSLGK GIR\SRSACTQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSQWL IFVF
5875	296	1848	LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVYQVRA LEFSGSLFPHAI CLGDVDNDTLNELVVGDTSGKVSUYKNDSDRP WLTCSQGM LTCVGVGDV CNKGNLLVAVSAEGWFHLDLTPAK VLDSAGHHETLIGEBQRPVFKQHI PANTKVMLISDIDGDCREL VVGYYTDRVVRFRWELLEGEPHLLTGQLVSLKKWMLGQVDSLS VTGLPLGLPELMVSQPGCAYAILLCTWKKDTGSPASEGPTDGS /SGDPSCPRRGAAPDIWPYPQQECLHSPNWQHQT\SHGTESGGS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GLFALCTLDGTLKLMEEEMEEADKLLWSVQVDHQLFALEKLDVTG NGHEEVVACAWDGGQTYIIDHNRTVVRFQVDENIRAFACAGLYACK RGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETKP\ST TACCRSWAWILTSL*LVPCPTKRSTIQTSHHSVLPQASRIFFPS WTCLIAEGGF*TPTLPPKGVFGSHCAAAGSITKQ
5876	1122	224	HLPLGVPSKVAGAAAMEPQEERETQVAWLKKIFGDHPIQYEV NPRTEILHHLSENRVRDRDYYLVIEDLKQKASEYESEAKYLQ DLLMESVNFSPANLSSSTGSRYLNALVDSVALETKDTSLASFIP AVNDLTSDLFRTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDV KKAELHLSTER\AKVDNRQNM\DFLKAKSEEFRTGIIAAGEQL SARGQ\DAFSVPISLVALIRENWPRLKQQTIPLK\KKLESYLD LMP\NPSHCSK*RIEBAK\RELA\SIEABLRRVS\MMEL
5877	2030	1907	GTLGKMAAASSSGEKEKERLGGGLGVAGGNSTRELLSALEDLEV LSRELIELLAISRNQKLLQAGEENQVLELLIHRDGEFQELMKLA LNQGIKHEMQVLEKEVEKRDSDIQQQLQKLEAEQILATAVYQ AKEKLKSIKARKGAISSEETIKYAHRIASNAVCAPLTWVPGD PRRPYPDTLEMRSGLLGQMNPSTNGVNGHLPDGDALA/RRKIAR CPCSTVS/NGSQMTCR*INIILILQKSVCEL
5878	950	2113	GLWKCMQLQCPHTRVQF*PTFRQQGPQ\VPVAVIAGNRPNYLY RMLRSLLSAQGVSPQMITYFIDGYEPMDDVVALFGLRGIQHTP ISIKNARVSQHYKASLTATFNLFPFAKFAVVEEDLDIAVDFFS FLSQSIHLEEDDSLYCISAWNDOGYEHTAEDPALLYRVETMPG LGWVLRRLSLYKEELEPKWPTPEKLWDWDMWMMRMEQRRGRECI PDVRSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSL KKEAYEVEVHRLLEAEVLDSKNPCEDSFLPDTEGHTYVAFIR MEKDDDFTTWTQLAKCLHIWDLVGRNHRGLWRLFRKKNHFLVV GVPA SPYSVKKPPSVTFIFLEPPPKKEGAPGAPEQT
5879	3	981	RLTEAAAGSGSRAAGWAGSPPTLLPLSPTSPPRCAATMASSDED GTNGGASEAGEDREAPGKRRRLGLFLATAWLTFYDIAMTAGWLVL AIAMVRFYMEKGTGHRGLYKSIQKTLKFFQTFALEIVHCLIGIV PTSIVITGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT EITRYSFYTFSLDLHLPYFIKWARYNFFIILYPVGAGELLTIY AALPHVKKTGMFSIRLPNKYNVSEFYLLITMASYIPLFPQL YFHLRQRKRLVHG\G*L*KRMK*SLQTRCFQNNQDYLSPSF NNKNKQCEISWIVWFLKI
5880	1138	1324	SLWCLVAGGLGLGPSSQNPLQAGILARPREARGTFSALTACSA SVTSKKGKSSSGMWPSAASDRDSPVPLRPPGFVQLPSGTGWVLS *KKKRGRCSS/WLSQPQHEREKEVLLRRSMAEGERARAASDVL CRSLANETHQLRRTLTATAHMCQHAKCLDERQHAQRNVGERS DQSEHTDGHTSVQSVIEKLEENRLLKQKVTHVEDLNKQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQBLAASRTARDAALERVQMLEQQILAYKDDFMSEADRE AQSRILEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGLQCPH CLQCFSDQGEELLRHVAECCQ
5881	26	441	GGIHPSPTAPRAQHLTMDCTWRILFLVAAATGTHAQVQLQSG SEVKKPGASVMVSCYVSGYTLTKLSMHVWRQAPGKLE*MGFPD LQDVETIYPQKFGQGRVSMTEETSTETTQ/AYLESSLRSSEDTAV HHCATDTV
5882	2407	2216	SGCVMELYSHSLEYNPEWISVQSAVAPAQLALNSDGL*LHSGE RTRRD*QLPEAGGPGLEPLQLGELDITSDEFILDEVG\VDLR HYSKQVELELQIEQKSIKDYIQESENIALHNQITACDAVLER MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG ELVDGLVVPALVTAILEAPVTEPRFLEQLQELDAKAAVREQE ARGTAACADVRGVLDRLRVKAATKIREFIIQKIYSFRKPMITNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYR SYLGRMLKVQYEEVAEKDDLMGVEDTAKKGFSSKPSLSRNTIF TLGTRGSVISPTLEAPILVPHTAQRGEQRYPFREALFRSQHYAL LDNSCREYLFICEFFVVSPPAAHDLFHAVMGRTLSMTLKHLDYS LADCYDAIAVFLCIHIVLFRFNIAAKRDVPALDRYWEQVLALLW

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALV SINQTI PNERTMQLLQQLQVEVENFVLRAABFSSRKEQLVFLI NNYDMMLGVLME*ERAADDSKEVESFQQLINARTQEFIEELLS PPFGGLVAFVKEAEALIBRGQAERLRGEARVTQLIRGFGSSWK SSVESLSQDVMSFTNFRNGTSIIQGALTQLIQ\LYHRPHRV\LSQQLRALPARAELINIHLMVELKKHKPNF
5883	2	1374	EFPGRRFRAVMEAGAGAGAGAAGWSCPGPGPTVTTLGSYEASEG CERKKGQRWGSLERRGMQAMEGEVLLPALYEEEEEEEEEEVE EEEEQVQKGSVGSLSVNKHRLSLTETELEELRAQVLQVLAEL EETRELQAGHEDDSLQLQLEDERLASAQAEVFTKQIQQLQG ELRSLREEISLLEHEKESELKEIEQELHLAQAEIOSLROAEDS ATEHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRAEME MKSSEPSGSLGLSDYSGLEELQELRERYHFLNBEYRALQESNS SLTGQLADLESERTQATERWLQSQTLSTMSAESQTSEMDFLEP DPEMQLLRQQLRDAEEQMHGMKNKCQELCCELEELQHHRQVSE EQRRRLQRELKCAQNEVLRFTSHS\SPSHPLPPIPPSSPCLL*A LVVISALLWCWAE*SS
5884	4261	2522	GVLARASARLRVPLTGVRAEPEVGAEPKAVAGAAEPDEDGGR SRLRDCGDYTPSERLPGKGAFLWFGGAI PAALATAKRSGAVFV FVAGDDHQSTQMAASWEDDKVTEASSNSFVAIKIDTKSEACLP SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTIRHKVRQM HLLKSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAELCE IPSTSDTKSDTATGGESAGHATSSQEPSCGSDQRPADLNRIVE RLTKKLEERREEKRKEEQREIKKEIERRTKGKEMLDYKXKQEE ELTKRMLBEERNREKAEDRAARERIKQQIALDRAERAARFAKTK EVEAAKAAALLAKQAEMEVRKESYARERSTVARIQFRLPDGSS TNQFPSPDAPLEEARQFAAQTVGNITYGNFSLATMFPRREFTKEY KKKLLDLELAPSASVLLP/ALFINF*AGRPTASIVHSSSGDIW TLGTVLYPFLAIWRLISNLFNPPPTQTSVRVTSEPPNPAS SSKSEKREPVRKRVLEKRGDDFKKEGKIYRLRTQDDGEDENNWT NGNSTQOM
5885	900	467	AAGGGRSRLRSRWSPTGPSKSPSGVRCGG\RR\AWEDKDEFLDV IYWFRQIIAVVLGVIWGVLPRLGFLGIAGFLINAGVLYLYFSN YLQIDEEYGGTWELTKEGFMTSFA/IVHGHLDHLLHCHPL*LM VYSSQVLP IQSKGPS
5886	86	1341	PFRGRALTLLKQPRFGVAPPSTLGTCHKSDPGRPAAQSPSPSGS GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSLEPPLKNG EVILLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVSKNVAL PKGTIVLASPGWTTTHSIDGKLEKLLTEWPDITPLSLALGTVG MPGLTAYFGLLEICGVKGGETVMVNAAGAVGSVVGQIAKLKGC KVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY DCYPDNVGGFESNTVIGQMKKFGRIAICGAISTYNRTGPLPPGP PPEIGIYQELRMEAFVYRWQGDARQKALKDLLKWLELPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIYKEYIIEGFE NMPAAFMGLKGDNLGKTIVKA
5887	1937	104	APGCRGCRATRCPCRGRWDSIGDEAARS PAAPGGAPGLLGLRE RPDRCHPGGDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPCSSVDFSVFS ACSVVPVVTGDSQFCSQKAVIYSLNFTANPPQRFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTS DGFTLNABSY VSFTTKLDIPTAAKYEYGVPLQTSDFSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBI LRVPDSRK KVPITVQSIYQSLNKTLLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYYTDAGEVTKADLSFVLGTSSVVVPLQQKFIEHFLQ ENTQPVPLSGNPGYVVGVLPLAAGFQPHKSGSIIQTTNRYGQITI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKRLRTGALPCQLVAQ KVKSLLWGQGFDPDYVAPFGNSQGP/ADMLDWVPIHFTQSFNK DSCQLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSFPAN SGNERTILISTAVTFVDVSAPEAGFRAPPAINARLPFNFFFPF V

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5888	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDSPRTPSNTPSAEADWSFG LELHPDYKKTWGPQVCSFLRRGGPEEPVLLKNIRENEITGALLP CLDESFRFENLGVSSLGERRKLLSYIQLRVQIHVDTKVINDPIH GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYVFPGASHNRFEH SLGVGYLAGCLVHALGEKQPELQISERDVLVCVQIAGLCHDLGHG PFSHMFDRGFIPLARPEVKWTHEQGSVMFEHLINSNGIKPVE QYGLIPEEDICFIKEQIVGPLESPEVDSLWPYKGRPENKSFLEY IVSNKRGIDVDKWDYFARDCHHLGIQNNPDYKRFIKFARVCEV DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT DAFLKADDYIEITGAGGKKYRISTAIIDMEAYTKLTDNIFLEIL YSTDPKLDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQEKNPIDHVS FYCKTAPNRAIRITKNQVSQLLP\EKFAEQ\LRVYCKKVDKRS LYA\ARQYFVQW\CADR\NFT\KPDGRCY*PPTP*HPQKKGW\ NDSTFSKPIPTRLPRRLPKSRV\QLFKDDPM
5889	1831	731	LPAACGRPVTAARPRQAEGRSGRPRDLDPYPPQVFPFRPDRVAI VTGGTDGIGYSTAKHLARLGMHVI IAGNNDKAKQVVSKEET LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLK FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMVFPQR KTRDGFEEHFGNLGHFLLTNLLDTLKESSPGHSARVVTVS SATHYVAELNMDLQSSACYSPPHAAQAQSKLALVFTYHLQRL AEGSHVTANVDPGVVNTDLYKHVFWATRLAKKLLGWLFPKT DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ LWSKSCMIGVLDVTL
5890	1322	200	FRRCWSAAGRAVPVAFCSRSISASSPRRPRGAVRLQSGTEAACRS GRPDPRPASAAGGHAGERSQRDVLVHLFAGGCGGTGVAITCP LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVS PGPLHCLKV ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCCKELNDVFD PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR RMGAFFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVYESI KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI AYPHEVVRTRLREEGTKYRSFFQTLSSLVQEEGYGSLYRGLTTH LVRQIP\NTAIMMATYELVYLLNG
5891	1322	200	FRRCWSAAGRAVPVAFCSRSISASSPRRPRGAVRLQSGTEAACRS GRPDPRPASAAGGHAGERSQRDVLVHLFAGGCGGTGVAITCP LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVS PGPLHCLKV ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCCKELNDVFD PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR RMGAFFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVYESI KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI AYPHEVVRTRLREEGTKYRSFFQTLSSLVQEEGYGSLYRGLTTH LVRQIP\NTAIMMATYELVYLLNG
5892	1764	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQVVLGHRLGPA DSGWMPPQAAPCLSGAPHASAADVVVHGRRTAICRAGRGGFKDT TPDELLSAVMTAVLKDVNLRPEQLGDCVGNVLQPGAGAIMARI AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVABR FGISREKQDTFALASQQAARAQSKGCFQAEIVPVTTHVDDKG TKRSITVTQDEGIRPSTTMEGLAKLPAFKKGSTTAGNSSQVS DGAAILLARRSKAEELGLPILGVLRSAVVGVPDIMGIGPAY AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCEKRLPP*EG *TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC PCAIGSWNGSPLPVFEYPWGT
5893	3	1653	ILSKRRQCQAKTKELMAKKVAVIGAGVSGLISLKCCEVDEGLEPT CFPERTDIGVWRFKENVEDGRASIYQSVVNTSKEMSCFSDFP MPEDFPNFLHNSKLLLEYFRIFAKKFDLLKYIQPQTTVLSVRKCP DFSSSGQWKVVTVQSNGEKQSAVFDAMVVCSGHHILPHIPLKSF GMEFRKGQYFHSRQYKHPDGFEKRIILVIGMGNLGS DIAVELSK NAAQVFISTRHGTWMSRISEDGYPNDSVFHTRFRSMLRNLVPR TAVKWMIBQQMNRWFNHNENYGLEPQNKYIMKEPVLNDDVPSRL CGAIVKSTVKELTETSAIFEDGTVEENIDVIFATGYSFSPFP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LEDSLKVENNMVSLYKIFPAHLDKSTLACIGLIQPLGSIFPT AELQARWVTRVFKGLCSLPSERTMMMDIIKRNEKRIDLFGESQS QTLQNTYVDYLDLEALEIGAKPDFCSLLFKDKPLAVRLYPGPCN SY*YRLVGPGQWEGARNAIPTQKQRIKPLKTRALKDSSNFSVS FLKILGLLAVVVAFF\COLQWS
5894	174	1673	RYSPPKVLQNKESLKLGMATALVSAHSLAPLNKKKEGLRVVRE DHYSTWEGQFKLQGNKGLGQEPCKQFRLRYEETGPREALS RLRELCCQWLQPEHTKHEILELLVLEQFLIILPKBLQARVQEH HPESREDVVVLEDLQDLGETGQQVDPDQPKKQKILVEEMAPL KGVQEQQVRHECEVTKEPEKEGEETRIENGKLIIVVTDSCGRVES SGKISEPMEAHNEGSNLERHQAKPKIEYKCSEREQRFIQHLD LIEHASTHTGKKLCESDVCQSSSLTGKKVLS*ERKVIQC/HGV LGKAFQSSSHLVHRQKIHLEKPYQCNECGKVFSONAGLLEHLR IHTGEKPYLCIHCGKNFRSSHLNRHQRIHSQEPCCKECCGKT FSOALLLTHHQRIHSHSKSHQCNECGKAFSLTSDLIIRHHRIHTG EKPKFCNICQKAFRLNSHLAQHVRIHNEKPYQCSECGEAFRQR SGLFQHQRYHHKDKLA
5895	2967	86	HPSSLGAIFFYPFPSSPWPPLLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGLFVLAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQDLSGNLYFSTSAICRYFF\LLSGWEQDDL TNQWLEW EATELQPTLSAALYYL\VVQGGKG\EDVLGSVRRTLTHIDHSL RQ\NCPFLAGETESLADIVLWALYPLLDQPAYLPEELSALHSW FQTLSTQ\EPQCR\AARRLVLKQ\QGVLA LR\PYLQKQPQPSA EGKGLSPIEPSEELATLSEETAMAVTAWEGLESPLPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADV FARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEC DKYHI IHA DIY\RFWNISFDIFGRITTPQQ\TKIT\QDIFQQLKRGFVLQD TVEQLRCEHCARF\LA DRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCP VVQSSQHLFLDLPLKLEKRL EEWLGR LPGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWF DATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHS LVPSSALGAEDNYTL\VSHLIATEVLYNEDG K\FSKSRGVGVFRDM\AHD TGIPPDISR FYL\LYIRPEGK\DSA FSWTDLLKNNS\ELNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPACSI LLTNFLCTL PAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAEVAKL LLDLKKQLA VAE KPPEAPKGGKKK
5896	2967	86	HPSSLGAIFFYPFPSSPWPPLLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGLFVLAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQDLSGNLYFSTSAICRYFF\LLSGWEQDDL TNQWLEW EATELQPTLSAALYYL\VVQGGKG\EDVLGSVRRTLTHIDHSL RQ\NCPFLAGETESLADIVLWALYPLLDQPAYLPEELSALHSW FQTLSTQ\EPQCR\AARRLVLKQ\QGVLA LR\PYLQKQPQPSA EGKGLSPIEPSEELATLSEETAMAVTAWEGLESPLPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADV FARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEC DKYHI IHA DIY\RFWNISFDIFGRITTPQQ\TKIT\QDIFQQLKRGFVLQD TVEQLRCEHCARF\LA DRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCP VVQSSQHLFLDLPLKLEKRL EEWLGR LPGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWF DATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHS LVPSSALGAEDNYTL\VSHLIATEVLYNEDG K\FSKSRGVGVFRDM\AHD TGIPPDISR FYL\LYIRPEGK\DSA FSWTDLLKNNS\ELNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPACSI LLTNFLCTL PAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LMDEVTKQGNIVRELKAKQADKNEVAEVAKLDDLKKQLAVAEG KPPEAPKGKKKK
5897	2967	86	<p>HPSLLGAIPFYPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDGNYLFTSAICRYFF\LLSGWEQDDL TNQWLEW EATELQPTLSAALYYL\VVQGGK\EDVLGSRVRLTHIDHSLRQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPQCR\AARRLVLKQ\QGVLA LR\PYLQKQPQPSPA EGKGLSPIEPSEELATLSEEEIAMAVTAWKGLSPLPRLPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADV FARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIHA DIY\RFWNISFDIFGRITTPQQ\TKIT\QDIFQQLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGR TL PGSDWTPNAQFITPFFGFREWP SKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWF DATIGYLSITANYTDQWERW\KNPEQVDLYQ FM\AKDNVPFHS LVPSSALGAEDNYTL\VSHLIATEYLYNEDG K\FSKSRGVGVFRDM\AHDGTGIPDISRFYL\LYIRPEGK\DSA FSWTDLLKNNS\ELNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGEADRQAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSI LLTNFLCTL PAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQIQIA LMDEVTKQGNIVRELKAKQADKNEVAEVAKLDDLKKQLAVAEG KPPEAPKGKKKK</p>
5898	2967	86	<p>HPSLLGAIPFYPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE MRLFVSDGVPGLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT RPKVPVLQLDGNYLFTSAICRYFF\LLSGWEQDDL TNQWLEW EATELQPTLSAALYYL\VVQGGK\EDVLGSRVRLTHIDHSLRQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW FQTLSTQ\EPQCR\AARRLVLKQ\QGVLA LR\PYLQKQPQPSPA EGKGLSPIEPSEELATLSEEEIAMAVTAWKGLSPLPRLPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIGCVLSADV FARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIHA DIY\RFWNISFDIFGRITTPQQ\TKIT\QDIFQQLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGR TL PGSDWTPNAQFITPFFGFREWP SKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWF DATIGYLSITANYTDQWERW\KNPEQVDLYQ FM\AKDNVPFHS LVPSSALGAEDNYTL\VSHLIATEYLYNEDG K\FSKSRGVGVFRDM\AHDGTGIPDISRFYL\LYIRPEGK\DSA FSWTDLLKNNS\ELNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGEADRQAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSI LLTNFLCTL PAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQIQIA LMDEVTKQGNIVRELKAKQADKNEVAEVAKLDDLKKQLAVAEG KPPEAPKGKKKK</p>
5899	326	1078	<p>NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKQIKHMAFIEQ EANEKAEIEIDAKAEFEFNIEKGRVLTQRLKIMEYEEKKEKQIE QKKILMSTMRNQARLKVLRANDLISDLLSEAKLRLSRIVEDP EVYQGLLDKLVLOGLLRLLEPVMIVRCRP\QDLLLLVEAAVQKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWVSGNQRIKVSNTLESRLDSAKQKMP EIRMLFGANTNRKFFI</p>
5900	64	1409	<p>KAASRDSPCLEFCFLCGVSSHDLQHRMWHRLSHLSRLQDLLK GGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHPEL KYANTVMRFDYVWLDRHCRSASCYNSKTHQRS LDTASVDLCIKP KTRLDDETTLFFTWPDGHVTKYDLNWLKNSYEGQKQKVIQPRI LWNAEIYQQAQVPSVDCQS FLETNEGLKKFLQNFLLYGIAFVEN VPPTQEHTEKLAERISLIRETIYGRMWYFTSDFSRGDTAYTKLA LDRHTDTYFQEPGCIQVFHCLKHEGTGGRTLLVDGFYAAEQVL</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QKAPPEEFELLKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG/YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPENEFWVKLPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVLNTARLLGLQA
5901	1	2121	VAIEQTSLSKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL KTHLDTVLPKLTCPQCNEFPNQESLLKHVTIHFMITSTYYICE SCDKQFTSVDDLQKHLDMHTFVFFRCTLCQEVFDSKVSILQLHL \AVKHSNEKKVYRCTSCNWDFRNETDLQLHVKNHLENQKGVHK CIPCGESFGTEVELQCHITTHSKYCNCKFCSKAFHAILLEKHL REKHCVFETKTPNCGTNGASEQVQKEEVELQTLLTNSQESHNSH DGSEEDVDTSEPMYGCDCGAAYTMETLLQNHQLRDHNIRPGES AIVKKKAELIKGNYKCNVCSRTFFSENGLRHMQTHLGPVKHYM CPIOGERFPPSLTLTEHKVTHSKSLDTGNCRICKMPLQSEEEFL EHCQMHFDLRNSLTGFRVCVCMQTVTSTLELKHGTFFHMQKTGN GSAVQTTGRGQHVQKLYKCASCLEKFRSKQLDLVKLDINGLPYGL CAGCVNLSKSASPGINVPPGTNRPGLGQENENLSAIEGKGVGGL KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP QVSPMPRISPSQSDEKKTQYQCIKCMVFYENWDIQVHVANHMID EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFIV FVQANKLQQHIFSAHQEDKIIDCTQCPQKFFQTELQNHMTMQ HSS
5902	712	209	LKNRRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF IPLKPRQ*ED*MFQSWLHAWGDTLEEAPEQCAMAMFGYMTDTGT VEPLQTVETVQGGDLQSLLFHFLDEWLYKFSADFFIP\GWGE EFSLSKHPQGTVEVKAITYSAMQVYNEENPEVFVIDI
5903	2106	735	DTPGPSLPSTTAPFSLRSLSPFSPRSYLLPFGDPQLQGRGLPTT PALFALSAPVPGAASPMPPSGLRLLPLLLPLLWLLVLTGPRPAA GLSTCKTIDMELVKRKRIEAIHQILSKRLASPPSQGEVPPGP LPEAVLALYNSTRDRVAGESAEPEPEPEADYAKEVTRVLMVET HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL KLVQEQHVELYQKYSNNWRYLSNRLAPSDSPEWLSFDVTGVV RQWLSRSGEIEGFRLSAHCSDSRDNTLQVDINGFTTGR\RGDL ATIHGMNRPFLLLMATPLERAQHLQS\SRHRQAL\DTNY\CFSE HGGRNCLRC/VHC*HLIFRKDL\GW\KWI\HE\PKGYHANFCL GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\ LPIVYY\VGRKPKVEQLSNMIVRSCKCS
5904	3	1126	MMEIENAINTFKEEQRLIYEELIKEEKTNNELSAISRKIDTW ALGNSETEKAFRAISSKVPVDKVTPTSLPEEVLDPEKFLQQTGG RQGAWDYDHDHQNFKVRNKHGKPTFMEEVLEHLPGKTQDEVQQ HEKWKYQKFLALEERKKESIQIWKTKKQKREBIFKLKEKADNTP VLFHNKQEDNQKQKEBQRKKQKLAVEAWKKQKSIEMSMKASQL KEEEEEKKEKHQKERQRFKLKLLLESYTQQKKEQEEFLRLEKEI REKAKEAEKRKNADEISRFOERDLHKLELKLDRQAKBDEKSO KQRRALKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR
5905	287	2912	MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLPVWSQCLQNFLLHGTKNVTNSSLRLPR QNSDGGQKNKPREHIDCGDIVWSLAPGSSVPEKQSRVCVNIWH RFRFGDQQLLATGLNSGRIGKIWDVYTGKLLNLVDHTGVVRDL TFAPDGLSILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\ SCAPSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*PNLKFLVLIFF*K*CIVSQVK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFLAVNLFACISICFSS*A QVGDPSSL*TSDYLKGRQCWSNNLLTLRFLSVYFFKNLVVSGKK REGGL*YLTFLISVYFS*LVFGINGFYQSFVVKLHCLYFMFRLI FKLTFRNRI*NRICMSALINLKTDFNLMTLSIFFKLLIYNA* YNLN*I*QF*YKMFVLCMSE*SYNICLFIAGF\LWNMDKYTM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			IRKLEGGHHHDVVACDFSPDGALLATASYDTRVYIWDPHNGDILMEFGHLFPPTPIFAGGANDRWVRSVSFSDHGLHVASLADDKMVRFWRIDEDYPVQVAPLSNGLCCAFSTDGSLVLAAGTHDGSVYFWATPRQVPSLQHLCRMISIRRVMTQEQVQLPISKLEFLSYRI
5906	146	2038	REGAGSGRMASGA\YNPYIEITEQPRQGRMFYKCEGRSAGSI PGEHSTDNNRTYPSIQIMNYGKGV\RITLVTK\NDPYKPHPH DLVGKDCRD\GYEAEFGQE\RRP\LFFQN\LGIRCVKKKEVKE A\IITR\IKAGINPFDVP*KQLNDIEDCDLDDVRLWFRVFLPDG HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCRVKNKCSVVRGG DEIFLLCDKVQKDDIEVRFLNDWEAKGIFSQADVHRQVAIVFK TPPYCKAITEPVTVMQLRRPSDQEVSESMDFRYLPDEKDTYGN KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLLELLTSGDPPTLAS QSAGITVNFPERPRPGLLGSIGEGRYFKKEPNLFSHDAVREMP TGVSSQAESYYPSPGPISGLSHHASMAPLSSSSWSSVAHPTPR SGTNTPLSSSFSTRTLPSNSQGIPLRLIPVGNLNASNACIYNN ADDIVGMEASSMPSADLYGISDPNMLSNCSVNMMTSSDSMGET DNPRLLSMNLNENPSCNSVLDPRDLRQLHQMSSSSMSAGANSNTT VFSQSDAFEGSDFCADNSMINESGPSNSTNPNSHVFVQDSQY SGIGSMQNEQLSDSFYEFFQV
5907	99	1873	TYLLSSWS*NLDTKIKSQVKV/RKGHKKISWPYPQPAKQNGK KATSKVPSAPHFVHPNDHANREAEKKKWVEEMREKQQAAREQE RQKRTIESYQCDVLRQEEFEHKEEVLQELNMFQLDDEATR AYYKEFRKVVEYSDVILEVLDARDPLGCRCFQMEEAVALRAQGNK KLVLVLNKIDLVPKEVVEKNLDYLRNELPTVAFKASTQHVKVNL NRCSVPVQASESLKSKACFGAENLMRVLGNYCRLGEVTRTHIR GVVGLPNVKGSSLSNLSKRSRACSVGAVPGITKFMQEVYLDKF IRLLDAPGIVPGPNSVGTILRNCVHVQKLADPVTVPETILQRC NLEEISNYGVSGFQTTEHFLTAVAHRLGKKKGGLYSQEQAOK AVLADWVSGKISFYIPPPATHTLPTLSAEIVKEMTEVPDIEDT EQANEDTMECLATGESDELLGDTDPLEMEIKLLHSPMTKIADAI ENKTTVYKIGDLTGCTNPNRHQMGWAKRNVDRPKNSNSMVDVC SVDRRSVLQRI METDPLQGGQALASALKNNKKMQKRAKIASKL SDSMMSALDLSGNADGVDG
5908	247	975	HCGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEETHPHTRA HTRTLRATLRRPPRSHSTRLRFPMLDGGGLASWK/PMRER* GWRPAPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI VTLWGKVVSSANHHKAHVKTGTCEVVALHRCCKNKIEERSQT VKCSFPQGVAGTTRAAPS CVDASIVEQKWWCHMQPCLEGBECK VLPDRKGWSCSSGNKVKTTRVTH
5909	1	5002	PAIPGSTIIWAPGSHSAARADGRHGSLSQSQAPGALCGARAPP SSNLRADRSIMICAQARAGKNLYHNRLGLAAMAFPSRNSQSLRR CKEPIRYSYNPDQFHNMDLRGGPHDGVTIIPRSTSDTLVTSDSR STLMGRSSYSIGHSQDLVIHWDIKEEVDAGDWIGMYLIDEVLS ENFLDYKNRGVNGSHRGQIWKIDASSYFVEPETKICFKYYHGV SGALRATTSPVTVKNSAAPIFKSIGADETVQGGSRRLISFSL DFQAMGLKKGMFPNDPYLKISIQPGKHSIFPALPHHGQERRSK IIGTNTVNIWQAEQFSFVSLPTDVLIEVKDFAKSRPIIKRFL GKLSMPVQRLERHAIGDRVSYTLGRRLPTDHVSGQLQFRFEI TSSIHDPDEEISLSTEPESAQIQDSFPMNLMESGSGEPRSEAPE SSESWKPEQLGEGSVDPDRGNQSIELSRPAEEAAVITEAGDQGM VSVGPEGAGELLAQVQKDIQAPSAEELAEQLDLGEBASALLLE DGEAPASTKEEPLLEEATTQSRAGREEEKEQEEGDVSTLEQG EGRLQLRASVKRKSRLPVSLETVIASACGDPETPRTHYIR IHTLLHSMPSAQGSAEEEDGAEESTLKDSSEKDGLEVDTV AADPSALEEDREEPEGATPGTAHPGHSGGHFPLSANGAAQDGD HPSTGSESDSSPRQGDHSCGCDASCCSPSCYSSSCYSTSCYS SSCYASCYSPSCYNGNRFASTRFSSVDSAKISESTVFSSQDD EEEENSASFESVPDSMQSPELDPESTNGAGPWQDELAAPSCHVER SPEGLESVPAGPSNRREGECPILHNSQFVSQPLSLRPEIHHYPT IDEPLPNWEARIDSHGRVYVDHVNRTTWTQRPATAATPDGMR RSGSIQMEQLNRRYQNIQRTIATERSEEDSGSQSCEQAPAGGG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GGGSDSEABESSQSSLDLRREGSLSPVNSQKITLLQLSPAVKFI TNPEFFTVLHANYSAVRVFTSSTCLKHMILKVRDARNFERYQH NRDLVNFNMFADTRLELPRGWEIKTDQOGKSFVDHNSRATTF IDPRIPLQNGRLPNHLTHROHLQRLRSYSAGEASEVSRNRGASL LARPGHSLVAAIRSQHQHESLPLAYNDKIVAFRLQPNIFEMLEQ RQPSIARNHTLREKIHVIRTEGNHGLEKLSCDADLVILLSLFEE EIMSYVPLQAAPHGYSFSPRCSPPQSPQSPGLQASARAPSP YRRDFEAKLRNFRKLEAKGFGQPGKIKLIIRDHLLGTFNQ VMAYSRKELQRNKLYTVFVGEGLDYSGPSREFFFLLSQELFNP YYGLFEYSANDTYTVQISPMASAFVENHLEWFRFSGRILG\LALI HQYLLDAFFT\RPFYKALL\RLPC\D\LSDELYLDEBFHQSLQW MKDNNITDILDLTFTVNEVFGQVTERELKSGGANTQVTEKNKK EYIERMVKWRVERGVVQTEALVRGFYEVVDSRLVSVPDARELE LVIAGTAEIDLNDWRNNTTEYRGYHDGHLVIRFWAAVERFNNE QRLRLQFVTGTSSVPYEGFAAPPWPMGLRRPLP*KKWGKITS LPPRG\HTCLQPDWDLPTVSPRTPMLYEK\LLTA\VEETSTFGT
5910	1526	446	VAEPAAEMFGRGTQIKLDPRTADLLEVLKTNVGTSPACFSQPPT AAQLLRALGPVELALTSILTLLALGSI AIFLEDAVYLYKNLTCP IKRRTLLWKSSAPTIVSVLCCFGLWIPRSLVLVEMTITSPYAVC FYLLMLVMVEGFGGKEAVLRLTRDTPMMVHTGPCCCCCPCCPRL LLTRKKLQ*R*CWALSNTPS**R**PWWACFSSPTASMTQQTFL RGAQLYGSTLSSA/CSTLLALWTLGIISQARLHLGEQNMGAKE ALFOVLLILTALQPSIFSVLANGGQIACSPPYSSKTRSQVMNCH LLIETFTLMTVLRMYRRDKHKVGYETFSSPDLDLNLKALRW AWTMKGCCTH
5911	109	595	QLPLAPCTIGKGLEMRSPKQSFIRSSSHSGAGLLVKNPSTPVF CGHRRGGAFFKYKPTPVVGPEQRPTGQKHMRRGGVSLSPLECS GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET GFHHVGOAGLELL/NVVIHLPRPPKVLGLQA
5912	924	277	MILNKALMLGALALTVMSPCGGEDIVADHVASYGVNLYQSYGP SGQYSHEFDGDEEFYVDLERKETVWQLPLFRFRFRFPDQFALT IAVLKHNLMNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNLI CLVDNIPFPVNVITWLSNGHSVTEGVSETRPSSPKSDHFLQDQ VTSFSPFE**DL**TAKVEQLGAWFEPLLKHGABIPPTL
5913	46	1198	QLRMAGAEGAAGRQSELEPVVSLVDVLEDEELENEACAVLGGS DSEKCSYSQGSVKRQALYACSTCTPEGEPEPAGICLACSIECHGS HKLFEIYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN FFGLYCIKRPYPDPDEIIPDEMIQCVVCEDNFWHGRHLGAIPPE SGDFQEMVCCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM E*/DDQEVIKPENGEHQDSTLKEDEVPEQKDDVREVKVEQNSEP CAGSSSEDLQTVFKNESLNABESKSGCKLQBLKAKQLIKKDTAT YWPLNWSKLCTCQDCMKMYGDLVFLTDEYDTVLAYENKGI AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ**FED
5914	960	124	NLGGSLEPPEALFIQVASMNRVDFYLASIEDMLVAI/GGRN ENGALSSVETYSFKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMSLGD IYSIGSDDNIESMERFDVLGVEAYSPOCNQWTRVAPLLHANSE SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP KAIAGGSACFIAP**SLGQTRKRKAKARGTRTGASDFSCASWDH PHRHLPGLCRPAATS
5915	1604	703	FPCRPTPLKLGRRRRRARI IQAPHCHSPRPRTCPPGALQAPEA PASRAEGPVAVVNGHTEGPAPARSAPKEPPGLPRPLGSPFCPT QEDFPALGGPCPPRPPSPGFSVAVLLKGTPPPPPPGLVPPIS KPPPGFSGLLPSPHP\PVSPAPPPPPQK/RPRLLPAP/PGLPS PRELPGEPSAHPVHQGLPAERRGPLQRVQEPRLRGVQTGPDLS PVLQELPGPAGGEFPEGL**AAGPAAH
5916	256	633	SPRWEIFGPWHRWESFLEGEWPSRIPEPSPDSTKGTSGKGR TVTGAVHRHLNHVAGIIPWVLSQLKPTAATAQDQWTSQQYPDH PTRLLIQ**NQATADKNN**TALLQPHQRL\VSPRMAEA
5917	1343	827	AHQILTYLEP/ICLVVNYNKILT VFLTKSVLEI**KFIHTPQTYR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5918	13	1247	<p>F*NDFFGIKEVYVSRRLRRTSF/RLAVTFLEQAVVSKCVPVDQ FMEHLPLSLLSLASDPVNPVRVLLAKALRQMLLEKAYFRNAGNP HLEVEETILALQSDRDQDVSFFAALEPKRRNIIDTAVLEKQN</p> <p>EGAQVARRRRRRQWRAGRCGRGGRRAERTGGRGPPGRPRPLP PGPARRRRRRMTFPYGDALSGLGGGASGGTFASPGRLFP APPTAAAGSMKKDALTLSEVAAALKPAPAPASYPPA\ADG APSAAPPDGLLASPDGLLKLASPELERLI IQSNGLVTTPTSS QFLYPKVAASEEQEFAEGFVKALEDLHKQNLGAGRAAAAAA AGGPGSGTATGSGAPGELAPAAAAPEAPVYA\NLSSY\AGGCRGL RGGAAT\VAFAAEPVFPFPPPPGALGPRRP/RLALQGRRPQTV PDVP\SFGESE\PLSPIET\DTPRRI\KAKRKRL\RNPIQIRAPK PASRKLGAQSRALERESDPS*SPHGSLASTASLLREQVAQLK QVLSHVNSGCQLLPQHQPVPAY</p>
5919	1	4254	<p>TSVQGDSTPTSSQGSINMHHWISQAIHGTTSTTSSSTQSG GSGAAHRLADVMAQTHIENHSAPPDVTTYSEHSIQVERPQGST GSRTAPKYGNAELMETGDGVVSSRSVSAKIQQVNTLKRPRRP LREFFVDDFEELLEVQPPDPNPQKPEGAQMLAMRGELGVVNTN PPSLEAALQRWGTISPKAPCLTMDTNGKPLYILTYGKLWTRSM KVAYSILHLGLTKQEPMPVRPGRVALVFPNNDPAAAFMAAFYGC LAEVVPVPIEVPLTRKDAGSQIGFLLGSCGVTVALTSDACHKG LPKSPGTGEIPQFKGWPKLLWFVTESKHLSPKPRDWF\PHIKDAN NDTAYIEYKTC\DGSVLGVTVTRTALLTHCQALTOACGYTEAE TIVNVLDFKKDVLWHGILTSVMNMHVVISIPYSLMKVNPLSWI QKVCQYKAKVACVKSMDHVALVHRDQORDINLSSLRMLIVADG ANPWSISSCDAFLNVFQSKGLRQEVIPCASSPEALTVAIRRP DASNQPPGRGVLSMHGLTYGVIRVDSEELSVLTQDVGVLVMPG AIMCSVKPDGVPLCRTDEIGELCVAVATGTSYGLSGMTKNT FEVFAMTSSGAPISEYFFIRTGLLGFVGPGLVFFVVGKMDGLMV VSGRRHNADDIVATALAVEPMKFVYRGRIVAVSVTVLHDERIVI VAEQRPDSTEEDSFQWMSRVLQAIDS IHQVGVCYCLALVPANTLP KTPLGGLHLSLTKQLFLEGLSLHPCNVLMCPHTCVTNLPKPRQKQ PEIGPASVMVGNLVSGKRIAQASGRDLGQIEDNDQARKFLFLSE VLQWRAQTTPDHILYTLNCRGAIANSLTCVQLHKRAEKIAVML MERGHLQDGDHVALVYPPGIDLIAAFYGCYAGCVPIITVRPPH QNIATTLPTVKMIVEVRSACLMTTQLICKLLRSREAAAADVVR TWPLILDITDD*PKRPAQICKPCNPDTLAYLDFSVSTTGMLAGV KMSHAATSFAFCRSIKLQCELYPSREVAICLDPYCGLGFLVWCLC SVYSGHQSLIPPSELETNPALWLLAVSQYKVRDTFCSYSVMEL CTKGLGSQTESLKARGLDLSRVRTCVVVAERPRIALTQSFSKL FKDLGLHPRVSTSPFCRVNLAIQLQGTSGPDPTTVYVDMRALR HDRVRLVERGSPHSLPLMESGKILPGVRIIANPETKGLGDSH LGEIWHSAHNASGYFTIYGDESQSDHFNRLSFGDTQTIIWAR TGYLGLRLRTELTDANGERHDALYVVGALDEAMELRGMRYHPID IETSVIRAHKSVTECAVFTWNTNLLVVVVELDGSQEALDLVPLV TNVVLEEHYLVGVVVVDIGVIPINSRGEKQRMHLRDGFLADQ LDPIYVAYNM</p> <p>QLGAVAHAGVSRIPP*LFPPPLHPTFLSLWCLHHKLP/HPPGASM VRPPVPPRRPPAHISSVRQASTQVPTVPHTQVAVANIGTQTGP SGVGCTPGRPPLPCKCSSAAHSTYRVQEPVHPIPGQEPLTASM LAAAPLHEQKQMIGERLYPLIHDVHTQLAGKITGMLEIDNSEL LMLSPESLHAKIDEAVAVLQAQAMEQPKAYMH</p>
5920	1381	1499	<p>VCPGTGGE*GLWGQLGGLPKETPLKPMDAFTGSGLKRKFDDVDV GSSVNSDDEISSSDSADSCLSNPPTTASFTPTSILKRQKQLR RKNVRFDQTVVYFARRQGFTSVPSQGGSSLGMAQRHNSVRSYT LCEFAQEQQEVNHRILREHLKEEKLHAKMKMLTKNGTIVESVAD GLTLDDVSDDEDIDVENVEVDYFFLQPLPTKRRRALLRASGVHR IDAEKQELRAIRLSREECGDCRLCYDPEACACSQAGIKCQVD RMSFPCCGSRDGCNMGRIEFNPIRVTRHYLHTIMKLELESKR Q\GAAQPPQ*GALPDCQLQDRSTGL*DPWSIGSKLSFTGKG AAATHLILRVINRGAEGKRK</p>
5921	727	157	<p>SYSNWGLFPVSFIQVPRSRGTGNLKPILFYSYYE\CMETLKG\T</p>
5922	2475	495	

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CLYNATQYKVCSPRNDRPDACYNPSEPAATTVFETRTGLLGDT SKIITRTEEKEIPKQITLRFDAACAINSKKLEIGCGSLN*ERS* RVENKYVCHESGVCKNCAYWPCVI*AT*KKKNDSVYLQKGEAN PSCAAGHCNPLELIITNPLDPHKKGERVTGLINRTGLKPQVVI LIKGEVHKCSPKPVFQTFYEELNLPAPELLKRTKNLFLQLAENV IFLLNGTSCYVRGGTTIGDRWPWEA*ELVPTDPAPDIPI*KAE ASNF*VLKTSIIRQYCIAREGKDFIIPVGKPNICGKLYNSTTK TIT*DLNHTKKNPFSKFSKLKTA*AHAEH*DWTPVSGLY*IC RHRAYFRLPNKWADSCVIGTIKPSFLLPIKMGELLGFSVYASR EKKGIVIGNWKDNEWPRERI IQYYGPATWAQDGSWGYR/TP/VY MLNWIIRLQAILEIISNETGRALTVLAWQETQMRNAIYQNRLLA DYLLVAEGGVCRKFNLTNCCQLINDQGVVKNIVRDMTKLAHP IQVWHKFDPESLFGKWFPATGGFKTLIVGVLVIRTCLLLPCVL PLLFQMIKGIVATLVHQKTSAHVNYMNHYSISQRDSKSEDESE NSH
5923	137	638	QLCGRRGQRFRTSIKRMHPI*RTCPNTNL/IILLSQENTQIRDL QQENRELWISLEEHQDALELIMSRYRQMLQMLVAKKAVDAEPV LKAHQSHSAEIESQIDRICEMGEVMRKAVQVDDQDFCKIQEKLA QLELENKELRELLISSESLOARKENSMDTASQAIK
5924	274	2146	EKGKVKDAGAEQWISLSLSCKGSWETQFSNHLNSLTPPTSVRRM PLITTVTLKLMVARHMKLLCSKAFSTQLQKIFLHSGMGIHQ SVCMKLPNTSHIISILMGQPMALVQLETLAPLTII IQFQOTD HMKFWKNLPLHSHHLTPSVPTQVTPKKTGSPEIKLKITKTIONG RELFESSLCGDLLENVQASE\Q*NQSIESRKEKRKSKNHDSR SEERKSHKIPKLEPEEQNRPNERNVDTVSEKPREEPVLKEGSPS ANTI FCSNNGSVHW\FKPQVGDVWVKVGTYPWWPCMVSSDPQL EVHTKINTRGAREYHVQFNSQPERAWVHEKRVREYKGHKQYEE LLAEATKQASNHSEKQKIRKPRPQEREAQWDIGIAHAEKALMT REERIEQYTFIYIDKQPEEALSQAKKSVASTEVKTRRPRSVL NTQPEQTNAGEVASSLSSTEIRRSQRRTSAEEEEPPPVKIAW KTAARKSLPASITMHKGSLLDLQKCNMSPVVKIEQVFALQATG DGKFIQDFVYSTKGIGNKTEISVRGQDRLIISTPNQRNEKPTQS VSSPEATSGSTGSVEKKQQRRISTRSESEKSTEVVPKKIKKE QVGFLHVES
5925	216	1911	MMTAESREATGLSPQAAQEKDGIVIVKVEEEDBHMWGDSTL QDTPPPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHQWL RPE INTKEQILELLVLEQFLSILPKELQVWLQEYRPSGEEAVTLL E DLELDLSGQVPGQVHGPEMLARGMVLDPVQESSFDLHHEAT QSHFKHSSRKPRLLQSRALPAHI PAPPHGSPRDQAMASALT ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGS AF PQGGENRNEEESTSKAETSEDSASRGBTGSRQKBFGEKRDG KKTGERQQKNPEEKTRKEKRDGPAIGKDKKTTITGERGPREGK GLGRSFSLSNFTTPEEVTGTGKSHRCDECGKCFTRSSSLIRHK I IHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LT KHQ RIHTGEKPYECSECGKAFNRNSYLI LHRRVHTREKPYKCTKCGK \AFTRSSTLTLHHRIHARERASEYSPASLDAGFAFLKSCV
5926	2	233	DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEBPPGAHEP SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS
5927	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAKYGIPLA YKKYGDKKLHEKKLPQKHQAHTPEKRVNTGEERRKISEEAA RRRLEFIEKEKKQKQDIISLMKAEQMKRQBERLERINRAREQG WRNVL SAGGSGEVKAPFLGSGGTIAPSSFSRGGQYEHYHAI FQ MQQRAEDNEAKWKREIYGRGLPERQKGLAVERAKQVEEFLQR KREAMQNKARAEHMGILQNLAA MYGGRPSSSRGKPRNKEEV YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGESEADM RRRK\IESLKAHANARA AVLKEQLERKRKEAYBREKKVVEEHLV AKGVKSSDVS PPLGQHETGGSPSKQQMRSVISVTSALKEVGVD S SLTDTRETSEEMQKTNNAISSKREILRLNENLKAQEDEKQKQ N LSDTTFEINVHEDAKEHREKSVSSDRKKWEAGGLVPLDELTL DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LQLQTELENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPFSEASPMQSLKLEGNLEPPDDLETEILQEPS GTNKDE\SLPCTITDVWISSEKETKETQSADRITIQENEVSDEG VSTVDQLSDIHIEPGTNDQSQSKCDVDKSVQPEFFPHKVVHSE HLNLVPQVQSVQCSPEESFAFRSHSLPKNKNKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLMVPTVGDVQRDNLEIDEI EDENIKEGPSDESIVFEETDTDLQELQASMEQLLREQPGEEYS EEESVLKNSDVEPTANGTDVAEDDNPSSSALNEEWHSDNSD GEIASECECDVSFNHLEELRLHLEQEMGFKEFFEVYKIKAIHE DEDENIEICSKIVQNILGNEHQHLYAKILHLVMDGAYQEDNDE
5928	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAKYGTPLA YKKGDKKLHEKKPLQKHQAQHTPEKRVNTGEERRKISEEAA RRLEFIEKEKKQKQDIISLMKAEQMKRQEKERLERINRAREQG WRNVLSAGGSSEVKAPFLGSGGTIAPSSFSRQYEHYHAI FDQ MQQRAEDNEAKWKREIYGRGLPERQKGLAVERAKQVEEFLQR KREAMONKARAEGHMGILQNLAAMYGGRPSRSGGKPRNKEEV YLARLRQIRLQNFNERQKIKALRGEKKEANHSEGESEADM RRKK\IESLKAHANARAVALKEQLERKKEAYEREKKVWEEHLV AKGVKSSDVSPPLGQHETGSSPSKQMSRVSISVTSALKEVGVD SLDTRTSEEMQKTNNAISSKREILRLNENLKAQEDKKGQN LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIFDELTL DTSFSTTERHTVGEVILGPNNGSPRRAGKSPDTSVLKILGEAE LQLQTELENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS AIVDSPVETKSPFSEASPMQSLKLEGNLEPPDDLETEILQEPS GTNKDE\SLPCTITDVWISSEKETKETQSADRITIQENEVSDEG VSTVDQLSDIHIEPGTNDQSQSKCDVDKSVQPEFFPHKVVHSE HLNLVPQVQSVQCSPEESFAFRSHSLPKNKNKNSLLIGLSTG LFDANNPKMLRTCSLPDLSKLFRTLMVPTVGDVQRDNLEIDEI EDENIKEGPSDESIVFEETDTDLQELQASMEQLLREQPGEEYS EEESVLKNSDVEPTANGTDVAEDDNPSSSALNEEWHSDNSD GEIASECECDVSFNHLEELRLHLEQEMGFKEFFEVYKIKAIHE DEDENIEICSKIVQNILGNEHQHLYAKILHLVMDGAYQEDNDE
5929	3	1558	LDFSMTQLPAYVAILLFVYSRASCQDTFTAAYVEHAAILPNAT LTPVSRREALALMNRNLDILEGATSAADQGAHIVTPEDAIYG WNFNRLSLYPYLEDIPDPEVNWIPCNRRNRFGQTPVQERLSCL\ AKNNSIYVANIGDKKPCDSDPQCPDGRYQYNTDVVF\DSQ KLVARVYHKQNLFMGENQFNVPKEPEIVTFNTTFGSFGIFTCFI LFHDPVAVTLVKDFHVDITVFPTAMNVLPHLSAVEPHSAWAMGM RVNFLASNIHYPSSKMTGSGIYAPNSSRAFYDMKTEEGKLLLS QLDSHPSHSAVNWTSYASSIEALSSGNKEPKGTVFDEFTFVK LTGVAGNYTVQKDLCHLSYKMSENIPNEVYALGAFDGLHTVE GRYVLQICTLLKCKTTLNLTGDSAEASTRFEMFSLSGTFTGTQ YVFPVLLSENQLAPGEFQVSTDGRLFLSLKPTSGPVLTVTLFGR LYEKDASNASSGLTAQARIIMLIVIAPIVCSLSW
5930	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLWVIPSERHGFEEASIKEERGDEVMMVLAENGGKAMVNKDDIQ KMNPKFKSKVEDMAELTCLNEASVLHNLKDRYSSGLIYTYSGLF CVVINPYKNLPIYSENI IEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDNH IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFI RINFV TGYIVGANIETYLLEKSRVRAQKDERTFHIFYQLLSG\AGEHL KSDLLEGFNNYRFLSNGYIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMETRAILTPRIKVGGRDYVQKAQTKAQADFAVEALA KATYERLPRWLVRINKALDRTRKQASFIGILDIAGFEI FELN SFEQLCINYTNEKLQQLFNHTMFILEQEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCEIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMRFTVGQLYKESLTKLMTALRNTPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFNNRIVFQEFQRQRYEILTP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEERDLKITDIIFFQAVCRGYLARKAFKKQQQLSALKVLQR NCAAYLKLHWWQWVRVFTKVKPLLQVTRQEEELQAKDEELLKV EKQTKVGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAACKQLEELIHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAESEKAKNLAKIRNKQEVMSIDLEE RLKKEEKTRQLEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSSELEALKTELEDTLDTAAQQELRTKRE QVVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKLACEVKVLQVQKAESEHKRKKLDAQV QELHAKVSEGDRRLRVELAEKASKLQNELDNVSTLLEAEKKGKIK FAKDAASLESQLODTQELLQEETRQKLNLSRIRQLEEEKNSLQ EQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA KKLLKDAEALSQRLEBKALAYDKLEKTKNRLQQLDLDLTVDL HQRQVASNLEKKQ\KKFDQLLAEKKSISARYAERDRABAEARE KETKALSLARALEEAEAKEEFERQNKQLRADMEDLMSKDDVG KNVHELEKSKRALEQQV\EEMRTQLEEELEDELQATEDAKLRLEV NMQAMKAQFERDLQTRDEQNEEKRLLIQKVRELEAELEDERKQ RALAVASKKMEIDLKDLAEQTEAANKARDEVIKQLRKLQAQMK DYQRELEEARASRDEIFAQSKSEKSKLSLEAEILQLQEEELASS ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE ELEEEQSNMELLNDRFRKTTLQVDTLNAELAERSAAQKSDNAR QQLERQNKELKAKLQLEGA VKSKFKATISALEAKIGQLEEQLE QEAKERAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA NARMQLKRQLBEAEBEATRANASRRKLQRELDDEANEGLSR EVSTLKNRLRRGGPISFSSSRSGRRQLHLLEGASLELSDDDTESK TSDVNETQPPQSE</p>
5931	113	6082	<p>RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLWVWPSERHGFPAASIKBERGDEVMLAENGKKAMVNDKDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTSGLF CVVINPYKNLPIYSENIEMMYRGKKRHEMPPIYAISESAYRCM LQDREDQSILCTGSGAGKTENTKKVVIQYLAHVASSHKGRKDNH IPGE\LERQLLQANPILESFGNARTVQNDNSSFQKGFIRINFDV TGYIVGANIETYLEKSRVRAQKADERTFHFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVSVVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVG RDYVQKAQTKAQADFAVEALA KATYERLFRWLVRINKALDRTRKQGSFIGILDIAGFIEFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVALLLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADWLKMNMDPLND NVATLLHQSSDRFVABLWKDQVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMTLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICQGFNPNRIVQEFQRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEERDLKITDIIFFQAVCRGYLARKAFKKQQQLSALKVLQR NCAAYLKLHWWQWVRVFTKVKPLLQVTRQEEELQAKDEELLKV EKQTKVGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAACKQLEELIHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAESEKAKNLAKIRNKQEVMSIDLEE RLKKEEKTRQLEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSSELEALKTELEDTLDTAAQQELRTKRE QVVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKLACEVKVLQVQKAESEHKRKKLDAQV QELHAKVSEGDRRLRVELAEKASKLQNELDNVSTLLEAEKKGKIK FAKDAASLESQLODTQELLQEETRQKLNLSRIRQLEEEKNSLQ EQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQEELDDLTVDLH HQRQVASNLEKKQ\KKFDQLLAEKKSISARYAERDRABAEARE KETKALSARALEBALEAKEEFERQNKQLRADMEDLMSSKDDVG KNVHELEKSKRALEQQV\EEMRTQLEEELEDELQATBDALRLLEV NMQAMKAQFERDLQTRDEQNEKKRLLIKQVRELEAELEDERKQ RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAMK DYQRELEEARASRDEIFAQSKSEKLLKSLEABILQLQEELAS ERARRHAEQERDELADEITNSASGKSALLDEKRLRLARIAQLEE BLEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR QQLERQNKELKAKLQEEGAVSKFKATISALEAKIGQLEEQLE QEAKERAAANKLVRTEKKLKEIFMQVEDERRHADQYKEQMEKA NARMKQLKRQLEEAEEATRANASRRKLQRELDDEANEGLSR EVSTLKNRLRRGGPISFSSSSRGRRLHLEGASLELSDDDTESK TSDVNETQPPQSE
5932	33	572	RHLEEICFLFLQKGRKLKLSGPRWEEGKPRGTGGLWVKAENMG FGATLAVGLTIFVLSVVTIIICFTSCCCCLYKTCRRPRPV\APP PHPP/PVVHAPYPQPPSVPPSYPGPSYQGYHTMPPQPGMPAAPP FMQYPPPYPAQPMGPPPAYHETLAGGAAAPYPASQPPYPNAYMDA PKAAL
5933	1	3190	GTRKLMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNRYNESARES LCDSPHQNLSPILLENKLLK AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEQ SDGNKVKTFRGGVVNAAKEEHETDEKRGKIYKPSRFFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKSNLELFKEELKQI QEERDERHKTGRLSRFEPPQSDSDGQRRSMDAPSRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLLKCCCEFGFRGFP LASVKIMWPRTDEERARERNCGFVAFMNRDAERALKNLNGKMI MSFEMKLGWGAVIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLQAIIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPLNPLYLHGMSEEQ ETEAFVEEPSKKGALKEEQDKLEELRGLTPRKNDIGDAMVFC LNNAEAAAEIIVDCITESLSILKTPPKKIARLYLVSDVLYNSSA KVANASYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQKQRM TCFRAWEDWAIYEPFLIKLQNIIFLGLVNIIEEKETEDVPPDDL GAPIEEELDGAPLEDVVGIPIDATPIDDLGVPKSLDDDLGVP PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESEEEENQNEEESDEEDTQSSKSEEHLYSNPIKEEMTE SKFSKYSEMSEBKRAKLEIELKVMKFQDELESGKRPKKPGQS QEQVEHYRDKLLQREKEKELEERERERDKKDEKLESRSKDKKEK DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPPSPKERSERSE SHKESRSRSSHKDSPRDVS KAKRSPSGSRTPKRSRRSRSP KKSGKRSRSQSRSPHRSHKSKGKTNTGRKFFKAVTYWKCDLF LCPERSVF
5934	1	3190	GTRKLMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNRYNESARES LCDSPHQNLSPILLENKLLK AFSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEQ SDGNKVKTFRGGVVNAAKEEHETDEKRGKIYKPSRFFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKSNLELFKEELKQI QEERDERHKTGRLSRFEPPQSDSDGQRRSMDAPSRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLLKCCCEFGFRGFP LASVKIMWPRTDEERARERNCGFVAFMNRDAERALKNLNGKMI MSFEMKLGWGAVIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLQAIIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPLNPLYLHGMSEEQ ETEAFVEEPSKKGALKEEQDKLEELRGLTPRKNDIGDAMVFC LNNAEAAAEIIVDCITESLSILKTPPKKIARLYLVSDVLYNSSA KVANASYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQKQRM TCFRAWEDWAIYEPFLIKLQNIIFLGLVNIIEEKETEDVPPDDL GAPIEEELDGAPLEDVVGIPIDATPIDDLGVPKSLDDDLGVP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESEEEENQNEESEDREDTQSSKSEEHLYSNPIKEEMTE SKFSKYSEMSEKRAKLREIELKVMKFQDELESGKRPKKPGQSF QEQVEHYRDKLLQREKEKELERERERDKDKEKLESRSKDKKEK DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKRSERSER SHKSSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRRSRSP KKGKKSRSQSRSPHRSHKKS KGTNTGRKFFKAVTYWKCDLF LCPERSVF
5935	3	4493	SYWLSGWRLSRPPRQFWAGWRGIRFGTMAPVHGDDCEIGASAL SDSGSFVSSRARREKSKKGRQEALERLKAKAGERKYKYEVEDF TGVYEEVDEEQSKLVQARQDDDWIVDDGIGYVEDGREIFDD LEDDALDADEKGDGKARNKDKRNVKLAFTKPNNIKSMFTACA GKKTADKAVDLSDGLLDIQLDNTETPQITPPVMILKKKRS IGASPFPVSHVATAVPSGKIAPSVSRKEPPLTPVPLKRAEFAG DDVQVESTEEQESGAMFEDGDFDEPMEVEVDLEPMAAKAWD KESEPAEEVKQEADSGKGTVSYLGSFLPDVSCWDIDQEGDSSFS VQEVQVDSSHLPLVKGADDEQVFHYWLDAYEDQYNQPGVVFLF GKVVIESAETHVSCVMVKNIERLTLYFLPREMKIDLNTGKETGT PISMKDVEEYFDEKIATKYKIMKFKSKPVEKNYAFEPIDVPEKS EYLEVKYSAEMPQLPQDLKGETFSHVFGTNTSSLELFLMNRKIK GPCWLEVKKSTALNQPVSWCKVEAMALKPDLVNVIKDVSPPLV VMAFSMTMQNAKNHQNIIAMAAALVHHSFALDKAAPKPPFQSH FCVVSKEPKDCIFPYAFKEVIEKKNVKEVAATERTLLGFFLAKV HKIDPDIIVGHNIYGFELVLLQRIINVCKAPHWSKIGRLKRSNM PKLGGRSFGGERNATCGRMICDVEISAKELIRCKSYHLSELVQQ ILKTERVVIPMENIQNMYSESSQLLYLLEHTWKDA\KFILQIMC ELNVLPALQITNAGNIMSRTLMGGRSERNEFLLHAFYENNY IVPDKQIFRKPQQLGDEDEIDGDTNKYKGRKKGAYAGGLVL DPKVGFYDKFILLDFNSLYPSIIQEFNICPTTVQRVASEAQKV TEDGEQEQIPELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD LNPDLILQYDIRQKALKLTANSYMGCLGFSYSRFYAKPLAALVT YKGREILMHTKEMVQKMNLEVIYGDTSIMINTNSTNLEBVKL GNKVKSEVNKLYKLEIDIDGVFKSLLLKKKKYAAALVVEPTSD GNYVTQELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDTIV ENIQKRLIEIGENVLNGSVPSQFEINKALTKDPQDYPDKKSLP HVHVALWINSQGGKVKAGDTVSYVICODGSNLTASQRAYAPEQ LQKQDNLTIDTQYLAQQIHPVVARICEPIDGIDAVLIATGWEL DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKPCPC TCGTENIYDNVFDGSGTDMEPSLYRCSNIDKASPLTFTVQLSN KLIMDIRRFIKKYDGLWICEPTCRNRTHLPLQFSRTGPLCP ACMKATLQPEYSDKSLYTQLCFYRIFDAECALEKLTDTHEKDK LKKQFFTPKVLQDYRKLNKNTAEQFLSRSGYSEVNLSKLFAGCAV KS
5936	1124	139	RGEEQDAEFRRFACLGFERLQEFSLRLRAVHRSRANTCYLAT RMLMATCCPSPTTACTGWPQAPPLRLLVQKREADSSGLAFAS NSLQRRKKGLLLRPVAPLRTPLLLISLPQDFRQVSSVIDVDLL PETHRRVRLHKGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMMVAN SHN\LIVTVKPAQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD SSDLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPLSD QEQASSGWGSRIRGDGSGFSL
5937	31	1600	PTSLKSTVOLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL YGLTSSYSLWMLRSSLKQYSFEALREKSNYSIDPDVKNDFAPI LHLADQYDPLYSKRFSIFLSEVSENKQLKQINLNNEWTVEKLKSK LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPVVKLPS AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMKG IPRWVFLKNLKELYLSGCVLPEQLSTMQLEGFQDLKLNRLTYL KSSLSRIPQVVTDLPLSLQKLSLDNEGSKLVLNLLKMMVNLSK LELISCDLERIPHSIFSLNLLHELDLRENNLKTVEETISFQHLQ NLSCLKLWHNNIAYIPAIGALSNLQSLDHNHNIENLPLQLFL CTKLHYLDLSYNHLTFIPPEIQYL\SNLQYFAVTNNNIEMLPDG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LFQCKKLQCLLLGKNSLMNLSPHVGELSNLTHREPIG\NYLETLPPELEGCSLKRNCILVEENLNTLPLPVTERLQTCCLKC
5938	395	1865	YKGEFFCNQEARGERRRKKKAMSSPNIWSTGSSVYSTPVFSQKMTVWILLLLSLYPGFTSQKSDDDYEDYASNKTWVLTPTKVPBGDVTVLNNLLLEGVDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINMETITDIFFAQTWYDRRLKFNSTIKVLRNLNSNMVGKIWIPTFFRN SKKADAHWITTPNRMRLRIWNGRVLVSLRLTIDAECQLQLHNP MDEHSCPLEFSSYGYPREIIVYQWKRSSVEVGDRSWRLYQFSFVGLRNTTEVVKTTSGDYVMSVYFDLSRRMGYFTIQTYPCTLI VVLSWVSFWINKDAVPARTSLGITTTLTMTLSTIARKSLPKVSYTAMDLFVSVCFIFVFSALVEYG\TLHYFVSNRKPSKDKDKKK KNPAPTIDIRPSATIOMNATHLQERDEEYGYECLDGKDCASF FCCFEDCRTGAWRHGRIHRIAKMDSYARIFFFTAFCFLNLYVW VSYLYL
5939	66	1404	IRPGYLKEVQENSPGHRAGLEFFDFIVSINGSRLNKDNDTLKD LKANVEKPVKMLIYSSKTLELRETSVTPSNLWGGQGLLGVSI R FCSFDGANENVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNE SBDLFSLIETHEAKPLKLYVNTDTDNCREVIITPNSAWGGEGLGCGIGYGYLHRIPTRPFEEGKKISLPGQMAGTPIITPLKDGFT VQLSSVNPSPSLSPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV PTVP\LLPPQVNVQSLTSVPPMESSYLHLPLGLMPFTRQGLPNLPQ PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I AFLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT TTAKADAASSLTVDVTPPTAKAPTVEDRVGDS TPVSEKPVSAADANASESP
5940	145	717	RRSASRSASPRQSAGTAVTTGTTRAGGTCLAAHHRMRWRADGRS LEKLPVHMLGVITEVEQEPSFSDIASLVVWCMAVGISYISVYDH QGIFKRNNRMLMDEILKQQQELLGLDCSKYSPEFANSNDKDDQV LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPDLDVDT LA\VTYLVQMVVILI
5941	13	6147	MCLGRMGASSERSPEVPGPPAPGLPFCCGGSLAVVLLALPVA WQCNAPAW\LPFARPTNLDEFEPIGTLYLNEYCRPGYSGRPF SIICLKNSVWTGAKDRCKRKRCPDPVNGMVHVIKGIQFGSQ IKYSC TKGYRLIGSSSATCIIISGDTVIWNETPICDRIPCGLPP TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFEVLGEP SIY CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLSL NEVVEFRCQPGFVMKGP RRVKCQALNKWEPELPSCSRVCQPPPD VLHAERTORDKDNFSPGQEVFYSCBPGYDLRGAASMRCTPQGDW SPAAPTCEVKS CDDFMGQLLNGRVLFPVNLQLGAKVDFVCEG FQLKGSSASVYCVLAGMESLWNSVVPVCEQIFCPSPPVIPNGRHTG KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQNG VSSPAPRCGILGHCAPDHFLFAKLKTQTNASDFPIGTSLKYE CRPEYYGRPF SITCLDNLVWSSPKDVCKRKSKCTPPDPVNGMVH VITDIQVGSRIYNSCTTGHRLIGHSSAECILSGNAHWSTKPPI CORIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV FELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL VSDNRSLSLNEVVEFRCQPGFVMKGP RRVKCQALNKWEPELPS CSRVCQPPPDVLHAERTORDKDNFSPGQEVFYSCBPGYDLRGA ASMRCTPQGDWSPAAPTCEVKS CDDFMGQLLNGRVLFPVNLQLG AKVDFVCEG FQLKGSSASVYCVLAGMESLWNSVVPVCEQIFCPS PVPVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI RCTSDPQNGVWSSPAPRCGILGHCAPDHFLFAKLKTQTNASD FPIGTSLKYE CRPEYYGRPF SITCLDNLVWSSPKDVCKRKSKCT PPDVNGMVHVITDIQVGSRIYNSCTTGHRLIGHSSAECILSGN TAHWSTKPPICQRI PCGLPPTIANGDFISTNRENFHYGSVVTYR CNLGRGRKVFEVLGEP SIYCTSNDDQVGIWSGPAPQCIIPNK CTPPNVENGILVSDNRSLSLNEVVEFRCQPGFVMKGP RRVKCQA LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC EPGYDLRGAASLHCTPQGDWSPAAPCAVKS CDDFLGQLPHGRV LFPNLQLGAKVSFVCEG FRLKGSSVSHCVLGMRS LWNNSVP VCEHIFCPNPPAILNGRHTGTPSGDIPYKGEISYTCDPHPDRGM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRAGHCKTPEQF PFASPTIPINDFEFPVGTSLNYECRPGYFGKMFISISLENLWVS SVEDNCRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCNEGFRLL IGSPSTTCLVSGNNVTWKKAPICEIISCEPPPTISNGDFYSNN RTSFHNGTVVTYQCHTGPGEQLFELVGERSIYCTSKDDQVGWV SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRFCRQPG FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEHTLSHQ DNFS PGQEVFYSCFPSYDLRGAASLHCTPQGDWSPEAPRCTVKS CDDFLGQLPHGRVLLPLNLQLGAKVSFVCEGFRLLKGRSASHCV LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI PYGKE VSYTCDPHPDGMTFNLIIGESTIRRTSEPHONGVWSSPAPRCEL PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGYLLVK GFI FCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMKKVYHY GDYVTLKCEDGYTLEGS PWSQCQADDRWDPLAKCTSRTHDALI VGTLSGTIFFILLIIFLSWIIKHKRKGNNAHENPKEVAIHLHSQ GGSSVHPRTLQTNEENSRLVP
5942	4509	688	YLYVVRMRANFLAYGISHKAYQIDPPL\RKHREQ\LVIE\VGRL DK\AQMRIFBERTGYFSSDGLRTASHYIKYNTIETFNELFDA HKTEGDI FAIVSKAEEDQIKVREEEIEELDTLLSNFCRLSTPG GVENSYGKINILLQTYINRGEMDSFSLISDSAYVAQNAARIVRA LFEIALRKRWPTMTYRLNLKSAIDKRLNGWASPLRQFSILP PH MLTRLEEKLTVDKLDKMRKDEIGHILHHVNIIGLVKQCVHQIP SVMMEAFIQPI TRTVLRLVLSIYADFTWNDQVHGTGEPWWI WV EDPTNDHIYHSEYFLALKKQVISKEAQLLVFTIPIFEPLPSQY I IRAVSDRWLGAEAVCI INFQHLILPERHPPHTELLDLQPLPITA LGCKAYEALYNFSHFNPVQTQIFHTLYHTDCNVLLGAPTSGGT VAAELAI FRVFNKYPTSKAVYIAPLKALVRERMDWKVRIEEL GKKVIELTGDVTPDMKSIKADLIVTTPEKWDGVSRSWQNRNRY QQVTILI IDEIHLGEEERGVL EVIVSRTNFISSHTEKPVRI V LSTALANARDLADWLNLIKQMGLENFRPSVRPVPLEVHIQGFPGQ HYCPRMASMNKPAQAIRSHSPAKPVLI FVSSRRQTRLTALELI AFLATEEDPKQWLNMDEREMENI IATVRDSNLKLTAFGIGMH AGLHERDRKTVEELFVNCKVQVLIATSTLANGVNFPAHLV I IKG TEYDYGKTRRYVDFPITDVLQMMGRAGRPOFDDQKAVILVHDI KKFYKFLYEPFPPVESSLGVLSDHNLAEIAGGTITSKQDALD YITWTYFFRRLIMNPSYVNLGDVSHDSVNKFLSHLIEKSLIELE LSYCIEIGEDNRSIEPLTYGRIASYYLKHQTVKMFKORLKPEC STEELLSILSDAREYTDLPVRHNEHDMNSELAKCLPIESNPHSF DSPHTKAHLLLQAHLSRAMLPCPDYDITDTKTVLQALRVQAML DVAANQGWLVTLNITNLQMVIQGRWLKDSLLTLPNIENHHL HLPKKWKPI MKGPHARGRTSIECLPELIHACGGKDHVFSMVS ELHAAKTQAWNFLSHLPEINVGISVKGSWDDLVEGHNELSVST LTADKRDDNKWIKLHADQYVVLQVSLQRVHFGFHGKGPESCAVT PRFPKSKDEGWFLILGEVDKRELIALKRVGYIRNHVVASLSPYT PEIPGRYIYTLYFMSDCYLGLDQQYD/NLSQRYTSESFCTGQHQ GL
5943	1	2274	DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQTLWLPNHVFLRLR EGLKNQSPTEAEKPASSSLPSSPPQLLTRNVVFLGGELFLWD GEDSSFLVVRLRGPGSGG\BEPALSQYQRLLCINPPLFEIYQVL LSPQTQHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVNCSTTP VAERFFTSSTSLTLKHAAYWYSEILDPHVVLLTSDNVIRIYSLR EPQPTTNVI ILSEABEESLVNLKGRAYTASLGATAVAFDFGPLA AVPKTLFGQNGKDEVVAYPLYIYENGETFLTYISLLHSPGN/I WKAVGSIAHAS\AARDNYGYDACAVALCLPCVPNIIIVATESGML YHCVVLEGEEDDHTSEKSWDSRIDLIPSLYVFECEVLELALKL ASGEDDPFDSDFSPVKLHRDPKCPSPRYHCTHEAGVHVSGLTWI HKLHKFLGSDDEEDKSLQELSTBQKCFVEHILCTKPLPCRQAP IRGFWIVFDIIGPTMICITSTYECLINPLLSTVHPASPPLLCR EDVEVAESPLRVLAETPDSFEKHRSILQRSVANPAFLKASEKD IAPPPECLQLLSRATQVFREQYILKQDLAKEEIQRRVKLLCDQ KKKQLEDLSYCREERKSLREMAERLADKYEEAKEKQEDIMNRMK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KLLHSFHSSELVLSDSERDMKKELQLIPDQLRHLGNAIKQVTMK KDYQQQKMEKVLSPKPTIILSAYQRKCIQSILKEEGEHIREMV KQINDIRNHVNF
5944	167	3428	FSIATFTDEPEVLTEPPSATTTTTIGISATWTTLAGSHGKRNNIT ITTSKKRKNRKNKITPENVOIIFDDPLPISYSQPEKVNAGESKS SSTSESGDSNDMRISSCSDSSNSNRRKSDNHSAPVTTTVSS KKQPSVLVTPPKEERKSVSGKASIKLSETISEGTSNSLSTCTKS GPSPLSSPNGKLTVASPKRGQKREBGEVVRSSKKVSPSTVI SRVIGRGGCNINAIREFTHAIDIDKQDKDTGDRIITIRGGTES TRQATQLINALIKDPDKEIDELIPKNRLKSSANSKIGSSAPTT TAANTSLMGIKMTTVALSSTSQTATALTVPASSASTHTIKNP VN\NVRPGFPVSPF\LAYPPQFAHALLAQTFQQIRPRLPMT HFGGTFPPAQSTWGPFPVRLSPARATNSPKPHMVPRHSNQNSS GSQVNSAGSLTSSPTTTSSASTVPGTSTNGSPSSPSVRRQLF VTUVKTSNATTTTVTASNNNTAPTATYPMPTAKEHYVSSP SSPSPPAQPGGVSRNSPLDCGSASPKNKVASSEGEAGSFPVET TNRTPPNSSSSSGSSAHSNQPPGVSQEPRLPQQSQVPPP EVRMTVPPLATSSAPVAVFSTAPVTYPMPTQPMGCPQPTPKMET PAIRPPPHGTTAPHKNSASVQNSSVAVLSVNHIKRPHSVPSVQ LPSTLSTQSACQNSVHPANKPIAPNFSAPLPFPFSTLFENSPT SAHAFWGGSVSSQSTPESMLSGKSSYLPSNDPLHQSDTSKAPG FRPPLQRPAPSPSGIVNMDSPYGSVTPSSSTHLGNFASNISGGQM YGPAPLGGAPAAANFNQRHFSPLSLTPCASSANDSSAQSVSS GVRAPSPAPSSVPLGSEKPSNVSDRKVPVPIGTERSARIRQTG TSAPSVIGSNLSTSVGHSGIWSFEGIGGNQDKVDWCNPGMGNPM IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHQHVPAGYMDFPK VGGMPFVSYGNAMIPVAPIDGAGGPIFNGPHAADPSWNSLIK MVSSSTENNGPQTWTGPWAPHMNSVHMNQLG
5945	1461	197	GVTHLFLFGKRKLNGTAEDLKGQADFFLLVSEAVVATGSPRA WLTCLILPLPGIIFSVLPKAMSRPLITFTPATDPSDLWKDQGO QPQPEKPESTLDGAAARAFYEALIGDESSAPDSQORSQTEPARER KRKKRRIMKAPAAEAVAEGASGRHGQGRSLEAEDKMTTHIRLRAA QEGDLPELRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG AAVSYLLGRGAAWVGCESGRDAAQLAEAGFPEVARMVRESH GETRSPENRSPTPSLQYCENDTHFQDSNHRSTAHLLSLSQGP QPPNLPGLGVPISSPGFKLLLRGGWEPGMLGPRGEGRANPIPTV LKRDOEGLGYRSAPQPRVTHFPADTRAVAGRE\TPPRVATLSW REERRREE\KDRAWERDLRTYMNLEF
5946	541	1666	ILGSYSYIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLF SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDV/TILTEAV YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG YIWEFKYLFVQCNYLTLENLELHTTPWSSCECLFDDDIRAITFKA KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPTASQ KIALNAHSSLSKISFSSLPNIYVTGCAKCGLELETDENRIYKQCF SCLPFTMKKIYYRPAALMTAIDGRHDVCIRVESKLEIKILLNISA DCLNRVIVPSSEITYGMVVADLFHSLLAWSAEPCVLKIQSLFVL DENSYPQQDFSLDFYPDIVKHGANARL
5947	3	1317	RGIPDRRRRGPIGRVNMMDLENKVKMGLGHEQGFGAPCLKCKEK CEGFELHFWRKICRNC\NVAKKSM\TVLLSNEEDRKVGKLFEDT KYTTLIAKLSKGIPMYKRNVMILTNPVAARKQVNSINTVYEW PPVQNALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD QDPSKCHELSPREVKEMEQFVKYKSEALGVGDVXLPCEMDAQG PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTQYSCYCKLSMKEG DPAIYAERAGYDKLWHPACFVCSSTCHELLVDMYIFWKNKLYCG RHYCDSEKPRCAGCDELIFSNEYTQAEQNWHLKHFFCCPDCSI LAGEIYVMVNDKPVCKPCYVKNHAVVCOGCHNAIDPEVQRVTYN NFSWHASTECLSCSSCKCLIGQKFMPEGMVFCVSECKKMS
5948	39	3370	YRERYPVSGSVLRSALVCWDFLSGLTEGSLLEGGFFSGPIDQ GNHYQMRKGRCHRGSAARHSPSPSVKHSPTRETLTYAQORM VEIEIEGRHLRISIFDPLEIILEDLTAQEMSECSNSENSERP PVCLRTKRRHKNRVRKKNALPSAHGTPASASALPEPKVRIVEY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>SPPSAPRRPPVYKFIKSAEELDNEVEYDMDEEDYAWLEIVNE KRKGDGCVPAVSQSMFEFLMDRFKESHENQKQGEQQSLIDEDA VCCICMDGECQNSNVILFCDCMCNLAVHQECYGVPIPEGQWLC/ RAHCLQSRARPADCVLCNKGGAFFKTTDDDRNGHV\VCALW\IP E\VGFAVTVFIEPIDGVNIPPARWKLTCNLCKEKGR/VGACI QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR KKAKKAKKALAEPCAVLPTVCAPYIPQRLNRANQVAIQKKQ FVERAHSYWLKRLSRNGAPLLRRLQSSLQSQRSSQRENDDEM KAAKEKLYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI KHPMDFATMRKRLAAGYKNLHEFEEDFDLIIDNCMKYNARDTV FYRAAVRLRDQGGVLRQARREVDSIGLEEASGMHLPERPAAAP RRPFSWEDVDRLLDPANRAHLGLEEQRLRELLDMLDLCAMKSSG SRSKRAKLLKKEIALLRNLSQQHSQPLPTGPGLEGFEEDGAAL GPEAGEEVLPRLETLQPRKRSRSTCGDSEVEEESPGKRLDAGL TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSNSPLCDSS FNAPKCGRGKPALVRRHTLEDRSELISCIENGYAKAARIAEV GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFVLFFDNKRSWQ WLPKSKMVLGIDETIDKLKMEGRNSSIRKAVRIAEDRAMNHL SRVHGEPTSDLSID</p>
5949	39	3370	<p>YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLEPGFFSGPIDQ GNHYQMRKGRCHRGSAARHPPSPCSVKHSPTRETLTYAQARM VEIEIGRLHRISIFDPLEIILEDLTAQEMSECNSENKENSERP PVCRLTKRHKNNRVKKNEALPSAHGTPASASALPEPKVRIVEY SPPSAPRRPPVYKFIKSAEELDNEVEYDMDEEDYAWLEIVNE KRKGDGCVPAVSQSMFEFLMDRFKESHENQKQGEQQSLIDEDA VCCICMDGECQNSNVILFCDCMCNLAVHQECYGVPIPEGQWLC/ RAHCLQSRARPADCVLCNKGGAFFKTTDDDRNGHV\VCALW\IP E\VGFAVTVFIEPIDGVNIPPARWKLTCNLCKEKGR/VGACI QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR KKAKKAKKALAEPCAVLPTVCAPYIPQRLNRANQVAIQKKQ FVERAHSYWLKRLSRNGAPLLRRLQSSLQSQRSSQRENDDEM KAAKEKLYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI KHPMDFATMRKRLAAGYKNLHEFEEDFDLIIDNCMKYNARDTV FYRAAVRLRDQGGVLRQARREVDSIGLEEASGMHLPERPAAAP RRPFSWEDVDRLLDPANRAHLGLEEQRLRELLDMLDLCAMKSSG SRSKRAKLLKKEIALLRNLSQQHSQPLPTGPGLEGFEEDGAAL GPEAGEEVLPRLETLQPRKRSRSTCGDSEVEEESPGKRLDAGL TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSNSPLCDSS FNAPKCGRGKPALVRRHTLEDRSELISCIENGYAKAARIAEV GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFVLFFDNKRSWQ WLPKSKMVLGIDETIDKLKMEGRNSSIRKAVRIAEDRAMNHL SRVHGEPTSDLSID</p>
5950	1166	373	<p>ESRSLTMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR CLCRQHRPVQLCAHRTCREALDVLAKTVAFRLNLPSPWQLPPQ DQRRLLQGCWGPFLFLGLAQDAVTFEVAEAPVPSILKILLEEP SSSGSGQLPDRPQPSLAQVWLQCCLESFWSLELSPKE\YACL KGPIILFNPDVGLQAASHIGHLQEAHWVLCVLEPWCAPQGR LTRVLLTASTLKS IPTSLGLDLPFRPIIGDVDIAGLLGDMLLLR</p>
5951	143	5449	<p>WNVVKPSLLVQLFKFSDEEHEQNDISIGKTGETGVEEMIATR VBQDSKETVLSHEDDHILEDAGSSDISSDACTNPNKNTENSLV GLPSCVDEVTECNLELKD TMGIADKTENTLERNKIEPLGYCEDA ESNRQLESTEFNKNLEVVDTSTFGPESNILENAICDVPDQNSK QLNAIESTKIESHETANLQDDRNSQSSSVSYLESKSVKSXHTKP VHSKQNM TTDAPKKIVAAYEVVHSKTKVNVKSVKRN TDVPS QQNFHRPVKVRKKQIDKEPKIQSCNSGVKSVKNQAHSVLKKTLQ</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>DQTLVQIFKPLTHSLSDKSHAHPCGLKEPHHPAQTGHVSHSSQK QCHKPQQQAPAMKTNHSHVKEELEHPGVEHFKEEDKLKLLKPEKN LQPRQRSSSKSFLDEPPLFIPDNIATIRREGSDHSSSFESKYM WTPSKQCGFCKKPHGNRFMVGCGRCDWFHGDVGLSLSLQAQVM GEEDKEYVCVKKCAEEDKKTEILDPTLENQATVBFHSGDKTME CEKLGSLSKHTTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD NEIKKWQLAPLRKMGQPVLPRRSSEKSEKIPKESTTVTCTGEG ASKPGTHEKQEMKKKKV\KGVNLNVHPAASAKPSADQIRQSVR HSLKDILMKRLTDSNLKVPEEKAATKIEKELPSFFRDTDAK YKNKYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIRMSPEELAS KELAAWRRRENRTIEMIIEKQREVERRPITKITHKEIEIESD APMKEQEAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS QHRQHLFDLNCCKICIGRMAPPVDDLSPKKVKKVGVARKHSDNE AESIADALSSTSNILASEFFEEKQESPKSTFSPAPRPPEMPGT EVESTFLARLNFVWKGFINMPVAKFVTKAYPVSGSPEYLTEDL PDSIQVGGRIISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDI SYTLFAYFSSSRKRYGVAANNMKQVKDMLYLIPLGATDKIPHLV PFDGPGLELHRPNLLGLIIRQKLKQHSACASTSHIAETPESA PPIALPPDKKSKIEVSTEEAPEEENDFFNSPTTVLHKQRNKPPQ NLQEDLPTAVEPLMEVTKQEPKPLRFLPGVLIGWENQPTTLEL ANKPLPVDDILQSLGTTGQVYDQ\AQSVMEQNTVKEIPFLNEQ TNSKIEKTDNVEVTDGENKEIKVKVDNISESTDKSAEIEISVVG SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSKQEETVESKE KTLKROLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN LVANTARSPQFINLKRDPQQAAGRSQPVTTSESKDGDSCRNGEK HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRFGSAVATSHFE VGNTCPSEFPKSKITFTSRSTSPRTSTNFSMPRPQQPNLQHLKS SPPGFPFPGPPNFPQSMFGFPFPHLPPLLPFGFG\FA\QNP VPWPPV\HLP\GQFQRMGGLSQASRYIGQNFYQVKDIRRPE RRHSDPWGRQDQQLDRPFNRGKGRQRFYSDSHHLKRERHEKE WEQESERHRRDRSQDKDRDRKSREEGHKDKERARLSHGDRTD GKASRDSRNVDKKPKPKSEDYBKDKEREKSKHREGEKDRDRYH KDRDHTDRTKSKR</p>
5952	3226	639	<p>PPARRSARDLFRALSMEARPSGSWNGALCRLL\LVTL\AFLIF ASDACKNVTLHVPSKLDKELVGRVNLKECFATANLIHSSDPDF QILEDGSSVYTTNTILLSSEKRSFTILLSNTENQEKKKIFVFLH QTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFLFLQVQ QSDTAQNYTIYYISIRGPGVDQEPNLFYVERDGTNLYCTRPVDR EQYESFEIIAFATTPDGYTPELPLPLIKIEDENDNYPIFTEET YTFTIFENCVRGTIVGQVCATDKDEPDMHTRLYSIIQGVPPS PTLFSMHPTTGVIITTSQDLRELIDKYQLKIKVQDMGQYFGL QTTSTCIINIDVDNHLPTFTRTSYVTSVEENTVDVEILRVTV DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLGVVVKPL NYEBKQMMILQIGVVNEAPFSREASPRSAMSTATVTVNVEDQDE GPECNPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGIRYKCL TDPTGWVTIDENTGSIKVFRLDRBAETIKNGIYNITVLASDQG GRICGTGLGIIQDVNDNSPFIKKTVIICKPTMSSAEIVAVDP DEPIHGPPFDLSLESSTSEVQRMWRLKAINDTAARLSYQNDPPF GSYVVPITVRDRMGSSVTSLDVTLCDICITENDCTHRVDRIGG GGVQLGKWAIIALLGIALFFCILEFTLVCGASGTSKQPKVIPPDD LAQQNLIVSNTEAPGDDKVYSANGFTTQTVGASAGVCGTVGSG IKNGGQETIEMVKGGHQTSSECRGAGHHHTLDSCRGGHTEVDNC RYTYSEBWSFTQPRLGEEISIRGHTLIKN</p>
5953	330	811	<p>PLLCNPDGWWYVWKQSEISKESQEMDARPKLDLGFKEGQTIK LCIGNITNKKGGASKPRTARGGGLSLLPPPGGKVTIPPPSS/V KLPSTNHVTPPSIPKSNHGGSDADILLDLSDPAPVTTTAPPTVS VSNLWGDFTASSSVNPQAPQPSNVVQF</p>
5954	32	2130	<p>PPPPPKLANMADLEAVLADVSYLMAMEKSKATPAARASKRIVL PEPSIRSVMQYLAERNEITFDKIFNQKIGFLLPKDFCLNEINE AVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSCSH</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PFSKQAVEHVQSHLSKKQVSTLTFQPYIBEICESLRGDIQKFM ESDKXFRFCQWKNVELNIHLMNEFSVHRIIGRGGFGEVYGCRK ADTGKMYAMKCLNKKRIKMKQGETLALNERIMLSLVSTGDCPFI VCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYA TEIILGLEHMHNRVYRDLPANILLDEHGHARIS\DLGLACD FSKKKPHASVGTGHYMAPEVLQKGTAYDSSADWFLGCMFLKLL RGHSPFRQHKTKDKHEIDRMTLTVNVELPDTFSPELKSLLEGLL QRDVSKRLGCHGGGSQEVKEHSFFKGVWDQHVYLYQKYPPLIPP RGEVNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERW QQEVTETVYEAVNADTKIEARKRAKNKQLGHEEDYALGKDCIM HGYMLKLGNPFLTQWQRRYFYLFPNRLWEWRGEGESRQNLITM ILSVERTQIKDKKCILFRKGGKQFVLQCESDPEFVQWKKELNE TFEQAQRLLRRAPKFLNKPRTSGTVLEPKPSLCHRNNSGL
5955	1726	444	KREREFRLAVCPRLRYPSAYESSPGTELRCEGLCRSQGBFADCR PANRQDVLSGWINLPVLQLTQDKPLKTPGRDLHGTRTAFIHHRQ VWKRCINIWDRDVLGVLNEIANSEEEVFVWKTASGWALALCR WASSLHGSLFPHLSLRSEDLIAEFAQVTNWSGCCLRVFAWHPH NKPAVALLDSDSVRVYNASTIVPSLKHRLQRNVASLAWKPLSAS VLAVACQSCILITWLTDPSTSLTRPSSGCAQVLSHPGHTPTVSLA WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLW SPDGSKILATTPSAVFRVWEAQMWTCERWPTLSGRCQTGCWSPD GSRLFTVLGEPLIYSLSPFERCGEGKG\ALEVQSQRRLWQICL RQYRHQMVRRGLGERLTPWSGTPVGNVWLCL
5956	1705	139	GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA TYVWSSIINTLQTOVEVKRRHRLKRHNDQFVGSEAVDVIFSHL IQNKYFGDVIDIPRAKVVRVQCALMDYKVFVAVPTKVFGDKKPT FEDSSCSLYRPTTIPNODSQLGKENKLYSPARYADALFKSSDIR SASLEDLWENLSLKPA NSPHVNISATLSPQVINEVWQEETIGRL LQLVDLPLLDLSLLKQGEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQDEWLSAAIDCSBYLPQDMVVEISRSFPEQPDRTDLVK ELLFDAIGRYSSREPLNLHSDVHNGIARLLVNGKTEIALEAT QLLLKLLDFQNRREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK RIFSKAIVDNKNLSXGKTDLVLVFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYQRIQDRDYSNNTKTTKDE LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD
5957	1479	451	ELQVAVAMDTLDRVVKPKTKRAXRFLEKREPKNENIKNAMLIK GGNANATVTVKLVKDVYALKKPYGVLYKKKNITRPEDQTSLEFF SKKSDCSLFMGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV SLKDIKNSKCEGTKPMILIFAGDDFDVTEYRRLKSLIIDFFRG PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLKKSGCRTPRIE LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPABRITEDHEKKS KRIKKLMELSQPLLFHCVLLKRIKHQS IQSFL
5958	1	3138	AAALGMLLWFPACQAFNLDVEXLTVYSGPKGSYFGYAVDFHIPD ARTASVLVGAPKANTSQPDIVEGAVYYCPWPAEGSAQCRQIPF DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP LLFTWRNFKPTPEKGPVGTCTYVAIQNFSAYAEFSPCGNSNADP EGQGYCQAGSLDFYKNGDLIVGGPGSFYWQQQVITASVADI IA NYSFKDILRLKAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSQ ELVAGIPRGAQNPFGVSIINSYDMTFIQNFTGEQMASYFGYTVV VSDVNSDGLDDVLVGAPLPMEREFESNPREVGOIYLYLQVSSLL FRDPOILTGTETFGFRGSAMAHGLDNLQDGYNDIAIGVFPAGKD QRGKVLIIYNGKDGTLNTPFKFCQGVWASHAVPSGFGFTLRGD SDIDKNDYPDLIVGAPGTGKVAVYRARPVVTVDAQLLHMPMIIN LENKTCQVPDSMTSACFSLRVCASVTGQS IANTIVLMAEVQLD SLKQKGAIKRTFLDNHQAHRVFPVVIKQKSHQCQDFIVYLRD ETEFDRKLSPINISLNSLDESTFKEGLEVKPILNYYRENIVSE QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHMLIINAR NEGEGAYEAEFLVMIPEEADYVGIERNKNGFRPLSCYKMNVT RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS NKDNPDNSNFVSLQINITAVAQVEIRGVSHPPQIVLP IHNWEPEE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EPHKEEBVGPLVEHIYELHNTIGPSTISDTILEVGVWPFSSARDEFL LYIFHIQTLGLPQCQPNPNINPQDIKPAASPEDTPELSAFLRNS TIPHLVRKRDVHVVEFHRQSPAKILNCTNIECLQISCAVGRLEG GESAVLKVRSLWAHTFLQRKNDPYALASLVSEVKMMPYTDQP AKLPEGSIAIKTSVIWATPNVSFSIPLWVILAILLGLLVLAAIL TLALWKCGLFDRARPPQEDMTDREQLTNDKTPEA
5959	1	1166	GTSGYAAQQLPSLLKEREPHLGLTNKVFASQWLNHRQVVCSTKC NTLFVVDVQTSQITKIPIILKDREPGGVTQGGCGIHAIELNPSRT LLATGGDNPNSLAIYRLPTLDPVCVGGDDGHKDWIFSIWISDTM AVSGSRDGSMLWEVTDVLTKSADARNVSRVPVYAHITHKALK DIPKEDTNPDCNKVRALAFNNKNKELGAVSLDGYFHLWKAENTL SKLLSTKLPYCENVCCLAYGSEWSVYAVGSAHVSEFLDPRQPSY NVKSVCSRERGSGIRSVSYFYEHIITVGTGQGSLLFYDIRAQRFL EERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF FPNAVYTHCYDSSGTLKFVAGGFLPSGLHGNVYAGLWS
5960	2853	870	FVWSDGGFRPRRGPAVGAGAAHLSDPWAMTPTANRATNPLNKE LDWASINGFCQLNEDFEGPPLATRLLAHKIQSPQEWAIQALT VLETCMKSCGKRFDHDEVGKFRFLNELIKVSPKYLGSRTSEKVK NKILELLYSWTVGLPEEVKIAEAYQMLKKQG\IVKSDPKLPDDT TFPLPPPRPKNVI FEDEEKSMLARLLKSSHPEDLRAANKLIKE MVQEDQKRMEKISKRVNAIEEVNNVKKLTEMVMSHSQGGAAAG SSEDL\MKEL\YQRCRMRPTLPTGRVDTEDND\EALAEILQA NDNLTQVINLYKQLVRGEEVNGDATAGSI PGSTSALLDLSGLDL PPAGTTYPAMPTRPGEQASPEQPSASVSLDDELMSLGLSDPTP PSGSLDGTGWNFSQSSDATEPPAPALAAQAPSMESRPPAQTSLP ASSGLDDLLGKTLTLLQQLPPESQQRWEKQQTPTRLTLRDLQ NKSSSCSSPSSSATSLHTVSPPEPRPPQPPVPTSLASITVP LESIKPSNLPVTVYDQHGFRILFHFARDPLGRSDVLVVVSM LSTAPQPIRNIVFQSAVPKVMKVLQPPSGTELPAFNPIVHPSA ITQVLLLANPQKEKVRRLRYKLTFTMGDQTYNEMGDVDQFPFPPET WGSLL
5961	198	3147	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCQLKHPISILELYNY FEDSNYVYLVELMCHNGEMNRYLKNRVKPPFSENEARHFMHQIIT GMLYLHSHGILHRDLTSLNLLLTRNMNIKIADFGLATQLKMPHE KHYTLGTPNYISPEIATRSAGHLESVDVSLGCMFYTLIGRPP FDDTIVKNTLNKVVLDAYEMPTFLSIEAKDLIHQLLRNRPADRL SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS STISGSLFDKRRLLIGQLPNKMTVFPKNKSSTDFSSSGDGNS FYTQWGNQETSNSGRGRVIQDAERPHSRYLRRAYSSDRSGTSN SQSQAKTYTMRCHSAEMLSVSKRSGGGENEERYSPTDNNANIF NFFKEKTSSSSGSFERPDNNQALSNHLCPGKTPFPFADPTPQTE TVQQWFGNLQINAHLRKTEYDSISPNRDFQGHDPDLQKDTSKNA WTDTKVKKNSDASDNAHSVQQNTMKYMTALHSKPEIIQECVF GSDPLSEQSKTROMEPFWGYNRTLSITSPLVAHRLKPIRQKT KKAVVSLDSEEVVELVKEYASQYEVKEVLQISSDGNITITYY PNGG\RGFPLA\DRPPSP\DNISR\YSF\DNLPEKYWRKYQYA SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVXI HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANEGHR ICLALESIISEERKTRSAFFPPIIGRKPGSTSSPKALSPPPS VDSNYPTRDRASFNRVMHSAASPTQAPILNPSMVTNEGLGLTT TASGTDISSNSLKDCLPKSAQLLKSQVVFVKNVGVATQ\LTSGAVW VQFNDGSQLVVQAGVSSISYTSPNGO\TTR\YGENEKLDPDIYKQ KLQCLSSILLMFSNPTPNFH
5962	20	2447	RVCSSASTASQAVMADAWEEIRRLAADFQRAQFAEATQRLSER NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVGR GRVNIQVLDQVINVLDLHIBNRIGDIIKSEKHVQLVLGQLIDEN YLDRLAEVNDKLQESGQVTISELCKTYDLPGNFLTQALQRLG RIISGHIDLNRGVIFTEAFVARHKARIRGLFSAITRPTAVNSL ISKYGFQEQLLYSVLEELVNSGRLRGTVVGGRODKAVFVPIYS RTQSTWVDSFFRONGYLEPDALSRLGIPDAVSYIKKRYKTTQLL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FLKAACVGGGLVDQVEASVEEAISSGTWVDIAPLLPTSLSVEDA AILLQQVMRAFASKQASTVVFSDTVVSSEKF\INDCTELFREIMH QKAEMKNPNVHLITEEDLKQISTLESVSTSKDKDKDERRRKA TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDSDDESQSSHTGK KKPEISFMFQDEIEDPLRKHIQDAPEEFISELAELYIKPLNKTY LEVVRVSFMSSTTSASGTGRKRTIKDLQEBVSNLYNNIRLFEKG MKFFADDTQAALT KHLKSVCTDITNLI FNFLASDLMMAVDDPA AITSEIRKKILSKLSEETKVALT KHLNLSNEKSIEDFISCLDSA AEACDIMVKRGDKKREKQILFQHRQALAEQLKVTEDPALILHLT SVLLFPQFSTHMLHAFGRCPVQIIAFLNSKIPEDQHALLVKYQG LVVVKQLVSQSKKTGGDYPLNNELDKEDVASTTRKELQELSS SIKDLVLKSRKSSVTEE
5963	62	1130	PWNPQDFPGRNGLMG\QKGEIGFP\GQQGKKGAPGMP\GLMSGN GSPGPGTTPGSGKSGEPGIQGMPGASGLKGPATGSPGEPGY MGLPGIQGKKGDKNQGEKGIQGGKGENGRQGI PGQGIQHHG AKGERGEKGPVGRGAIGSKGESVDGLMGPAGPKGPGDPGPQ GPPGLDGKPGREFSEQFIRQVCTDVIRAQLPVLQSGRIRNCDH CLSQHSGSPIPGPPGPIGPEGPRGLPGLPRDGVPLVGVVGRP GVRGLKGLPGRNGEKGSGQGFYPPGEGGPPGPPGEGPPGISKEG PPGDPGLPGKGDHKGKPGIQGQPPGPGICDPSLCSFVIARRDPF RKGPNY
5964	3	2147	SCRTRGRLSPLQPREAGSSRGRSEPRPGMEEACQVQTTK RGDPHELRLNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNS PKIVQLLAGVADQTKDGLISYQEFALAFESVLCAPDSMFIVAFQ FDKSGNGEVT FENVKEIFGQTI IHHHIPFNWDCEFIRLHFGHNR KKHLNTEFTQFLQELQLEHARQAFALKDKSKSGMISGLDFSDI MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAPNSLLNM ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ LADLYNASGRITLADIERIAPLAEGALPYNLAEQRRQSPGLGR PIWLQIAESAYRFTLGSVAVGATAVYPIDLVKTRMQNRQSG SVVGLMYKNSDFCKKVLRYEGFFGLYRGLIPOLIGVAPKAI KLTVNDFVRDKFTRRDGSPVLP AEVLAGGCAGGSQVIFTNPLEI VKIRLQVAGEITTGPRVSALNVLRLDGI FGLYKGAACFLRDIP FSAIYFPVYAHCKLLADENGHVGGNLNLAAGAMAG\VPAAASLV TPADVIKTRLQVAARAGQTTYSVGDICFRKIL\REEGPSAFWKG TAARVFRSSPQPG\VTLVTYELLQRGFYIDFGGLKPGASEPTPK SRIADLPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA VVQPKAAVAATQ
5965	1	1498	MVTWLYRFLPTSNMAAKLRSLPPDLRLQFWLHARLQKCFLSRG CGSYCAGAKASPLPGKMAMGLMCGRRELRLQLSGRRVHVSAGP SQWL GKPLTTRLLFPAAAPCCCRPHYLFLAASGPRSLSTSAISFA EVQVQAPPVVAATPSPTAVPEVASGETADVQTAAEQSFAELGL GSYTPVGLIQNLLEFMHVDLGLPWGAIAACTVFARCLIFPLIV TGQREARAIHNLPEIQKFSSRI REAKLAGDHIEYYKASSEMAL YQKKHGIKLYKPLILPVTQAPIFISFFIALREMANLPVPSLQGT GLWNFQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW MRNVIRMMPLITLPI TMHFTAVFMYWLSNLFSLVQVSLRIP AVRTVLKIPQRVVHDLKLPREGFLESFKKGWKNAMTRQLRE REQMRNQLELAARGPLRQTTHNPLLQPGKDNPPNIPSS\SSS SSKPKSKYPWHDTLG
5966	102	1925	RSKQVMARLTKRQADTKAIOHLWAAIBIRNOKQIANIDRITK YMSRVHGMHPKETTRQLSLAVKDLIVETLTVGCKGSKAGIEQ GYWLPGBEIDWETENHDWYCFBCHLPGEVLICDLCFRVYHKSCL SDEFRLRDSSSPWQCPVCRSIIKKNTNKQEMGTYLRFIVSRMKE RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYSYEE FKADAQLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC KNCFYLANARPDNWFYPCIPNHELDWAKMKGFWFPAKVMQKE DNQVDVRFEGHHQRAWIPSENIQDITVNIHRLHVKRSMGWKA CDELELHQRFLREGRFWKSKNEDRGEEEAESSISSTSNEQLKVT QBPRAKKGRNQSVFEPKKEPEPETEAUSSSQEIPTMPOPIEKV SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KDRMKS DHKRETERV VREALEKLRSEMEEEKRQAVNKAVANMQG EMDRKCKQVKECKEEFVEEIKKLATQHKQLISQTKKKQWCYNC EEEMHYHCCWNTSYCSIKCQEHWAHAKRTRCRKR
5967	102	1925	RSKQVMARLT KRRQADTKAIQHLWAAIBIIRNQKQIANIDRITK YMSRVHGMHPKETTQRLSLAVKDGLIVETLTVGCGKSGKAGIEQE GYWLPGEIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL SDEFRLRDSSSPWQCPVCRSIIKKNTNKQEMGTYLRFIVSRMKE RAIDLNKKGKDNKHPMYRRLVHSAVDVFTIQEKVNEGKYRSYEE FKADAQLLLHNTVIFYGADSEQAD IARMLYKDTCHEL\DELQLC KNCFYLANARPDNWFYPCIPNHELD WAKMGFGFWPAKVMQKE DNQVDVRFPGHHHQRRAWIPSENIQDITVNIHRLHVKRSMGWKA CDELELHQRFLEGRFWKSKNEDRGEAEASSISSTSNELQKVT QEPRACKGRNRQSVEPKKEPEPETEAVSSSQEIPMPQPIEKV SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF KDRMKS DHKRETERV VREALEKLRSEMEEEKRQAVNKAVANMQG EMDRKCKQVKECKEEFVEEIKKLATQHKQLISQTKKKQWCYNC EEEMHYHCCWNTSYCSIKCQEHWAHAKRTRCRKR
5968	81	1288	VRFPRRGAPPTVLTGPRQGVFLGPQRPGSEPDIPARGQPHFP RPVGVSTSAQAQVQPPAMHRRRLALGLGFCLLAGTSLSVLWVYL ENWLPVSYPVYLPCEIFNMKLHYKREKLPQPVVWSQYPPQKL LEHRTQLLTLTPWLAPIVSEGTFPNPELLQHIYQPLNLTIGTV FAVGN/HFLESAAEFFMRGYRVHYIIFTDNPAAVPGVPLGPHRL LSSIPIQGHSHWEETSMMRMETISQHIakrahevdyLFCLDVD MVFRNPWGPETLGLDVAIHPSYAVPRQQFPYERRRVSTAFVA DSEGDFFYGGAVFGGOVARVYEFTRGCHMAILADKANGIMAAWR EESHLNRHFI SNKPSKVLSP EYLWDDRKPPPSLKLIRFSTLDK DISCLRS
5969	1126	503	DVGFINIKRRCDLDFLES PRKPSGRDRAPKORRIANAKCLC TGVREGEPPS/TTSQKVEAGRDFTYLIIVVLFGISITGGLFYTI FKELFSSSSPSKIYGRALEKCRSHPEVIGVFGESVKGYGEVTRR GRRQHVRFTEYVKDGLKHTCVKPYIEGSEPGKQGTVYAQVKENP GSGEYDFRYIFVEIESYPRRTIIIEDNRSQDD
5970	316	4712	SQDNIGHRLQLQKHGWKLQGLGKSLQGRDTPIPVVKYDVMGMG RMEMELDYAEDATERRRVLEVEKEDTEELRQKYKDYVDKEKAIA KALEDLRANFYCELDKQYQKHQEFDNHINSYDHAHKORLKDOLK QREFARNVSSRSRKDEKKQEKALRLHLEAEQRKQAECAFGSGP MFKPTTVAVDEEGEDDKDESATNSGTGATASCGLGSEFSTDKG GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLTGPLQKLGVSF SFAXKAPVKLESIASVFKDHAEEGTSEDGTPKDEKSSDQGLQKV GDSGSSNLDGKKEDDPQDGGSLASTLSKLKRMKREEGAGATE PEYHYIIPAHCKVKPNFPFLFMRASEQMDGDNTHPKNAPES KKGSSPKPKSCIKAAASQGAETVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETS LATPA GKESQEGPKHPTGFFFPVLSKDESTALQWPELLIFTKAEPSSIS YSCNPLYDFDKLSRNKDARTKGT EKPDKIGSSSKDHLQGLDPGE PNKSEVGGEEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKHKKSSKHKKRKHADTEEK SSKAESGEKSKRKRKRKRKNKSSAPADSERGPKPEPPGSGSPA PFRRRRAQDDSQRRSLPAEEGSSGKKDEGGGSSSDHGGGRKH KGELPPSSCQRAGTKRSSRSSHRSQPSGDESDSDASSHRLHQ KSPSYSEEEEEEDSGSEHSRSRSRSGRRHSSHRSRSRSYSSSS DASSDQSCYSRQRSYSDSYSDYSRDRSRHRSKRSHSDSDSYAS SKHRSKRHYSSDDDYLSQSRSRSRSHTRERSRSRGRSRS SSCSRSRSKRRSSTTAHWSQRSRSYSRDRSRSTRSPSQRSGR KRSWGHESEERHSGRRDFIRSKIYRSQSPHYFRSGREGPGKK DDGRGDDSKATGPPSQNSNIGTRGSEGDSPEDKNSVTAKLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPSS LGNKPVLP LIGKLPATRKPNKKCEESGLERGEQEQS ETEBGP GSSDALFGHQFP\SEETTGPLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDP TISHNYLPDPSDGNLTLESLSQSGPPVSSSL LP IAFDLEHFPSYAPPSGDPSEISTDGAEDA\SLAPLESQPI TF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>TPEEMEXYSKIQQAQQHIQQQLLAKQVKAPPASAAALAPATPALQPIHIQQPATASATSIITVQHAILQHHAATAAIGIHPHPHPQPLAQVHHIPQPHLTPIISLHLSHSIIPGHPATFLASHPTIIPASAIHPGPPTFHPVPHALYPTLLAPRPAATAALHLHLPLHPIFSGQDLQHPPSHGT</p>
5971	53	2149	<p>SFLYFVGVMDNPIGNWDGRFDGVQLCSFACVESTILLHINDIIPESVTQERRPPKLAFMRSRGVDKGGSSSHNKPATGTSSTDPGNRRSELYFTLNGSSVDSQPQSKSNWTYIDEVAEDFAKSLTEISTDFRSPPLQPPPVNSLTENRFHSLPFLTKMPTNGSIGHSPLSLSAQSVMBELNTAPVQESPLAMPFGNSHGLEVGSLAEVKENPFYGVIRWIGQPPGLENEVLAGELEDEECAG\CTDGT/REGTRYFTCALKKALFVKLKS CRPDSRFASLQPVSNQIERCNSLAIWEAYLSEVVEENTPTQKWEKEGLEIMIG\KKKGIQGHYNSCYLDSTLFCFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRIYGYVCATKIMKLRKILEKVEAASGFTSEEDPEEFLNIFLPHILRVBPLLKIRSAGQKVQDCYFYQIFMEKNEKVGVTIQQLLEWSFINSLKFAEAPSCLIIQMFRFGKDFKLFKKIFPSLELNITDLEDTPROCRICGGLAMYECRECYDDPDISAGKIKQPKCTCNTQVHLHPKRLNHKYNPVS LPKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYKGKDDSAWLPFDSMADRDGGQNGFNIPQVTEPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAIYVPCQSPMTSLYK</p>
5972	440	1761	<p>ILLAGSPSPRDQCSQRQSSGGDKELVTRGCTFSTAVVSPSAMTQEPFREELAYDRMPTLERGRQDPASYAPDAKPSDLQLSKRLPPCFSHKTVVFSVLMGSCLLVTSGFSLYLGNVFPAMDYLRCAGSCIPSAIVSFTVSRNNANVINPQILFVSTFAVTTTCLIWFGCKLVLNPSAININFNLI LLLLLLELLMAATVIAARSSEEDCKKKKGSMSDSANILDEVFPFARVLKYSVVEVIAGISAVLGGI IALNVDDSVSGPHLSVTFFWILVACFPASIAASHVAECPNKCLVEVLIAISSLTSPLLFTASGYLSFSIMRIVEMFKDYPPAIKPSYDVLLLLLLLVLLLQA/GPQHGHRRHPVRALQGGCKAAGCILGHPERPAGAPGWGGQGEPPGVQRQGESLESRRGANGFVTPRRGNRVAAPSLAPGMETHNP</p>
5973	65	2007	<p>NGDGKDLFGHIWAWRSNGIISNFRSPHAGMAEDEPDASKPKTGGRAPPGGAEEAGEPTTLQLRLRGITISKAVQNKVEGILQDVQKPSNDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHLEEHTDTCCLKQSVYDAYRKYCESLACCRPLSTANFGKIIREIFPDIKARRLGGRGQSKYCYSGIRRKTLVSMPLPLGLDLKGSSEPEMGP EVTPAPRDELVEAACALTCDAERILKRSFSSIVEVARFLLQOHLISARSAHAHVLKAMGLAEDEHAPRERSKPKNGLENPEGGAHKKPERLAQPPKDLARTGAGPLARGERKKS SVVSSAPANNLQVNALVARLP LLLPRAPRSLIPPIPVSPPI LAPRLSSGALKVATLP LSSRAGAPPAAVPI INMILPTVPALPGPGPGGRAPPGGLTQPRGTENREVGIGGDQGPDKGVKRTAEVPVSEASQAPPAKAAKQDIEDTASDAKRKRGRPLKSGSGSERNSTPLKSAAAMESAQSSRLPWETWGSSEEGNSAGGAERPGPMGEARKGAVLAQG\QGDGTVSKGGRGPSQHTKEADKIPLVPSKVSIVKGSRSQKEAFPLAKGEVDTAPQGNKDLKEHVLQSSLSQEHKDPKATPP</p>
5974	4293	2200	<p>LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENTGDKG\BIDLESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNIKVRRTV\ASIKNDPPS\RDNRVVG SARARPSQFPEQFSSAQONGSV\SDISPVQA AKKEFGPPSRKSNVCVEKLEKREKRRLOQQELBKRAQDV DATNPNYEIMCMIRD FRGSLDYRPLTTADPIDEHRICVCVRKRPLNKKETQMKDLQVITIPSKDVVMVHEPKQKVDLTRYLENQTRFRDYAFDDSAFNEMVYRFTARPLVETIFERGMATCFAYGQTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKLELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQVQVVLGLREVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRS HAVFQIILRRKGKLGKPSLIDLAGNERGADTSSADRQTRLEGAEINKSLALKECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPGMASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPNQi\DDLETQWGVGSSPQRDDLKLLCEQNEEVSPQLFTFHEAVSQMVEM</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EEQVVDHRAVPQESIRWLEDEKALLEMTEEVYDVSATQLE AILEQKIDILTELDRKVKSFRAALQEEEOQASKQINPKRPRAL
5975	4293	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWENGDTKKG\ EID LESIFSLNP\ DL\ VPDGEIEPSP\ ETPPPPASSAKVNIKVNRR TV\ ASIKNDPPS\ RDNRVGVSARARPSQFPEQFSSAQNGSV\ S DISPVQAAKKEFGPPSRKSNVCVKEVKLQEKREKRLQOQELR EKRAQDVADATNPNYEIMCMIRDFRGSLDYRLTTADPIDEHRIC VCVRKRPLNKKETQMKDLVDITIPSKDVMMVHEPKQKVDLTRYL ENQTFRFDYAFDDAPNEMVYRFTARPLVETIFERGMATCFAYG QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKQ LELQVYATFFEIYSGKVFDDLNRKTKLRVLEDGKQVQVVLGLQE REVKCVEDVLKIDIGNSCRTSGQTSANAHSSRSRAVFQIILRR KGLHKGKFLIDLAGNERGADTSSADRQTRLEGAEINKSLALAK ECIRALGRNKPHTPPFRASKLTQVLRDSPIGENSRTCMATISPG MASCENTLNTLRYANRVKELTVDPATAAGDVRPIMHHPNQi\ DD LETQWGVGSSPQRDDLKLLCEQNEEVSQFLFTFHEAVSQMVEM EEQVVDHRAVPQESIRWLEDEKALLEMTEEVYDVSATQLE AILEQKIDILTELDRKVKSFRAALQEEEOQASKQINPKRPRAL
5976	20	2949	VHHLHLTRVSVVNLDIILRIAQQMGIKTLNLVLG\ LKRA\ LEF PEVSWMEVKDPMKMGAMLTNTGKYAIPITIDA\ EAYAIGKKEKPP FLPEEPSSSEEDDPIPELLCLICKDIMTDAVVI CCGNSYCD BCIRTALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNNFKNE TGyTKRLRKQLPSPPPP PPPRPLIQRLQPLMRSE ISRQODPL MIPVTSSSTHPAPSISSLSNQSSLAPPVSGNPSSAPAPVPDIT ATVISVHSEKSDGPFPRDSNKLPAALASEHSGTSS AITA LMEEKGYQVPVLGTPSLLGQSLHGLQI PTTGPVRINTARPGGG RPGWEHNSKGLYLVSPQQIRRGERSCYRSINRGRHHSERSQRT QGPSLPATPVFVPVPPPLYPPLPHTLPLPPGVPPPQFSPQFP GQP\ PPAGYSVPPPGFPAPANLSTPWVSSGVQTAHSNTIPTTQ APPLSREEFYREQRLKEEEKKSKLDEFTNDFAKELMEYKKIQ KERRRSFSRSKSPYSGSSYSRSTYTSKRSRGSTRSRSYSRSFS RSHRSYSRSPPYPRGRGKSRNYSRSRSHGYHRSRSRSPPYR RYHSRSRSPQAFRGQSPNKRNVPOGETEREYFNRYREVPPPYDM KAYYGRSVDFRDPFEKERYREWERKYREWYKYYKGAAQAQPR PSANRENFSPERFLPLNIRNSPPTGRREDVVGQSHRSRNIGS NYPEKLSARDGHNQKDN TKSKEKES ENAPGDGKGNKHKHKRKR KGESEGLNPELLETSRKSREPTGVEENK TDSL FVLP SRDDAT PVRDEPMDAESITFKSVSEKDKREB DKP KAGDKTKRKN DGS AV SKKENIVKPAKGPQEKVDG\ DVRD LLD NL\ QLKKPKEETPKDL TILNHLPLRRMKKSL\ EPP\ EKLTLNQKQ\ TPRNKTSQRGKSE EGLFQRCQIRKANN
5977	1363	1336	FLEDRGQVLSHFQCLSLHSINHLHPGAGVAGPATGW\ REYLT PVLKESKPKETGVITPEEFVAGDHLVHHCPTWQWATGEELKVK AYLPTGKQFLVTKNVPCYKRCQMEYSDELEAI EEDDGDGGWV DTYHNTG TGITEAVKE ITLENKDNIRLQDCSALCEEEDEDEG EADMEEYEEESGLLETD EATL DTRK IVEACKAKTDAGGEDAILQ TRTYDLYITYDKYYQTPRLWLFYDEQROPLTVEHMYEDISQDH VKKTVTIENHPLPPPPMCSVHPCRHA EVMKKI IETV AEGGGEL GVHMYLLIFLKFVQAVIPTI EYDYTRHFTM
5978	160	3213	RDGARRWGGCCSPLTWAPGFYRRFDLATSGRRRLRGQTAEPAGRQ RPRREPEAMDEQSVESIA BVFRCFICMEKLRDARLCPHCSKLCC FSCIRRWLTEQRAQCPHCRAPLQLREL VNCRWAEV TQQLD TLQ LCSLT KHEEN EKD CENH EKL SVFCWTC CKCIC HQCALWGGMH GGHTFKPLAEIYE QHVT KVNEE VAKLRRRLMELISLVQEVERNV EAVRN AKDERV EIRNAVEMMIARLD TQLKNKLI TLMGQKTS LT QETELLESLLQVEV HQLRSCSKSELISKSEILMMFQOVHRKPM ASFVTTTPVPDFTSELVPSYDSATFVLENFSTLQRQADPVYSPP LQVSGLCWRLKVYPDGNVVRGYLSVFL EL SAGLPETS KYEYR VEMVHQS CNDPT KNI IREFASD FEV GECWGYNRFR LDLLAN EG YLNQNDT VILRPQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ INN KERLTI ELSR TQKSRDLS PPDNHLS PQND DALETRAKKSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CSDMLLER\GPYSAS\VREAKEDEEDEEKIQNEDYHHELSGDGL DLDLVYEDEVNQLDGGSSSSASSTATSNTEENDIDEETMSGENDV BYNNMELEEGELMEDAAAAGPAGSSSHGYVGSSSRISRRLHCSA ATSSLLDIDPLILIHLLDLKDRSSIENLWGLQPRPPASLLQPTA SYSRKDKQQRKQAMWRVPSDLKMLKRLKTMMAEVRCKMTDVKX TLSEIKSSSAASGDMQTS\LFSAQAALAACGTENSGRLQDLGME LLAKSSVANCYIRNSTNKKSNPKPARSSVAGSLSLRRVDPGE NSRSKGDQCTLSEGS PGSSQSGSRHSSPRALIHGSIIGDILPKTE DRQCKALDSDAVVAVFSGLPVAVKRRKMVTLGANAKGGHLEGL QMTDLENNSETGELQPVLPBGASAAPEGMSSSDSDIECDTENE QEEHTSVGGFHDSEFMVMTQPPDEDTHSSFPDGEQIGPEDLSFNT DENSGR
5979	212	3665	LPDMYMLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE TTTLSPSGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETK LFTAKLVNENVECGNNTCTNNEVHNLTECKNASVISHSNSTA PDKTILIDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC DTQNTYRFQCGNMIFDNKEIKLENLEPEHEYKCDSEILYNCHK FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPQORSFHN FTLCYIKETEKDCLNLDKNLIKYLQNLKPYTKYVLSLHAYIIA KVQRNGSAAMCHFTTKSAPPSQVWMTVSMSTSDNSMHVKCRP DRNGPHERYHLEVEAGNTLVNESHKNCDFRVKDLQYSTDYTFK AYFHNGDYPGEPFILHHS\SYNSKALIAFLAFLIIVTSIALLVV LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLET YKRKIADDEGRFLAEFQSI PRVFSKFPKEARKPFNQKNRYVD ILPYDYNRVLSSEINGDAGSNYINASYIDGFKPRKYIAAQGPR DETVDDFWRMIWEQKATVIMVTRCEEGRNKKCAEYWPMEEGT RAPGECCCKDLTKHKRCP\DYIIQKLNIVNKKKATGREVTHIQ FTSWPDHGVDPEDPHLLKLRRRVNAFNSNFFSGPIVHCSAGVGR TGTYIGIDAMLEGLEAENKVDVYGVVVKLRRQRCLMVQVEAQYI LIHQALVEYNQFGETEVLSELHPYLHNMKKRDPPEPSPLEAE FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHSDSDSDSDSDSEEPSKYINASFIMSYWKP\EVMI AAQGPLKETIGDFWQMI FQRKVKVIMVLTTELKHGDQEIQAQYWG EGKQTYGDIIEVDLKDIDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNSVVEQLPAEPKELISMIQVVKQLPQKNSSEGNKHHKSTPL LIHCRDGSQQGTGIFCALLNLLSEAEETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCNVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS
5980	3	2363	DAWGCKLRLRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTHHALLQEVDDVVVAPCOGLR PTVDVLGDLVNDFLPVITYALHKDELSEDEQELQEI RYKFSFP VFFFKVPKLGSEIIDSSTRMESERSPLYRQLIDLGLYSSSHWN CGAPGQDTKAQSMLEQSEKLRHLSTFSHOVLQTRLVDAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKNELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVI VPENGE VGTREIKCCIRIQELIISRLNQAVANKLISSVDYLRSEFVGT ERCLQSLKESQDVSVHITSNLYKQILNAAHYHEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQPFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRLQDVLLHRKPKLGQELGRGQYGVVLYCDN WGGHFFCALKSVVPPDEKHWNDLALFHYMRSLPKHERLVLDLHG SVIDYNYGGSSIAVLLIMERLHRDLTYGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLVNLLDKQNRKAITDLGPFCKPEA MMSGSI VGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQMEACWDG DPLKRPLLGIQPMLOQIMNRLCKS\NSEQPNRGLDST
5981	1	2519	GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPSTLSQDR DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\DEECGRVRDFVAKLANTHQHVFDLGRGSVLSWVGDSGTG ILVLTTFHVPLVIMTFGQSKLYRSEYDGKNFKDITDLINNTFIR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTD LPFHPLTQMYSPOQNSDYLLALSTENGLWVSKNFGGKWEIHK VCLAKWGSNDNTIFFTTYANGSCKADLGALELWRTSDLGKSFKTI GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDDQGTWSMAQLP SVGQEQFYSLAANDDMVFMHVDPEPGDTGFGTIFTSDDRGIVYS KSLDRHLYTTTGGGETDFTNVTSLRGVYITSVLESDNSIQITMITF DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYISQKLNVP MAPLSEPNAGVIVIAHGSVGDAISVMVPDVYISDDGGYSWTMML EGPHYITLDSGGIIAIEHSSRPINVIKFSTDEGQCWQTYTTF RDPYFTGLASEPGARSMNISIWGFTEFLTSQWVSYTIDFKDI LERNCEEKDYTIWLAHSTDPEDEYDGCILGYKEQFLRLKSSVC QNGRDYVVTQPSICLCSLEDFLCDFGYRPPENDSKCQVEQPELK GHDLFCFLYGREEHLTTNGYRKIPGDKCQGGVNPVREVLDLKKK CTSNFLSPEKQNSKNSVPIILAIVGLMLVTVVAGVLIVKKYVC GGRLFLVHLYSVLQQH\AEA\NGVDGVDALDTASHTNKGHYHDDS DEDLLE
5982	56	2316	ATRPGRSSWCRQFSRTASAPGRSNMLRI PVRKALVGLSKSPK GCVRTTATAASNLIIEVFVDGQSVMEVPGTTVLQACEKVGMIIPR FCYHERLSVAGNCRMLVEIEKAPKVVAACAMPVMKGNILNTS EKSKKAREGVMEFLLANHPLDCPI CDQGGCEDLDQDSMMFGNDR SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD LGTTRGRNDMQVGTIYEKMFMSSELSGNIIDICPVGALTSKPYAF TARPWETRKTESIDVMDAVGSNIIVVSTRTGVEVMRILPRMHEDIN EEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV AGMLQSFQGDVAAIAGGLVDAEALVALKDLNLRVDSDTLCTEB VFPTAGAGTDLRSNYLLNTTIAGVEEADVLLVGTNPRFEAPLF NARIRKSWLHNDLKVALIGSPVDLTYTDHLDGDSPKILQDIASG SHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAIVSSIAQKIRM TSGVTGDWKMNIHLRIASQVAALDLGYKPGVEAIRKNPPKVLV LLGADGGCITRQDLPKDCFIYQGHGVDVGAPIADVILPGAAYT EKSATYVNTGRAQQTQKAVTTPPLAREDWKIIIRALSRIAGMTL PYDTL\DOVRNRLEEVSPLVRYDDIEG\ANYFQQANELSKLVN QQLLADPLVPPQLTMKDFYMTDSISRASQTMACKVAVTEGAQA VEEPSIC
5983	248	1763	EARGDGGRRRRHRASRRRAGRGEF\AGLKSQGGRAVFKRAVARGG RQ\YSAALALEPAGSEIADDDLSILYNRAACYLKEGNCSGCTQ DCNRALHLHPFSMKPLLRAMAYETLEQYKAYVDYKTVLQIDC GLQLANDSVNRLSRILMELDGNWREKLSLIPAVPASVPLQAWH PAKEMISKQAGDSSSHRQGGITDEKTFKALKEGNCQVNDKNYK DALSKYSECLKINNKECAIYTNRALCYLKLQCFEAKQDCDQAL QLADGNVKAFYRRALAHKGLKNYQKSLIDLKLVILLDPSII EAK MELEBEVTRLLNLKDKTAPFNKEKERRKIEIQEVNEGKEEPPGRPA GEVSTGLASEKGGKSSRPEDPEKLP IAKPNNAVEFGQIINAL STRKDKEACAHLLAITAPKDLPMFLSNKLEGDTPLLLIQSLKNN LIEKDPSLVYQHLLYLSKAERFKMMLTLISKQKELIEQLFEDL SDTPNNHFTLEBDIQALKRQYEL
5984	755	1193	SSVCMACTYVSNLGGKQSVSFLASGLMRVSTGPRLRLHHSFVL TGDVGRRICRLLVGLFTKGTSSKRVHPFSPGPFLLCDLARVG SSPKINVSPFYQN\QTSTORSTVFVWQRCSLVGPFQVTVFTMY FHSLRSISRFSG
5985	22	1408	RRVARPGTAEPFAKARRTVRRGRARRDLACAERKAGVSEBGDSGR RRPNPISPSAAGMSHIQIPPLTELLQGYTVEVLRRQPPDLVE FAVEYFTRLREARAPASVLPATPRQSLGHPPEPGPDRVADAK GDSESEDEDELEVVPVSFRNRRVSVCAETYNPDEEEDTDPRVI HPKTDQRCRLQEA CKDILLFKNLQEQLSQVLDAMFERIVKAD EHVIDQGGDDGNFYVIERGTIDILVTKDNQTRSVGQYDNRGSGF ELALMYNTPRAATIVATSEGSWLGLDRVTFRRIIVKNNAKKRM FESFIESVPLLSLEVSRMKIVDVIGEKIYKR/DGERIITQGE K\ADSFYIIESGEVSIILRSRTKSNKDGNGQVEIARCHKQGYF GELALVTNKPRASAYAVGDVVKCLVMDVQAFERLLGPMCDIMKR NISHYEEQLVKMFGSSVDLGNLQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5986	1806	484	DAWKSTSLTFHWKLWGRHRRGRRGLAHPKNHLSPOQGGATPQVP SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPVPSPGPPMEED GLRWTFKSPLDPSGLLSCTLPNGFGGQSGPEGERSLAPPDASI LISNVCSIGDHVAQELFQGSDDLGMMAEEAERPGEK\AQHSPRLRE EHVTCVQSILDEFLQT\YGLSLIPLSTDEVVEKLEDIFQQEFSTP SRKGLVLQLIQSYQRMFGNAMVRGFRVAYKRHLVTMDLGLTYG QNWLNQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG VWRWTKNVDIFNKELELLPIHLEVHWSLISVDVRRRTITYFDSQ RTLNRRCPKHIAKYLAQEAVKDRDLDFHQGWKGYFKMNVARQNN DSDCGAFVLQYCKHLALSQPFSTQDMPKLRQIYKELCHCKL TV
5987	1806	484	DAWKSTSLTFHWKLWGRHRRGRRGLAHPKNHLSPOQGGATPQVP SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPVPSPGPPMEED GLRWTFKSPLDPSGLLSCTLPNGFGGQSGPEGERSLAPPDASI LISNVCSIGDHVAQELFQGSDDLGMMAEEAERPGEK\AQHSPRLRE EHVTCVQSILDEFLQT\YGLSLIPLSTDEVVEKLEDIFQQEFSTP SRKGLVLQLIQSYQRMFGNAMVRGFRVAYKRHLVTMDLGLTYG QNWLNQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG VWRWTKNVDIFNKELELLPIHLEVHWSLISVDVRRRTITYFDSQ RTLNRRCPKHIAKYLAQEAVKDRDLDFHQGWKGYFKMNVARQNN DSDCGAFVLQYCKHLALSQPFSTQDMPKLRQIYKELCHCKL TV
5988	1292	410	FKKYFLSFLGLESSHSDRIHNLVLMFLATHNLVWVFTCRFQ RLDCIYNAGIMPNPQNLKALLFGLFS\ABGLLTQGDKITADG LQEVFETDVFGHFIILIRELEPLLCHSDNPSQLIWTSSRNARKSN FSLEDFQHSKGEKYSSSKYATDLSVALNRNFNQQLYSNVAC PGTALTNLTYGILPPFIWTLMPAILLLRFPANAFTLTPYNGTE ALVWLFHQKPSLSNPLIKYLSATTFGGRNYIMTQKMDLEDTAE KFYQKLELEKHIRVTIQTNDQARLSGSC
5989	194	2610	AMDFFQHSQHVLEQLNQQRQLGLLDCDTFFVVDGVHFAKHAVALA ACSEYFKMLFVDQKDVVHLDISNAAGLGQVLEFMYTAKLSLSP NVDDVL\AVATFLOQMODIITACHALKSLAEPATSPGNAEALAT EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPRDLKEERGGQQA SAASGAEQTEKADAPREPPVELKPDPTSGMAAAEAALSESS EQEMEVEPARKGEEBQKEQEEQEEGAGPAEVKEGSGLENSEA PEENENEEAGTDSQELGSEARGLRSGTYGDRTESKAYGSVH KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTHSPLKPYGCEECGKSYRLISLLNLRKRHSGEARYRCED CGKLFTTSGNLKRHLVHSGEKPYQCDYCGRSFSDPTSKMRHLE THDTDKEHKCPHCDKKNQVGNLKAHLKIHADGPLKCRECGKQ FTTSGNLKRHLRIHSGEKPYVCIHCQRQFADPGALQRHVRIHTG EKPCQCVMCQKAPTQASSLIAHVQRHTGEKPYVCERCGRFVQS SQLANHIRHHDNIRPHKCSVCSKAFVNVGDLKHI IHTGEKPY LCDKCGRGFNRVDNLRSHVKT VHQKAGIKILEPEEGSEVSVVT VDDMVTLATEALAAATAVTQLTVVPVGAATADETEVLKAEISKA VKQVQEEEDPNTHILYACDSCGDKFLDANS LAQHVR IHTAQALVM FQTDADFYQQYGGGTTWAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAE
5990	2	4700	FGPGPDSGGGARGSGWGRSQAPYGTGLGAVSGGEQVLLHEEAGD SGFVSLSRSLRDKDLEMEELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVMSLPDPSWDFSPSPFLETSSPKLPSWRPPRSR FRWGQSPPPQQRSDGEEEEEVASFSGQILAGELDNCVSSI PDPF MHLACPEBEDKATAEAMVPAAGDESISSLSLVAMHPYCLPN LTHLASLEDELQEOPDDLTLPPEGCVVLEIVGQAATAGDDLEIPV VVRQVSPGPRPVLDDSLTSSALQLLMPLESETAAVPKVT LSEKEGLSLNSEELDSACLLKPREVVEPVVPKEPQNPANAAF GSQARARKGRKKKSKQPAACVEGYARRLRSSSSRGQSTVGTETS QVDNLQKQPQEEELQKESGPLQKGPRAWARAWAAALENSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNP IPTHLSLVDSAGAS PMPVDSVEADPTAVGPVLAVGPVDPGLVDLASTSSSELVEPLPA EPVLINPVLADSAAVDPAVVPISDNLPVDAVPSGPAPVDLALV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DPVPNDLTPVDPVLVKSRTDPRRGAVSSALGGSAPQLLVESES LDPPKTI IPEVKEVVDLSKIESGTSATTHEARPRPLSLSEYRRR RQROAETEERSQPPTGKWPSPETPTGLADIPCLVIPPAPAK KTAQRSPETPLEICLVPGSPASPSPEPPVSKPVASSPTEQV PSQEMPLLARSPSPVQSVSPAVPTPPSMSAALPPFAGGLGMPPS LPPPLQPPSLPLSMGPVLPDPFTHYAPLPSWPCYPHVSPSGYP CLPPPTVPLVSGTPGAYAVPPTCSVPWAPPAPVSPSYSTCTY GPLGWGPGQHPFWSVTVPPLPPASIGRAVPQPKMESRGTPA GPPENVLPLSMAPPLSLGLPGHGAPQTEPTKVEVKVPVPSHPK HKVSALVQSPQMKALACVSAEGVTVEEPASERLKPETQTRPRE KPPLPATKAVPTPRQSTVPKLPVHPARLRKLSFLPTPRTQGSB DVVQAFISEIGIEASDLSLLEQFEKSEAKKECPPAPADSLAV GNSGGVDIPQEKRLDRLQAPELANVAGLTPPATPPHQLWKPLA AVSLLAKAKSPKSTAEGLTKPEGVTEAKHPAAVRLQEGVHGGS RVHVGSGDHDYC\VRSTPPKK\MPALLIPEVGSRWNVKRQDI TIKPVLSLGPAAPPPPCIAASREPLDHRSTSEQADPSAPCLAPS SLLSPEASPCRNDMNTTTPPEPSAKQSRMRCYRKACRSAPSSQ GWQGRGRNRSRVSSGNSRTSEASSSSSSSSSSSSSSSSSSSS HKRWRSSSCSSSGSRRCSSSSSSSSSSSSSSSSSSSSSSSSSS PSFRRSDRRRRYSYRSHDHYQRQVQLKERAIEERRVFIGK IPGRMTRSELKQRFVSGEIEECTIHFVRVQGDNYGFVTTYRABE AFAAIESGHLRQADEQPFDLCPGGRQFCRKSYSDLDSNREDF DPAPVSKPDSLDFTLLKQAQKNLRR
5991	334	1379	RLSSHFSQCSPSIYC\TKFDKQGNVTSFERKKTLYQELGLQAR DLRFPQVMSITVRNNRIIMRMEYLKAVITPBCILLIDYRNLNLK QWLFRELPSQLSGEGQLVTYPLPFEFRAIEALLQWINTLQGLK SILQPLILETLDALGDPKHSSVDRSKLHILLQNGKSLSELETDI KIFKESILEILDEELLEELCVSKWSDPQVFEKSSAGIDHAEEM ELLLENYYRLADDLSNAARELRVLIDDSQSIIFINLDSHRNVM RLNLQLTMTGTFSLSLFGLMGVAFGMNLESSLEEDHRIFWLITGI MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGL
5992	2	609	AGPDFRLVCGVSGSGFPGGRQGGQATEWRPLRPWNGAMEKLRRVL SGQDDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFACFVC GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGVPK QLKMKFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ FLSMTWYSLSYIPYARDAVIKCCSSLLS
5993	1650	594	AEGLGSAVWAGLWAGRHMEAGGATGALGVGCKLPSAFCFPGS SVAMDMPQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM EGVPTAIREISLLKELKHPNIVRLLDVHNRKLYLVFEFLSQ DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSPCHSHRVIHRDLK PQNLLINELGAIKLADFLARAFGVPLRTYTHEVVTWLYRAPEI LLATRFYTTAVDIWSIGCIFAEMVTRKALFFGDS\EIDQ\LFRI FRMLGTPSEDTPWPGVTQLPDYKGSFPKWTRKGLIEIVPNLEPEG RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF RH
5994	394	1934	AGEVQLHWIRGMRIQPQ/KAAAIIDLDPDFEQSRPRSCWTPL PRPEIANQPSKPPVEPDLGEKVHTEGRSEPIILLPSRLPEPAGG PQPGILGAVTGPRKGGSRNNAWGNQSYAELISQAIESAPEKRLT LAQIYEWVTRTPYFKDKGDSNSAGWKNSIRHNLHLHSKFIVK HNEATGKSSWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA PKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNRREADMWTT FRPRSSSNASSVSTRLSPLRPESEVLAEIIPASVSSYAGGVPTT LNEGLELLDGLNLTSSSHLSLSRSGLSGFSLQHPGVTGPLHTYSS SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTOVD PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLBAPGPSLVPTL SMIAPPPVMASAPIPKALGTPVLTPTTEAASQDRMPQDLDDMY MENLECDMDNIISDLMDGEGLDFNFEPDP
5995	2	2437	RPPGPGPASGAWLCTRARGSAFVFPPLPRPPSRGARRRRRLPGR GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSSREERGAASAAAA AEMMEELHSL\DP\RRQELLEAF\TGLGVSKGPLNSESNSQL CSVGSLSKDEKETPEKKQNDQRNRKRKAEPYETSQKGTGPRGHK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ISDYFERRVEQPLVGLDGSAAKEATEEQSALPTLMSVMLAKPRL DTEQLAQRGAGLCFTFVSAQQNSPSSSTGSGNTEHSCSSQKQISI QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLRANCCLR RQI\DEQQKMLEKYK\ERLNRCFDNEPRNFLIEKSKQEKMACRD KSMQDRRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQRINSQ REEIERQRKMLAKRKPPAMGQAPPATNEQKQRKSKTNGAENETL TLAEYHEQEEIFKLRLGLHLKKEAEIQAELERLERVRNLHIREL KRIHNEDNSQFKDHPTLNDRYLLHLHLGRGGSFSEVYKAFDLTEQ RVVAVKIHQLNKNWRDEKKNYHKKACREYRIHKELDHPRIVKL YDYFSLDTSDFCTVLEYCEGNDLDFYLLKQHLKMEKEARSIMQ IVNALKYLNEIKPPIIHVDLPKGNILLVNGTACGEIKITDFGLS KIMDDDSYNSVDGMELTSQAGATYWLPPPCFVVGKEPPKISK NKVDVWSVGVIIFYQCLYGRKPPFGHNQSQDILQENTILKATEVQFP PKPVTPEAKAFIRRCCLAYRKEDRIDVQQLACDPYLLPHIRKSV STSSPAGAAIASTSGASNNSSN
5996	1612	981	DQQAQLGLMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCE LFSIVVFGSIVNEGYNLSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSSEPHPA FWAFLWFTGDS CYL\ANQWQVSKPKDNPLNEGTASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAP
5997	1612	981	DQQAQLGLMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCE LFSIVVFGSIVNEGYNLSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSSEPHPA FWAFLWFTGDS CYL\ANQWQVSKPKDNPLNEGTASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAP
5998	1612	981	DQQAQLGLMLTLEFGILEFDFSWIGSWTQR/SWVSWRSRPGCE LFSIVVFGSIVNEGYNLSASEGEEFCIYNRNPNACSYGVAVGVL AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSSEPHPA FWAFLWFTGDS CYL\ANQWQVSKPKDNPLNEGTASPGRPSPFS FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAP
5999	2	1790	RPPMEKARRGGDGVPRGPVLHIVVGFHKKGCQVEFSYPPPLIP GDGHSHTLPEEWKYL PFLALPDGAHNYQEDTVFFHLPPRNGNG ATVFGISCYR\QIEAKALKVROADITRETQKSVCVLSKLPLYG LLOAKLQILITHAYFEEDKFSQISILKELYEHMNSSLGASLEGS QVYLGLSPRDLVLHFRHKGILILFKLILLEKKVLFYISPVNKLVG ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD FVSASTADVSHNTLGTIRKVMAGNHGEDAAMKTEEPFQVEDSS KGEQPNDTNQYLKPPSRPSPDSSESDEWETLDPVLEDPNLKERE QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE EDQYGMPLAIFTKGYLCLPYMALQQHLLSDVTVRGFVAGATNI LFRQKHLSDAIVEVEEALIQIHDPBLRKLNLNPTTADLRFADLV VRHVTENRDDVFLDGTGEGGDEWIRAQFAVYIHALAATLQLV LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK TA\MSSWLSTFTTSTSQSLETPPEDEKP
6000	101	1561	TEPCRTAENCTATMSENNKNLSLESSLRQLKCHFTWNLMGENSL DDPEDKVYFRTFQNRFEKATMCNLLAYLKHLKGQNEAALECLR KAEELIQEHADQAEIRSLVTWGNAYVYHYMGRSLSDVQIYVDK VKHVCEKFSSPYRIESPDLCEEGWTRLKCGGNQNERAKVCFEK ALEKKPKNPEPTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNDP NQYLKVLALKLHMKREEGEEGEGEK\LVEEALEKAPG\VTDV LRSAA\KFYRGKDEPKAIELLKALEYIIP\NNAYLHCQIGCCY RAKVPQVMNLRNGMYGKRKLLELIGHAVAHLKKADEANDNLFV VCSILASLHALADQYEDAEYFFQKEFSKELTPVAKQLLHLYGN FQLYQMKCEDKAIHFFIEGVKINQKSREKEKMKDKLQKIAKMR LSKNGADSEALHVLAFQLNEKMQQADEDSERGLESGSLIPAS SWNGE
6001	176	1038	AFASPSRGRHRTHTHTPRHTPRCTMAESHLQSSSLITASQFBEI WLHFDADGSGYLEGKELQNLIELQQAARKAGLEBSPMKTFVD QYQQRDDGKIGIVELAHVLPTEENFLLFRQQLKSCE\EFMKT WRKYDTHDSGFIETEELKNFLKDLLEKANKTVDDTKLAEYTDLM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LKLFDSNNDGKLELTEMARLLPVQENFLKFGQIKMCKGEFNKA FELYDQDGNQYIDENELDALLKDLCEKNKQDLINNITTYKKNI MALSDGGKLYRTDLALILCAGDN
6002	977	81	LAPPGGGLHIPPRTPLSHSRPSPSHHAPHSPPLPLPPADLHPHS SMAQRSDLELDCQLTRDRVVVSHDENLCROSGLNDRDVGSLDF EDLPLYKEKLEVYFSPGHFAHGSDDRMVRLDLFQRFPRTPMSV EIKGKNEELIREQ/VLVRVYDRNBITIWASEKSSVMKKCKAANP EMPLSFTISRGFVWLLSYLLGLLPFIPIPEKFFFCFLPNIIINRT YFPFSCSCLNQLLAVSVKWLIMRKSILRHLEERGQVVFVWCLNE ESDFEAAFSVGATGVTIDYPTALRHYLDNHGPAARTS
6003	140	4098	GKLAFRGMRRLLICKRICDYKSFDDDEESVDGNRPSSAASAFKVP APKTSNPNANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVREACITVA HLSTVLGNKFDHGAEAIPTLFNLVPSNAKVMATSGCAAIRFII RHTHVPRLLIPLITSNCTSKSVPVRRRSFEFLDLLQEWQTHSLE RHA AVL VETIKKGIHDADA EARVEARKTYMGLRNHPGEAETLY NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS KWSTANPSTVAGRVSAAGSSKASSLPQSLQSRSDIDVNAAGAG AHHAAGQSVRSRGLGAGALNAGSYASLEDTSDKLDGTASEDGRV RAKLSAPLAGMGNADSRGRSRTKMVSQSQPGSRSGSPGRVLT TTALSTVSSGVQVRVLSASQAQKRSKIPRSQGCSEASPSRLSV ARSSRI PRPSVSQGCSEASRESSRDTSPVRSFQPLASRHHRS TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLTGSDVEEA VADALLLGDIRTKKKPARRRYESYGMHSDDDANS DASSACERS YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDPI QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES FPNDLQFNILMRFTVDQTQTTPSLKVVAIILKYIETLAKQMDPGD FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFEINTPE FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP RSPANWSSPLTSPNTSNTLSPSAFDYDTENMNSEDIYSSLRG VTEAIQNFSFRSQEDMNEPLKRDSSKDDGDSMCGGPG\MSDPRA GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPNYSDSIS PFNKSAKKEAMFDDDDAQFPDDLSDHSDLVABLLKELSNHNER VEERKIALYELMKLTQESFSVWDEHFKTILLLLETGLDKEPT IRALALKVLEIREILRHQPARFKNYAELTMKLTLEAKDPHKEVVR SAEEAASV\LATSI\SPBQCIVLCP I IQTADYPINLAAIKMQT KVIERSVKETLNLNLLPEIMPLIQGYDNSESSVRKACVFCLVAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDDVS GQS
6004	140	4098	GKLAFRGMRRLLICKRICDYKSFDDDEESVDGNRPSSAASAFKVP APKTSNPNANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVREACITVA HLSTVLGNKFDHGAEAIPTLFNLVPSNAKVMATSGCAAIRFII RHTHVPRLLIPLITSNCTSKSVPVRRRSFEFLDLLQEWQTHSLE RHA AVL VETIKKGIHDADA EARVEARKTYMGLRNHPGEAETLY NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS KWSTANPSTVAGRVSAAGSSKASSLPQSLQSRSDIDVNAAGAG AHHAAGQSVRSRGLGAGALNAGSYASLEDTSDKLDGTASEDGRV RAKLSAPLAGMGNADSRGRSRTKMVSQSQPGSRSGSPGRVLT TTALSTVSSGVQVRVLSASQAQKRSKIPRSQGCSEASPSRLSV ARSSRI PRPSVSQGCSEASRESSRDTSPVRSFQPLASRHHRS TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLTGSDVEEA VADALLLGDIRTKKKPARRRYESYGMHSDDDANS DASSACERS YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDPI QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES FPNDLQFNILMRFTVDQTQTTPSLKVVAIILKYIETLAKQMDPGD FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFEINTPE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FTMLLGALPKTFQDGATKLLHNLRLNTGNGTQSSMGSPLTRPTP RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPNYSDSIS PFNKSALEAMFDDDDAQFPDDLSDHSDLVAEALLKELSNHNER VEERKIALYELMKLTQEESFSVWDEHFKTILLLETLGDKPEPT IRALALKVLRILRHQPARFKNYAELTVMKTLAHHKDPHKEVVR SAEEAASV\LATSI\SPEQCIKVLCPITQTADYPINLAIAKMQT KVIERSVKETLNLLEIPIMPGLIQGYDNSESSVRKACVFCVAV HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS GQS
6005	133	5955	RSSGRRQEQLGQFPGRERKGMASGLGSPSPCSAGSEEDMDALL NNSLPPHPENEEDPEEDLSETETPKLKKKKPKKPRDPKIPKS KRQKKERMLLCRQLGDSSEGGEPEFVEEBEEVALRSDSEGSDYTP GKKKKKKLGPKKEKKS KSKRKEEEEDDDDDSKPKSSAQLL EDWGMEDIDHVFSEEDYRTLNTYKAFSQFVRPLIAAKNPKIAVS KMMVLGAKWREFSTNNPFGSSGASVAAAAAAVAVVSMVTA TEVAPPPPPVEVPIRAKTKEGKGNARRKPKGSPRVPDAKKPK PKKVAPLKIKLGGFGSKRRSSSEDDDLVDSEDFDASINSYSV SDGSTSRSSSRKKLRTTKKKKKGEEVTAVDGYETHQDYCEV COQGEIILCDTCPRAYHMCVCLDPDMEKAPEGKWSCPHCEKEGI QWEAKENDSEGEIILREVGGDLEEDDHMEFCRVCKDGGELL CDTCPSSYHIIHCLNPLPEIPNGEWLCPRCTCPALGKVKQKILI WKWGQPPSPPTPVPRPPDADPNTSPKPLEGRPERQFFVKWQMS YWHCSWVSELQLELHC\QVMFRNYQRKNDMDPEPSGDFGDEEK S\RRRKNKDPKFAEMBERFYRYGIKPEW\MMIHRILNHSVDKKG HVHYLIKWRDLFPYDQASWESEDEVEIQDYDLFKQSYWNHREL MRGEEGRPGKLLKKVLRKLERPPETPTVDPVTKYEROPEYLDATGG TLHPYQMEGLNWLRFSAWAQGTDTILADEMGLGKTQTAVFLYSL YKEGHSKGFPLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGD DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE LITIDMAILGSIIDWACLIVDEAHLKNNQSKFFRVLNGYSLQHK LLLTGTPLQNNLEELFHLNFLTPERFHNLEGFLEEFADI QIKKLHDMLG\PHMLRRLKADVFNMPKTELIV\RVLSPPM\Q KKYYK\YILHSKFLKALN\ARGGGNQVSLNVMMDLKCCCNHPY LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH RVLIFSQMTKMLDLEDLEHEGYKYERIDGGITGNMRQEAIDR FNAPGAQQFCFLSTRAGGLGINLATADTVIYDSDNPHNDIQ AFSRAHRIGQNKVMYIRFVTRASVEERITQVAKKKMMLTHLVV RPGLGSKTGSMSKQELDDILKFGTEELFKDEATDGGGDNKEGED SSVIHYDDKAIERLLDRNQDETETELQGMNEYLSFFKVAQYVV REEEMGEEEVEREIIKQEEVDPDYWEKLLRHVYEQQEDLAR NLGKGKIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDE DFDERSEAPRRPSRKLNDKDKPLPPLARVGGNIEVLGFNAR QRKAFLNAIMRYGMPQDAFTTQWLVRDLRGKSEKEFKAYVSLF MRHLCEPGADGAETPADGVPREGLSRQHVLTRIGVMSLIRKKVQ EFEHVNGRWSMPELAEEVENKMSQPGSPSPKPTPTPSTPGDTQP NTPAPVPPAEDGIKIEENSLKEESIEGEKEVKSTAPETAIECT QAPAPASEDEKVVVEPPEGEKVEKAEVKERTPEMETEPKGGK AADVEKVEEKSAIDLTPIVEDKEEKEEKEEKEVMLQNGETPK DLNDEKQKKNIKQRFMFNIDAGGFTELHSLWQNEERAATVTKKT YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFGKEM NRGNFLEIKNKFLLARRFKLLEQALVIEQLRRAAYLNMSDPSH PSMALNTRFAEVECLAESHQHLKESMAGNKPANAVLHKVLKQL EELLSDMKADVTRLPATIARIIPVAVRLQMSERNILSRLANRAP EPTPQVVAQQQ
6006	1	965	DNDFLRNTVHRHPPVTAEPILRLAENEDVVVVDKPSIPVHPC GRFRHNTVIFILGKEHQLKBLPLHRLDRLTSGVLMFAKTAAS ERIHEQVRDRQLEKEYVCRVEGEFPTEVTCKEPILVVSYKGV CRVDPRGKPCETVFQRLSYNGQSSVVRCPRLTGRTHQIRVHLQF LGHPI LNDPIYNSVAVGPPSRGRGGYIPKTNEELLRLVAEHQAK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QSLDVLDLCEGDLSPGLTDSTAPSSSELGKDDLEELAAA\QKME EVAAAPQELDTIALASEKAVETDVMNQ\RQT\TLCRVPAGATG SLAPRPCDVPTCTTL
6007	3	2351	HELQVEYVFTDKTGLTENEMQFRECSINGMKYQEINGRLVPE GPTPDSSEGNLSYLSLNLNLSHLTSSSFRTSPENETELIK EHDLFKAVSLCHTVQINNVDCTGDGPWQSNLAPSQLEYVAS SPDEKALVEAAARIGIVFIGNSEETMEVKTGLKERYKLHLILE FDSRRRMSVIVQAPSGEKLFLAKGAESSILPKCIGGIEKTRI HVDEFALKGLRLTLCIAYRKFTSKEYEIDKRIFEARTALQQR\B EKLAAVFQFIEKDLILGATAVEDRLQDKVRETIEALRMAGIKV WVLTGDKHETAVSVLSGCHFHRTMNI LELINQKSDSBCAEQLR QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV LCCRMAPLQKAKVIRLIKISPEKPI TLAVGDGANDVSMIQEAHV GIGIMGKEGRQAARNSDYAIARFKFLSKLLFVHGHHFYIRIATL VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLYNICFT SLPILYSLLEQHVDPHVLQNKPTLYRDISKNRLLSIKTFLYWT ILGFSAHFIFFPGSVLLIGKDTSLGNGQMFGNWTFTLVFTVM VITVTVMMALETHFTWVWHLVWGSIIFFVFSLFYGGILWPF LGSQNMVVFVFIQLSSGSANFAIILMVVTCFLFDI IKKVFDRLH HPTSTEKAQLTETNAGIKCLDSMCCFPPEGEAACASVGRMLERVI GRCSPTHSRSWSASDPFYTNDRSILTSTMDSSC
6008	4554	1089	AGVRRAGARRGPGRALPAGATAVPPPSARRRRRCPAPEHAGPAR ASRPSQETMPQLPVNMLGSLRKARKTVKKILSDIGLEYCKEHIE DFKQFEPNDFYLNKTWEDVGLWDPSTLKNQDYRTKPFCCSACP FSSKFFSAYKSHFRNVHSEDFENRIILNCPYCTFNADKKTLETH IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK KCTYRDPLEYIVRKHIYREHFQHVAAPIAKAGEKSLNGAVPLG SNAREESSIHCKRCLFMPKSYEALVQHVIEDHERIGYQVTAMIG HTNVVVPKSKPLMLIAPKPDQKSMGLPPRIGSLASGNV\RSLP SQQMVNRLSIPKPNLSTGVNMMSSVHLQNNYGVKS SVGGYSV GQSMRLGLGGNAPVSI PQQSQSVKOLLPSGNGRSYGLGSEQRSG APARYSLQSANASSLSSGQLKSPSLSQSASRVLGQSSSKPAAA ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFEKEHKAKEVP AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHLIHGLSCPYCRS TFNDVEKMAAHMRMVHIDEEMGPKDSTLSFDLTQQGSHTNIH LLVTYTNLRDAPAESVAYHAQNPPVPPKPKQKVEKADIFVKS SPQAAVYPYKDVGKTLCPCLFSLKGPISDALAHLRERHQVIO TVHPVEKKLTYSKIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRNLNQSPLAPVKRTYEQMEFPLKKRKLDDSDSP SFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPY TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVDRCEKYKPGVL LGFNMKELNKKVHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESNESGSPFDPVFEVEPKISNDNPEBH VLKVIPEDASESEKLDQKEDGSKYETIHLTEPTKLMHNASDS EVDQDDVVEWKDGASPSSESGPGSQQVSD FEDNTCEMKPGTWSDE SSQSEDARSSKPAKKKATMQGDREQLKWNSSYGVKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDEQFDNMTDGVAE MHGSLAGVKLSSQQA
6009	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*CAVRSEEKSI*GSPSC HLVLGVLPVARQSSHSAGPAQSAFR* TGTGSGTPKAAEQSGYW EAYTLGHQHWNFPIQRPLVMKGRIMCGKCEK*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPODGEVGFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGA LDVAFLLHLTLVCSFNVAY*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQELHDMVAGAGVQVQW DPFVVGLAGIFHLIDDPHQIELSFQRRV*EQCQGVKPDSPQVP RPLRVGLLQVGPLVRGGGRVAGRGKRCWRDLLFPWRWGLSHRT RDLLRGGDRGHVVVIVLCRLGSLVGGLGTDELLWFGGR*LIIG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			I**RGRLSGEWGCGLGRGELFQVSIIGVSIHVIGQGDHEVLGG AGLVERGALHATGQGVEALVQQLLDVGPAGALGLCDGAALFQGP GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPQALHGAAI CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRG*TR R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLVEHGVYGT*IHCL GSFPGRLLWP*PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVRG TWRYGNPLNLL*GAWLGGAACGGQGGPLSTWQACTGPGQAAP LPPFGACRPRTRQCRTWVCFIAWRQLLAYTRD
6010	1	3533	IMPCGSSRLRLGCVTHPNEPVSDDLSTYFDCIESVMENSKVLGESH AGISQNAKTGDLPAFGCECVGIASKALCGLTEAAQAAYLVGIFD PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGFSEDNRNKCRITAPLIEAVENLTAFASNPEFVS IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAASVQSLATRDDISVEALQEQLTSSVQEIHLIDP IATAARGEAAQLGHKGTQLASYFPEPLILAAVGVASKILDHQQM TVLDQTKTLAESALQMLYAAKEGGNPKAQHTHDAITEAAQLMK EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTSD YGHLEFQGMMAATAEPPEIGFQIRTRVQDLGHGCIPLVQKAG ALQVCPTDSYTKRELIECARAVTEKVSILVLSALQAGNKGTOACI TAATAVSGIIADLDTTIFATAGTILNAENSETFADHRENILKTA KALVEDTKLLVSGAASPDKLAQAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAKDVAKALSDLSATKGAASKPVDDPSM YQLKGAAKVMVNTVTSLLKTVKAVEDEATRGTRALEATIECIKQ ELTVFQSKDVPEKTSPEESIRMTKGITMATAKAVAAGNSCRQE DVIATANLSRKAVSDMLTACKQASFPDVSDEVTRALRFGTEC TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA EAMKGTENVDPEPTVIAETELLGAAASIEAAKKLEQLKPRK PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQK VGSIPANAADDGQWSQGLISAARMVAATSSLCEANASVQGH SEEKLISAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV KRASDNLVRAAQKAAGKADDDVVVKTKFVGGLIAQIIAAQEEM LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6011	446	1835	LLQFAMRKSPGLSDCLWAWILLSTLTGRSYGQPSLQDELKDNT TVFTRILDRLLDGYDNRLRPLGERVTEVKTIDIFVTSFGPVS DMEYITIDVFFRQSWKDERLKFQGPMTVLRNLNLMASKIWPDTF FHNGKKSVAHNMTMPNKLRLITDGTLLYTMRLTVR\AECPMF GRDFPM\D\AHACPLKFGSYAYTRADEVVYEWREPARSVVVAED GSRNLQYDLLGQTVDSGIVQSSSTGEYVVMTHFLKRRKIGYFVI QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSIS ARNSLPKVAYATAMDFIACVAFVFSALIEFATVNYFTKRGYA WDGKSVVPEKPKKVDPLIKKNNTYAPTATSYTPNLARGDPGLA TIAKSATIEPKEVKPETKPEPKKTFNSVSKIDRLSRIAPPLLF GIFNLVYVATYLNREPQLKAPTPHQ
6012	351	5013	PAELFQSFATWHKELYDWRIGPWNQCQPVISKSLKPLECICKGE EGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLIPOQD CIVSEFSAWSECSKTCGSLQHRTRHVAPPQFGSGGCPNLTEF QVCQSSPCEAEELRYSLHVGWPSTCSMPHSRQVRQARRRGKNKE REKDRSKGVKDPARELIKKNRNRRQNRQENKYWDIQIGYQTR EVMCINKTGKAADLSFCQKEKLPMTFQSCVITKECQVSEWSEWS PCSKTCHDMVSPAGTRVTRTIRQFPISGEKECPEFEEKEPCLS QGDGVVPCATYGWRTTEWTECRVDPPLSQDKRRGNQALCGGG IQTRREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNNT QLCHIPCPTCEVSPWSANGPCTYENCNDQGGKGFKLKRRIT NEPTGGSGVTGNCPHLLAIPCEEPACYDWAVALGDCPEPDKG ECGPGTQVQEVVCCINSDEEVDRLCRDAIFPVPACDAPCPK CIVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP NSSALQEVRS CNEHPCTVYHWQTGPWQGCIEDTSVSSFNNTTTW NGEASCSVMQTRKVICVRVNVGQVGPKKCPESLRFETVRPCLL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVITQLPAN GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS VQDQSP\GAQEGCGPGRQARAITCRKQDGGGAGIHECLQYAGPV PALTOACQIPQDDCQLTSWSKFSSCNGDCGAVRTRKRTLGVKS KKKECKKNSHLYPLIETQYCPCKYNAQPVGNWSDCILPEGKVE VLLGMKVQGGDIKECGQGYRYQAMACYDQNGRLVETSRCSNHYI EEACII PCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLRKPYN GGRPCPKLDHVNQAQVYEVVPCSDCNQYLWVTEPWSICKVTFV NMRENCGEVQTRKVRMCQNTADGPSEHVEDYLCDEEMPLGSR VCKLPCPEDCVISEWGPWTQCVLPQNSQSSFRQSRADPIRQPADE GRSCPNAVEKEPCNLNKNCHYDYNVTDWSTCQLSEKAVCGNGI KTRMLDCVRS DGKSVDLKYCEALGLEKNWQMNSTCMVECPVNCQ LSDWSPWSECSQTCGLTGKIMIRRTVTQPPQDGRPCPSLMDQS KPCPVKPCYRWQYQWSPCQVQEAQCGEGTRTRNISCVSDGSA DDFSKVVD BEFCADIELIIDGNKNMVLBSCSQPCPGDCYLKDW SSWSLQCLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCEQML ETKSCYDGGQCYEYKWMASAWKSSRTVWCQRSDGINVTGGCLVM SQPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQ CTLIPVVLP TMEDKRGDVKTSRAVHPTQPSNPAGRGRTWFLQ PFGPDGRLKTWVYVGAAGAFVLLIFIVSMIYLACKKKPKPQRRQ NNRLKPLTLAYDGDADM
6013	1161	710	GAFIAGVPVQPVLIIRY PNLDTTSWAWRGPGVLKVLWLTASQPC SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE FVGS LPIVVGRLKVALEPQL/WGTGKSASEGVAWRWLCGRWGR ARPESNDQPGRVCAATAL
6014	2857	613	EAVAGGMEKSRMNL PKGPD TLCPDKDEFMKEDFDVDHFVSDCRK RVQLEELRDDLELYKLLKTAMVELINKDYADF\VNLS TNLVGM DKALNQLSVPLGQLREEVLSLRSSVSEGI RAVDERMSKQEDIRK KKMCVLR LIQVIRSEKIEKILNSQSSKETSALAEASSPLLTGQI LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE GLLLEGLQTS DVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI DEVII EQFVESH?NGLQVMYNKLEFVPHHCRLLREVTGGAISS EKGNTVPGYDFLVNSVWPQIVQGLEEKLP SLFNPGNPD AFHEKY TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI RFREIAGSLEAALTDVLEDAPEASPYCLLASHRTWSSLRRCWSD EMFLPLLVRHLWRHLSGRFWARYSVFV\N\ELSLRPISNESPK IKKPLVTGSKEPSITQGNTE DQSGSPSETKPVVSISRTQLVYV ADLDKLEQLPELLEI IKPKLEMIGFKNFSSISAALDSQSSFS ACVPSLSSKIIQDLSDCFGFLKSALEVPRLYRRTNKEVPTTAS SYVDSALKPLFQLQSGHKDKLQAI IQQWLBGTLSESTHKYYET VSDVLNSVKMEESLKRKLQARKTTPANFVPGSGGMSDDDKIRL QLALDVEYLGEIQKLGLQASDIKSFSALAEVAAAKQATAEQ P
6015	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGM DLVWSAWYGK VKGKGS LPLSAHGIVVAWLSRAEWDQVTVYLP CDDHKLQRYALN RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGTDELRLLY GMALVRFVNLI SERKTKFAKVP LKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCROLENSLRETWELEEFR EGIEEEDQEEDKNIVDDITEQKFPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKELYERARELLVS YEEEQFTVLEKFRYLP KAIKAWNNSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT FEQLAALQIEYEENVLDNDVLVPKPFSSQFWQPLLRLHLSQNFQT ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARF SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPC WASPQLLR II F\KAMGQGLQDE\EQEKLRLICSIYTQSGENSLVQEGSEASPIG KSPYTLDSLYWSVKPASSSFGSEAKAQQEEQGSVNDVKEEKE EKEVLDPQVEEEEENDDQEEEEDEDEDDEEDRMEVGPFTSG QESPTAENARLLAQKRGALQGS AWQVSSSEDVRWDTFF\LGRMPR SRPRTPAELMLENYDTHVIFWTKPVL\EQRLPESTCK\TDTLGL \SCGVGS\GNCSNSSSNFRGAFLLRARGSLH\GL\KTGLQLF
6016	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGM DLVWSAWYGK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VKGKGS LPLSAHGIVVAWLSRAEWDQVTVYLFCDHKLQRYALN RITVWRSRSGNELPLAVASTADLRCKLLDVTGGLGTDELRLLY GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPHINDCRRGCYFVLDWLQKTYWCRLQENSLRETWELEEFER EGIEEEDQEEDKNIWVDDITEQKPEPQDDGKSTESDVKADGDSK GSEEVDSHCKKALSHKELYERARELLVSYEEQFTVLEKFRYLP KAIKAWNNPSPRVECVLAEKGVTCENREAVLDAFLDDGFLVPT FEQLAALQIEYEENVLDNDVLVPKPFSQFWQPLLRLGHSQNFQ ALLERMLSELPAIGISIRPTYILRWTVELIVANTKTORNARRF SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPOLLRRI F\KAMGQGLQDE\BQEKLLRICSIYQSGENSLVQEGSEASPIG KSPYTLDSLWVSKPASSSSFGSEAKAQQEEQGSVNDVKEEKEE EKEVLPDQVEEEENDDQEEBEEDEDEDEDEDEDEDEMEVGPFS TGQESPTAENARLLAQKRGALQGSAAQVSSDVRWDTFF\LRMPR SRFRTPAELMLNETHVIFWTKPVL\BQRLPESTCK\TDITGL \SCGVGS\GNCSSSSSNFRGAFLEARGSLH\GL\KTGLQLF
6017	203	3469	SHQETEQNSAMAPKRGGGSGISFIFCCFRNNDHEITYRLRND NFALQTMPEPALPMPVEELDMFSELVDELDTDKHREAMFALP AEKKWQIYCSKKKQDEENKGSATSWPEFYIDQLNSMAARKSLAL EKEEEERSKTIESLKTALRTKPMRFVTRFIDLGLSCILNFKL TMDYETSESRIHTSLIGCIKALMNNSQGRAHVLHSEINVIAQ SLSTENIKTKVAVLEILGAVCLVPGGHKKVLQAMLHYQKYASER TRFQTLINDLDKSTGRYRDEVSLKTAIMSFINAVLSQAGVESL DFRLHLRYB\FLMLGIHPVMDKLRKHENSTLDRHLDFFEMLRNE DELEFAKRFELVHIDTKSATQMFELTRKRLTHSEAYPHFMSILH HCLQMPYKRSQNTVQYWLDDRIQQIVIQNDKGQDPDSTPLEN FNKNVVRMLVNEVEVKQWKEQABKMRKEHNELOQKLEKKEREC DAKTQKEEMMQTLNKMKEKLEKETTEHKQVKKQVADLTAQLHE LSRRAVCASIPGGSPGAPGGPFSSVPGSLPPPPPPPLPGGM LPFPPLPFGGPPPPPPGPPPLGAIMPPPGAPMGLALKKSIPO PTNALKSFNWSKLPENKLEGTVWTEIDDTKVFKILDLEDLERTF SAYQROQDFFVNSNSKQKEADAIDDTLSSSKLVKELSVIDGRR QNCNILLSRLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFVPE KSDIDLLEEKKHELDMAKADRFLFEMSRINHYQRLQSLYFKK KFAERVAEVKPKVEAIRSGSEEVFRSGALKQLEVVVLAFGNYMN KGQRGNAYGFKISSLNKIADTKSSIDKNIITLHYLITIVENKYP SVLNINNEELRDIPOAAKVNMTLEDKEISTLRSGLKAVETELEYQ KSQPPQPGDKFVSVVVSQFITVASFSFSDVEDLLAEAKDLFTKAV KHFGEAGKIQPDFFGIFDQFLQAVSEAKQENENMRKKKEEEE RRARMAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV FDKDL SKLRNRKRITNQMTDSSRERFITKLN
6018	13	2510	TISQSGGIRRRREAVWFEVVMDFSRHLMYSPPQCVPTGTY ALSSSYSSDALDFETHEKLDPVFDSPRMSRSLRLATTACTLGD GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSASF INHVSQV TSSGVSYGGTVSLQDAVTRRPPVLDES WIREQTTVDHFWGLDDD GDLKGGNKAAIQGNGDVGAGAAATGHNGFFCSN CNMLESERKDVLT AHPAAGPVS RVYSRDRNQKCDCKGXRHLDAHPGRAGTLWHIW ACAGYFLLQILRRIGAVGQAVSRTAWSALWLA VVAPGKAASGVF WWLGIGWYQPVTLISWLVFLTRCLRNICKFLVLLIPLFLLLG LSLRGQG\NFFSFLPVLNWSMHRTQVRVDDPQDVFKPTTSRLKQ PLQGDSEAFPHWMSGVEQQVASLSGQCHHGENLRELTTLQK LQARVDQMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHV RMS HLEDILGKLEKSEAIQKELEQTQKTI SAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREVMKLLFSD QGGSLQELLQRFSSQFVSKGDLQTMRLDLQLQLRNVTHHVS TKQLPTSEAVVS AVSEAGASGITEAQARAI VNSALKLYSQDKTG MVDFALES GGGSILSTRCSETYETKTALMSLFGIPLWYFSQSPR VVIQPDIIYPGNCWAFKSGQGYLVVRLSMMIHPAAFTLEHI PKTL SPTGNISSAPKDFAVYGLENEYQEEGQLLGQFTYDQDGESLQMF QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK
6019	2	1066	TPNDREPPQRPSSRRASHLAQEITSAASLGQDTQILGSLTTA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PVITSAIRSMPGISSQILTNAQQQVIGTLPWVNSASVAAPAPA QSLQVQAVTPQLLLNAGQVIATLASSPLPPVAVRK\ PSTPES LLKSEVQPIKPTPTVPQPAVVIASPAPAAKPSASAPIITCSET PTVSQLVSKPHTPSLDEEDGINLEEIREFAKNFKIRRLSLGLTQT QVGQALTATEGPAYSAICRFEKLDITPKSAQKLPVLEKWLN EAEARNQEGQNLMEFVGGEPSSKKRRRTSFTPAIEALNAYFE KNPLPTGQEITEIAKELNYDREVVRVWFCNRRQTLKNTSKLVNF QIP
6020	4953	549	EAIQFEVSIIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYLWP AHTKPVVTLTSYWEDISHRLDAVNILLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKMLQLTE EPQNSMPDII IWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIIFLKYPQEKNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP CGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWAAEKMYHTRRRRLVRKRKLD LTQTASSTAGAMELQDQEGWEYASLIGWKFWHKQRSSDTFRRR RWRKMAPSETHGAAAI FKLEGALGADTTEDGDEKSLEKQKHS A TTVFGANTPIVSCNFRDRYIYHLRCYVYQARNLLALDKDSFSDP YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPTVLQ NPPKVMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAFNLYMVP QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV ESVVIKNLKKTNPFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR DIVIEMEDTKPLLASKCLSSMSTALS KMAS PATVHLTEKEEIV DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAFEGLT DFDSTFKLYRGKSDENEDPSVVGFEKGSFRIYPLPDDPSVPAPP RQFRELPSVQECTVRIYIVRGLELQPDNNGLCDPYIKITLG KKVIE\DRDHYIPNTLNPVFRMYELSCYLPQEKDLKISVYDWD TFRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW RDSLRL\PTQ\LLQNVARFKGFPQPILEDGSRIRYGGRDYSLDE FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYLRLVIWNTKDVILDEKSI TGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGEKNFNWRFPFPDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIQIW\DNDFKS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDLPNRPETSFLWFTNPKTMKFIWRRFKWVIIGLLELLILL LFVAVLLYSLPNYLSMKIVKPNV
6021	4953	549	EAIQFEVSIIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYLWP AHTKPVVTLTSYWEDISHRLDAVNILLAMAERLQTNIEALKSGI QGKIPANQLAELWLKLIIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKMLQLTE EPQNSMPDII IWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC GKTQTIIFLKYPQEKNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP CGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR AVDEKGWEYGITIPPDHKPKSWAAEKMYHTRRRRLVRKRKLD LTQTASSTAGAMELQDQEGWEYASLIGWKFWHKQRSSDTFRRR RWRKMAPSETHGAAAI FKLEGALGADTTEDGDEKSLEKQKHS A TTVFGANTPIVSCNFRDRYIYHLRCYVYQARNLLALDKDSFSDP YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPTVLQ NPPKVMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAFNLYMVP QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV RSVVIKNLKKTNPFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
			<p>DIVIEEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEIV DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT DFSDFKLYRGKSDENEDPSVVGFEKGSFRIYPLPDDPSVPAPP RQFRELPDSVPQECTVRIYIVRGLELQPDNNGLCDPYIKITLG KKVIE\DRDHYIPNTLNPVFGMYELSCYLPQEKDLKISVYDYD TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPBEYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFPQILSEDSRIRYGGRDYSLDE FEANKILHQHGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRLVIWNTKDVLDEKSI TGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGEENFNWRFVFPFDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIQIW\DNCKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMI PDLKAMNPLKAKTASLFEQKSMKGWW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDLPNRPETSFLWFTNPCKTMKFI VNRFRKWI IGLLFLILL LFVAVLLYSLPNYLSMKIVKPNV</p>
6022	4953	549	<p>EAIQFEVSI GNYGNKFD TCKPLASTTQYSRAVFDGNYYYLFW AHTKPVVTLTSYWDISHRLDAVNTLLAMAERLQTNIEALKSGI QGKI PANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI RKLRSRSLSQIHEAAVRMRSEATDVKSTLARI EDWLDKLMQLTE EPQNSMPDIIIMIRGEKRLAYARIPAHQVLYSTGENASGKYC GKTQITFLKYPQEKNNPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGRHKPSDVTGKIKLKREF FLPPKGEWEGEWIVDPERSLLEADAGHTEFTDEVYQNESRY GGDWKPAEDTDTDANGDKAASPELTCPGWEWEDDAWSYDINR AVDEKGEWEGITIPPDHKKPSWVAEKMVHTHRRRLVRKRKDO LTQTASSTAGAMEELQDQGEWYASLIGWKFWKQSSDTFRRR RWRKMAPSETHGAAAI FKLEGALGADTTEDGDEKSLKQKXSA TTVFGANTPIVSCNFDYDIYHLRCVYQARNLLALDKDSFSDP YAHICFLHRSKTTEI IHSTLNPWTWDTI IFDEVEIYGEPTVLQ NPPKVMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW HPVMNGDKACGDVLTABILI RKGKGSNLPILPPQAPNLYMVP QGIRPVVQLTAIEILAWGLRNMKNPQMASITSPSLVVECGGERV ESVVIKNLKKTPNPFSSVLFMKVFLPKEELYMPLVIKVIDHRQ FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR DIVIEEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEIV DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT DFSDFKLYRGKSDENEDPSVVGFEKGSFRIYPLPDDPSVPAPP RQFRELPDSVPQECTVRIYIVRGLELQPDNNGLCDPYIKITLG KKVIE\DRDHYIPNTLNPVFGMYELSCYLPQEKDLKISVYDYD TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPBEYCVSGVNTW RDSLR\PTQ\LLQNVARFKGFPQILSEDSRIRYGGRDYSLDE FEANKILHQHGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRLVIWNTKDVLDEKSI TGEEMSDIYVKGWIPGNEE NKQKTDVHYRSLDGEENFNWRFVFPFDYLPAEQLCIVAKKEHFW SIDQTEFRIPPR\LIQIW\DNCKFS\LDDYLGFPRTLTCRHTI HFLQKSPGGNC/RGLDMI PDLKAMNPLKAKTASLFEQKSMKGWW PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDLPNRPETSFLWFTNPCKTMKFI VNRFRKWI IGLLFLILL LFVAVLLYSLPNYLSMKIVKPNV</p>
6023	102	916	<p>SQELGMFVELNNLLNTTPDRAEQGKLTLLCDAKTDGSFLVHHFL SFYLANCKVCVVALIQSFSSHYSIVGQKLGVS LTMARERGQLVF LEGL/IVCSGR/VFQAQKEPHPLQFLREANAGNLKPLFEFVREA LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVLDFIHYCRAT VCWELKGNMVLVHDSGDAEDEENDILLNGLSHQSHLILRAEGL ATGFCRDVHGQLRILWRRPSQPAVHRDQSFYQYKIQDKSVSFF AKGMSPAVL</p>
6024	3	3260	<p>FLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSFWEAB LPAELFQKKVASFPRTVLSTGMDNRYLVAVNTVQNKEGCEK RLVITASQSLENKELCILRNDWCSPVPEPGDI IHLEGDCTSDTW IIDKDFGYLILYPDMLISGTSIASSIRCMRAVLSETFRSSDPA TRQMLIGTVLHEVFQKAINNSFAPEKLQELAPQTIQEI RHLKEM</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			YRLNLSQDEIKQEVEDYLPSCFKWAGDFMHKNTSTDFPQMQLSL PSDNSKDNSTCNIEVVKPMDIEESIWSRPFGLKGKIDVTVGVKI HRGYKTKYKIMPLELKTGKESNSIEHRSQVVLTYLLSQERRADP EAGLLLYLKTGMYPVPANHLDKRELLKLRNQMAFSLFHRISKS ATRQKTQLASLPQIIIEEKTCKYCSQIGNCALYSRAVEQQMDCS SVPIMLPKIEEETQHLKQTHLEYFSLWCLMLTLESQSKDNKKK HQNILWLPASEMEKSGSCIGNLIRMEHVKIVCDGQYLHNFQCKH GAIPTVNLMDGDRVIVSGEERSLFALSRGYVKEINMTTVTCLLD RNLVSVLPSTLFRDQEEKNCDIDTPLGNLSKLMENFTVSKKLR DLIIDFREBPQFISYLSVLPDADKTVCILKGLNKPQRQAMKK VLLSKDYTLIVGMPGTGKTTTICTLVRILYACGFSVLLTSYTHS AVDNILLKLAKFKIGFLRSR\QIQKVHPAIQQFTEHEICRSKSI KS\LALEELYTSQLIDATTCMGINHPIFSRKIFDFCIVDEASQ ISQPICLGPPLFFSRRFVLVDHQQPLPLVLNREARALGMSSELF KRLEQNKSAVVQLTVQYRMNSKIMSLSNKLTIEGKLECGSDKVA NAVINLRHFKVDVKLELEYFADYSDNPWLMGVFEPNPNVCFNLTD KVPAPEQVEKGGVSNVTEAKLIVFLTSIFVKAGCSPSDIGIAP YRQQLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSVFVRSN KDGTVGELLKDWRRNLNVAITRAKHKLILLGCVPSLNCYPPEKL LNHLNSEKLIIDLPSREHESLCHILGDFQRE
6025	3977	89	GGFPAQSDHLPVPFPLRSDLLITMSTLYVSEHPDAFFSLRALIA ARYGEAGEGPGWGGAHPRICLQPPPTSRTSFPFRLPALEQGGP GLVWVGATAVLAQLLWPAAGLGGPGSRAAVLVQQWVSADTELIP AACGATLPALGLRSSAQDPQAVLGALGRALSPLEEWLRLHTYLA GEAPTADLAAVTALLLPFRYVLDPPARRIWNVTRVFTCVRQ PEFRAVLGEVVLVSGARPLSHQPGPEAPALPKTAAQLKKEAKKR EKLEKFOQKQKIQQQPPPEKKPKPEKREKRDGPVITYDLPTP PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGFFKPEYGRPNVS AANPRGVFMMCIPPPNVTGSLHLGHALTNAIQDSLTRWHRMRGE TTLWNPAGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLEVV KWKEEGDRIYHQLKGLSSLDWDRACTMDPKLSAAVTEAFVR LHEEGIIYRSTRLVNWSCTLSAISDIEVDKKELTGRLLSVPG YKEKVEFGVLVSFAKVKQGSDESDEEVVATRIETMLGDVAVAV HPKDTRYQHLKGNVIHPFLSRSLPIVFDEFVMDDFGTGAVKIT PAHDQNDYEVGQRHGLEAISIMDSRGALINVPPFGLGLPRFEAR KAVLVALKERGLFRGIEDNPMVPLCNRSKDVVEPLLRPQWYVR CGEMAQAASAAVTRGDLRLPERHQRTWHAMDNIRE\WCMFPFG KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYVWSGRNEABARE KAAKEFGVSPDKISLQQDEVDLDTWPFSSGLFPLSILGWPNQSED LSVFYPTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNLNLSNLDPS EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINDVN RILGYRHFNCNLWNATKFAIRGLGKGFVPSPTSQPGGHESLVD WIRSRLEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC LKPVLNGVDQVAECARQTLTYTCLDVGLRLLSPFMPFVTEELFQ RLPRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGGP QAQVVVAEAPWGLPAP\QCAVALASDRCSI\HLQLQG\LLDP ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ERRA\ASGNPVKVPL\E VQEADEAKLQOTEAEELRVDEAIALFQKML
6026	2674	514	GPITFLKKKAKMKDMLRIHVLLGLAITTLVQAVDKKVDPCRLC TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLQ TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV YLEENKLTPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK PLINLRSLVIAGINLITEIPDNALVGLLENLESIFYDNRLIKVPH VALQVVNLKFLDLNKNPINRIRRGDFSNNLHLKELGINNMP ISIDS LAVDNLPLDKIEATNPNRLSYIHPNAFFRLPKLESML NSNALSALYHGTIESLPNLKEISHSNPIRCDCVIRWMNMNKT IRFMEPDSLFCDVPPFPQGGQNVQVHFRDMMELCLPIAPESFP SNLNVEAGSYVSFHCRTA\EPQPEIYWITPSGQKLLPNT\LT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KFYVHSEGLTDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG SFPQDNNGSLNLIKIRDIQANSVLVSWKASSKILKSSVKWTAFAVK TENSAAQASARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNR KKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLIS CLSPMNCDGGHSYVRNVLQKPTFALGELYPPLINLWEAGKEKS TSLVKVATVIGLPTNMS
6027	5254	4148	GGRRAPGRPGRSIKDEEBETVFEVVSFSPDPLPVRYDKDITTK PISFYLSLEELLAWKPRLEDGFNVALEPLACRQPLSSQRPRPT LLCHDMMGYLLDRFIQGSVVQTFYAFYHWQCIDVFVYFSHTV TIPPVGWNTTAHRHGVCVLGTFITENEGGRLCEAFLAGDERSY QAVADRLVQIT\RFRRFDGWLINIENSLSLAAVGNMPPFLRLYT TQLHRQVPGGLVLWYDSVVQSGQLKWQDELNQHNRFVFDSCDGF FTNYNWREHLEMLGQAGERRADVVGVDVFARGNVVGGRFDT DKVGGGFRPRASGFPVPLGPHFLMDLFFPSAPQRNDSSCSSQSG DPVALNRNCPAPAKLCPH
6028	120	3432	NCLLLQAKGFHGETEDLQOWLTDTERHLLASKPLGGLPETAKEQ LNVHMEVCAAFEAKEETYKSLMQKGQMLARCPKSAETNIDQDI NNLKEKWESEVETKLNER\KT\KLEEALNLA\MEFHNSL\QDPIN WLTQAEQTLNVA SRPSLILDTVL FQIDEHKVFANEVNSHREQII ELDKTGTHLKYFSQKQDVVLIKNLLISVQSRWEKVQRLVERGR SLDDARKRAKQFHEAWSKLMWLEESEKSLDSELEIANDPDKIK TQLAQHKFEQKSLGAKHSVYDTTNRTRGRSLKEKTSLADDNLKLD DMLSELDRKWDITCGKSVERQNKLEEA\LLFSGQFTDALQALID WLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAFQKELGKRTSSVQ ALKRSARELIEGSRDDSSWVKVQMQLSTRWETVCALSISKQTR LEAALRQAEFEHVSVHALLLEWLAEAEQTLRFHGVLPDDEDALRT LIDQHKEFMKKLEEKRAELNKATTMGDTVLAICHPDSTITIKHW ITIIIRARFEEVLAWAKQHQQRLASALAGLIAKQELLEALLAWLQ WAETTLTDKDKVIPQIEIEVKALIAEHQTFMEEMTRKQPDVDK VTKYKRRADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSGQT QIETKNPRVNLVSKWQVWLLALERRRKLNDALDRLEELREFA NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKQDQGITRQEFID GILSSKFPTSRLEMSAVADIFDRDGDGYIDYEFVAALHPNKDA YKPI TDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFLGNO FGDSQQLRLVRI LRSTVMVRVGGGWMALDEFLVKNDPCRAGRT NMELREKFI LADGASQGMAAFRRPRRRSRPSSRGASPNRSTSVS SQAQAASQPVPATTPKILHPLTRNYGKPLWLTNSKMSPTCKAA ECSDFPVPSABGTPIQGSKLRLPGYLSGKGPHSGEDSGLITTA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRSGSDASDFDISE IQSVCSDEVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK LDKSSKR
6029	1	3533	IMPCGSSRLRLRCWTHPNEPVSDLSYFDCIESVMENSKVLGEM AGISQNAKTGDLPAFGECEVGIASKALCGLTEAAAQAYLVGIFD PNSQAGHQGLVDP IQFARANQAIQMACQNLVDPGSSPSQVLSAA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL VKTIKALDGDSEDRNRNKCRIATAPLIEAVENLTAFASNPFFVS IPAQISSEGSQAQEPILVSAKPMLESSYLIRTARSLAINPKDP PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAQLMK EAVDDINVTLINEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD YGH LAFQGGMAAAATAP EEEIGFIQIRTRVQDLGHGCI FLVQKAG\ ALQVCPTDSYTKRELIECARAVTEKVS LVL SALQAGNKGTQACI TAATAVSGIIADLDTTIFATAGTLNAENSETFADHRENILKTA KALVEDTKLLVSGAAS TPDKLAQAQSSAATITQLAEVVKLGAA SLGSDDPETQVVLINAIKDVAKALSD LISATKGAASKPVDDPSM YQLKGAAKVMVNTVTSLLKTVKADEATRGTRALEATIEICIKQ BLTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQBE DVIATANLSRKAVSDMLTACKQAS FHPDVSDVTRALRFGTEC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA EAMKGTEDVDPEDPTVIAETBLLGAAASIEAAKKLEQLKPRAK PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK VGSIPANAADDGQWSQGLISAARMVAATSSSLCEANASVQGH SEEKLISSAKQVAASATALLVACKVKADQDSEAMRRLQAAGNAV KRASDNLVRAAQKAAFGKADDDVVVKTFFVGGIAQIIAAQEM LKKERELEEARKLAQIRQQQYKFLPTELREDEG
6030	3	1777	FPGRGSPALQLEVLICGLMGLERLNLVLAIFVYRNIVNLLTEN APWNSLAWTVTSYVFLKFLQGGGTGSGTFVSNLRTFLWIRVQQF TSRRVELLIFFSHLHELRLRHLGRRRTGEVLRIADRGTSSTVGLL SYLVFNVIPTLADIIIGIIFYSMFFNAWFLIVFLCMSLYLTLT IVVTEWRTKFRAMNTQENATRARAVDSLNFETVKYNAESYB VERYREAI IKYQGLEWKSSASLVLLNQTNQNLVIGLGLLAGSLC AYFVTEQKLQVGDYVLFGTYYIQLYMLNWFGTYYRMIQTNFI MENMFDLLKK\ETEVDLPAGGPFPRFQKGRIEFENVHFSYADGR ETLQDVSFTVMPGQTLALVGPSPGAGKSTILRLFRFYDISSGCI RIDGQDISQVTQALFRFHWELCPKDTVLFNDTIADNIRYGRVT AGNDEVEAAQAAGIHDAMAFPEGYRTQVGERGLKLSGGEKOR VAIARTILKAPGIIILLDEATSALDTSNERAIQASLAKVCANRTT IVVAHRLSTVNNADQILVIXKGCIVERGRHEALLSRGGVYADMW QLQQGQETS EDTKPTMER
6031	160	1694	LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVEGADEALQKATKS DSSSPQRVQRPHSSPPRFVTVBELLETARGVTNMLAHEIVVNG DFQIKPELPELNSLKKRVKEIVHKAFWDCLSVQLSEDPAYDHA IKLVGEIKETLLSFLLPGHTRLRNQITEVLDLDLIKQEAENGAL DISKLAEFIIGMMGTLCAPARDEBVKLKDKEIVPLFREIFSV LDLMKVDMANFAISSIRPHLMQSSVEYERKKQEIILERQPNLD FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVQN YAYLKLLKWDHLQRFPETVLMQSRFHELQQL\REQLTILGAV LLVTFMSMAAPGISSQADFAEKLKMIKILLTDMHLPFHLKDV LTIGEKVCLVSSCLSLCGSSPFTTDETVLKGQIQAVASPD IRRIMESRILTFLETYLASGHQKPLPTVPGGSPVQRELEVAI KFARLVNNKMFVCPYYDAILSKILVRS
6032	39	2415	AARLCRAQPTKSAWMIRDLSKMPQTRHPAPHQPAQPFKFTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIDKDKKHNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSSESKKQKTEEKEIAARYDSGEEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKDKAPISP ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTPRDAPTGS NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFPGIVPHAG MNGELTSPGAAYAGLHNISPQMSAAAAAAYGRSPVVGFD PHHMRVPAIPNLTGIPGGKPAYSFHVSADGQMOPVFPFPDAL IGPGIPRHARQINTLNHGEVVCATISNPTRHVYTGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLPDGRTLIVGGEASTL SIWDLAAPTPIKAELTSSAPACYALAI SPDSKVCFSCCSDGNI AVWDLHNQTLVRQFQGHDTGASCIDISNDGTLWTGGLDNIVRS W\DLREGRLQQHD/FFTSPVFSGLGYCP\TEEWLAVGMENS\N EVLHVTKPDQYQLHLHESCVLSLKFACGKWF\VSTGKDNLLNA W\RTPYG\ASIF\QSKESS\VLSCDI\SVDDKYIVTGS\GDK\ RATVYEVY
6033	39	2415	AARLCRAQPTKSAWMIRDLSKMPQTRHPAPHQPAQPFKFTISE SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYEMS YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP PIGSSAGLLALSSALGGQSHLPIDKDKKHNDHQRDRDSIKSS SVSPSASFRGAEKHRNSADYSSSESKKQKTEEKEIAARYDSGEEK SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKDKAPISP ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTPRDAPTGS NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFPGIVPHAG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MNGELTSPGAAYAGLHNISPQMSAAAAAAYGRSPVVGFD PHHMRVPAIPPNLTGIPGGKPAYSPHVSADGQMOPVFPFDAL IGPGIPRHARQINTLNHGEVVCATISNPNTRHVTGGKGCVKVW DISHPGNKSPVSQLDCLNRDNYIRSCRLPDGRTLIVGGEASTL SIWDLAAPTPIKAELTSSAPACYALAI SPDSKVCFSCCSGNI AVWDLHNQTLVRQFQGHDTGASCIDISNDGTLKWTGGLDNTVRS W\DLREGRLQQHD/FTSPVFSGLGYCP\TEEWLAVGMENSN/V EVLHVTKPKDYQLHLHESCVLSLKFAHCGKWV\VSTGKDNLLNA W\RTPYG\ASIF\QSKSSS\VLSCDI\SVDDKYIVTGS\GDK\ RATVVEVY
6034	2683	714	ESGRRRLKRRRSPCPGTAGGPGETNPGPGACPRGPREEAAAA EIAQAEAPVPGADGDIIEAPAEAGSPSPASPPADGRLKAAAKR VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLC RQIPKLLRQLQEFDTLGHRLDCLDLKGEKLDYKTCEALEEVFKR LQFKVVDLEQTNLDEDEGASALFDMIEYYESATHLNISFNKHIGT RGWQAAAHMMRKTSCLYL\DARNTPLLDHSAFFVARALRIRSS LAVLHLENASLSGRPLMLLATALKMNMLRELYL\ADNKLNGLO DSAQGLNLLKFNCSLQILDLRNNHVLD SGLAYICEGLKEQKRG VTL\VLWNNQLTHTGMAFLGMLTLPHTQSLLETNLGHNPIGNEGV RHLKNGLI SNRSVLRGLASTKLTCGAVAVAEFIAESPRLLRL DLRENEIKTGGLMALSLALKNHSLRLDLDREPKEAVKSFIE TQKALLAEIQNGCKRNLVLAREREKEQPPQLSASMPETTATEP QPDDEPAAGVQNGAPSPAPSPDSDSDSDEEEEEEEGERDET PSGAIDTRDTSSEPQPPPEPPRSGPPLPNGLKPEFALALPPEP PPGPEVKGSGCGLEHLSCKNEKELEELLEASQESQETL
6035	19	404	SVTYLGIILHKNITGALPADPVQLISQTPPTSTKQQLLSFLGMVG YFYLWIPGFAITKPLCKLTENLADIDPKSFSSHSSFRSLKTA LENASTLALPDSSQPF\SLHTAEVQGCVEILTQGLGPLPV
6036	1745	356	LPDVEKLRGRGRKMDSVEKAATSVSNFRGRPSRGRPPKLRN SRGGQGRGVEKPPHLAALILARGSGKGIPLKNIKHLAVPLIG VLRALDSGAFQSVWVSTDHDEIENVAQFGAQVHRRSSEVSKD SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRHQFRWSEIQKGVREVTEPINLNPAPKRRQD WDGELYENGSGFYFAKRHLIEMGYLQGGKMAYEMRAEHSVDIDV DIDWPIAEQRLRYGYFGKEKLEIKLLVCNIDGCLTNHGIYVS GDQKEIISYDVKDAIGISLLKSGIEVRLISERACSKQTLSSLK LDCKMEVSVSKLAVVDEWRKEMGLCWKEVAYLGNEVSDDEECLK RVGLSGAPADACSTAQKAVGYICKNGGRGA\IREFAEHIC\LL MEKGLINFMKRNRLAVNIGKK
6037	2936	1919	WTSWWMSSVLTILLFSLQGNKMLNYSAPFAGGYLLPRKPVGTPA GGGFPRRHSVTLPPSSKFRQNLSSSLKGEPAFALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSRYKT\ELCRPFEEENGACKYG DKCQFAHGIHELRLSLTRHPKYKTEL CRTFTHTIGFCPYGPRCHFI HNAERRALAGARDLSADRPRQLQHSFSPAGFPSAAATAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSES PHMFDSPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD
6038	1450	426	SSALQEFGRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQSVTAKDSAKTIFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBAKRL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNSGSTIKAFPRAGVKGKGPVNGKNTGLQNKTFHCEICD VHVNSETQLKQHISRRHKDRAAGKPPKPKYSPYNKLOKTAHPL GVKLIVFSKEPSKPLAPRILNPLAAAAAAAVAVSSPFSRLTAP AATLFQTSALPPALLRPA GPPIRTAHTPVLPVFPY
6039	4073	1000	LDEYARLTLANLDDFEEDNEDDENRVNQEEKAKITELINKL NFLDEAEKDLATVNSNPFDDPDAEALNPFDPDSEEPITETASP RKTEDSFYNNSYNPFKEVQTPQYLNPPDEPEAFVTIKDSPPQST KKKNIRPVDMSKYLADSSKTEEEELDESNNPFYEPKSTPPNNL VNPVQBLETERRVKKAPAPPVLSPKTGVLNENTVSAGKDLSTS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PKPSPIPSPVLGRKPNASQSLLVCKEVTKNYRGVKITNFTTSW RNGLSFCAILHHFRPDLIDYKSLNPQDI KENNKKAYDGFASIGI SRLLPESDMVLLAIPDKLTVMYLYQIRAHFSGQELNVVQIEEN SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA VDFLSQDDSVFVNDSSGVGESESEHQTPDDHLSPTASPYCRRTK SDTEPQKSQQSSGRTSGSDDPGICNTDSTQAQVLLGKRLKLLKA ETLELSDLYVSDKKKDMSPFFICEETDEQKLQTLDIGSNLEKEK LENSRSLSECRSDPESPIKKTSLSPSTSKLGYSSRDLDLAKKHA SLRQTESDPDADRTTLNHADHSSKIVQHRLLSRQELKERARVL LEQARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEERRRQLRER ARQLIAEARSGGKMSLPSYGERAAEKLKERSKASGDENDNIEI DTNEEIPGFGVGGDELNTLENDLDTPEQNSKLVDLKLKLLLE VQPQVANSPPSSAAQKAVTESSEQDMKSGTEDLRTERLQKTERF RNPVVFSSKSDTVRKTQLQSFQSYIENRPEMKRQRSIQEDTKKGN EEKAAITETQRKPSSEDEVNKGFKDS\SQYVVGELAALENEQKQ IDTRAAALVEKRLRLYMDTGRNTEEEAMQEWFLVNKKNALIR RMNQLSLLEKEHDLERRYELLNRELRAMLAIEDWQKTEAQKRRE QLLLDELVALVNKRDAI VRDLDAQEKQAEEDDEHLERTLEQKNG KMAKKEKCVLQ
6040	475	1052	PTALMTAPSCAFFVQFRQPSVSGLSQITKSLYISNGVAANNKLM LSSNQITMVINVSVEVNTLYEDIQYMQVPVADSPNSRLCDFFD PIADHHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMSL LDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPV GMIPDIYEKEVRLMIPL
6041	2	3886	TEKDEKTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS NLLQVLQKPKGSLKSSKKKNGKVRPADEILESNEKENEKCVSSEG EKIECWELTTEPSLTHNSSGLSLPLRKKPLEDLVCKLADISINY VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKQSIQAKPLE IAKLQKQNPVQFLYQKLIGWLNEDQKDFGFLVDILYSALRCC DNDMERKKVLDLTKVDLKNWSLLKIEKACPSDDKHALVTPWL KGDILGEKLVNLADCLCNEDLESRVSSSESHFSEWTLSSVLVSQ HVKNLYLIGDVYVERIIVRLHETLFPKTKKLSEASSDSSVSFIC DVAYNYFSSAKGCLMPSSBDLLLTFLQCAQSKEKTHLPDFLI CKLNTWLSGVNLVHQTDSYKESTFLHLSALWLKNQVQASSL DINSQVLLSAVDLLNTLLESEDSYLMGVYIGSVMPNDSEWEK MRQSLPMQWLHRLPLEGRSLNLYECFKTDFKEQDIKTLPSHLCT SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP IFLIGFCEILQKMNITYDNLRVLGNMGLLQLLFNRSREHGTW SLIIAKLILSRSSSDEVKPHYKRKESFFPLTEGNLHTIQSLCP FLSKEEKEFSAQCIPALLGWTKKDLCSNNGFGHLAIFNSCLQ TKSIDDGELLHGILKIIISWKKEHEDIFLFCNLSEASPEVLGV NIEIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL YSIPLVQLFACVSCDLACDLSAFFDSTLTDTIGNLPVNLISEWK EFFSQIHSLLLPILVTVTGENKDVSETS FQNA MLKPMCELTLY ISKEQLLSHKLPARLVADQKTNLPEYLQTLNLTAFLLFRARP VQIAVYHMLYKLMPELPQYDQDNLSYGDSEEPALSPPAALMS LLSIQEDLLENVLGCI PVGQIVTIKPLSEDFCYVLGYLLTWKLI LTFKFAASSOLRALYSMLRKTKSLNKLHYHLFRLMPENPTYAR TAVEVPNKDPKTFTEELQLSIRETTMLPYHILPHLACSVYHMTL KDLPA MVRLWWSSEKRVFNI VDRFTSKYVSSVLSFQEI SSVQT STQLFNGMTVKARATTREVMATYTI EDIVIBLI IQLFSNYPLGS IIVESGKRVGVAVQQWRNWLQLSTYLT HQNGSIMEGLALWKN VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSACL KWTSSNKTCSLCRETFF
6042	1306	253	MAELAPASPSDIKASVSNNGDTTLLCSRRQSCGMNEVRQVSLTYP GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSSLAAQKKE LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFPYLLHQDWVE QYQDDTPVAPREFDVNAPDLYIPAMAFITYVLVAGLALGTDRFS PDLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVAFL GYKYVGMIGGVLMGLLFGKIGYLVVLGWCCVAIFVMIRTLRLK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6043	403	599	ILADAAAEGVPVRGARNQLRMYLTMAVAAAQPMMLMYWLTFLHVR LCLFFPFFCATPVLPLPSLISAL/CLSHLSVSSWFPCQPPLPC PLPPLQNKTAAGSLSTEQSERG
6044	793	412	KLEWNTFLISKVKISREVTMIASKFGIGQQVRHSLGVLGVV DIDPVYSLSESPDELAVNDELRAAPWYHVVEDDNLFPVHTYL AEAQLSSELQDEHP\EQPSMDELAQTIRKQLQAFRLRN
6045	155	2299	SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDLQRQPFPFPPPG AHSFGATPGPGTATAERSSGVAPASPAAPSPGSSGGGGFFSSSL SNAVKTATAAAATFSEQVGGSGGAGRGGAASRVLLVIDEPHT DWAKYFKGKKIHGEIDIKVEQAEFSDNLVAHANGGFSVDMVL RNGVKVVRSLKPDFVLRQHAFSMARNGDYRSLVIGLQYAGIPS VNSLHVSYNFCDKPWVFAQMVRLLHKKLGTEEFPLIDQTFYPNHK EMLSS\TTPVTVVMGHGTLWGKGKVKVDNQHDFQDIASVVALT KTYATAEPFIDAKYDVRVQKIGQNYKAYMRTSVSGNWKNTGSA MLEQIAMS DRYKLWVDTCEIFGGLDICAVEALHGKDGDRDHIIE VVGSSMPLIGDHQDEDKQLIVLVNKMMAQALPRQRDASPGR GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPGGGPPQPGPGP QRQGPPLQQRPPPGQQLSLGLPPAGSPLPQRLPSPTSAPQQP ASQAAPPTQGGQRQSRPVAGGPGAPPAARPPASPSQRQAGPPQ ATROTTSVSGPAPPKASGAPPGGQQRQGPQKPPGPGPTROASQ AGPVPTGPPPTTQPPRPSGPGPAGRPKPLAQKPSQDVPPPPATA AAGGPPHPQLNKSQLTNAFNLPEPAPPSPSLSQDEVKAETIRS LRKSFASLPSD
6046	212	1075	EGLTGPCERVFFLLGRGPPHAGTRAGHRRRAVRWAGPESLPPLPR SLIMDSPRAGTHQGPLDAETEVGADRCTSTAYQEQRQVEQVGK QAPLSPLGAMGGPGPGPCEDPAGAGGAGAGGSEPLVTVTQGA FTVALRARRGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH WVPIPEEESLQRAWQDAAACPRGLQLQCRGAGRPVLYQVVAQH SYSAQGPEDLGFQGDITVDVLCEVDQAWLEGHCDGRIGIFPKCF VVPAGPRMSGAPGRLPRSQQGDQP
6047	49	1405	PVLVTSLRMREADTLRFPQLMEVSADIISTVEFNHTGELLATGD KGRVVFVIFQREPESKNAPHSQGEYDVYSTFQSHEPEFDYLSLE IEEKINKIKWLPOQNAHSLSTNDKTIKLWKITERDKRPEQYN LKDEBEGKLKDLSTVTSLQVPVLKPMDLMEVSPRRIFANGHTYH INSISVNSDCETYMSADDLRLNLWHLAITDRSFTP\NIVDIKPA NMEDLTEVITASEFPHHCNLFVYSSSKGSLRLCDMRAALCDK HSLKEEPEDPSNRSFSEIIS\SVSDVKFSHSDRYMLTR\DYL TVKVVLDL\NMBARPIETQVHDYLRSLCSLYENDCIFIKFECA WNGSDSVIMTGA\YNNPFRMFDRNTKRDVTL\EASRESSKPRAV LKPRRCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA TNNLYIFQDKVNSDMH
6048	1	3194	GIRTPKFCDSPTSLEMRNNGRGRKMRPNSNTPVNETATASDS KGTNSSSKTRAGANSKGRRGSONSSEHRPPASSTSEDKASPSS ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSA TGPLPGTKV EPTVLDNRNCPSPVLIDCPHPNCNKYKHINGLYHQAHATDDD SKPEADGDSEYGEPI LHADLGSCNG\ASVSQK\GSLSPARSAT PKVRLVEPHSPSPSKFSTKGLCKKLSGEGDIDLGALSNDGSD DGPSVMDETSNDADFSLERKCKMEKCKPKPSLKEKIPSKSLK SARPI/APLAIPPQOIYTFQTATFTAASPGSSSGLTATVAQAMP NSPQLKPIQPKPTVMGEFFTVPALTPAKDKKKDKKKKESKE LESPLTPGKVCRAEAGKSPFRESSNGMKMEGLLNGSSDPHQR LASIKAEADKIYFTDNAPSIPSGSSRLNTPPTQPLTPLHV TQNGAEASSVKTNSPAYSDISDAGEDGEGKVDVSKSDAEQLVK EGAKKTLFPQPQSKDSPYQGFESYSPSYAQSSPGALNPSSQ AGVESQALKTKRDEEPESIRGKVNNDICEKKPELSSSSSQPSV IQORPNMYQSLYNNQYAYVPPYGYSDQSYHTLLSTNTAYRQ YEEQKQKQSLQEQQRGVDKKAEMGLKEREALKEEWKQKPSIPP TLTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDSSSKLPGQ APEGLKVKLS DASHLSKEASEAKTGAECGRQAEMDPI LWYRQEA EPRMWTYVYPKYSDIKSEDERWKEERDRKLKEERSRSKDSVPK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
.			EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTQHQS IPYMHGYSYSQSYDPNHPSYRSMMPAVMMQNYPGSYLPSSYSFSP YGSKVSGGEDADKARASPSVTCKSSSES KALDILQHASHYKSK SPTISDKTSQERDRGGCGVVGGGSCSSVGGASGGERSVDRPRT SPSQRLMSTHHHHHLGYSLLPAQYNLPYAAGLSSTAIVASQOG STPSLYPPRR
6049	215	1089	AMTGVFDRRVPSIRSGDFQAPFQTSAAAMHHPQSSEPTLPESAT DSDYYSPTGGAPHGYCSPTSASYG\KALNPYQYQYHGVNGSAGS YPAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTEPEVRMV NGKPKKVRKPRTIYSSFLAALQRRFQKTQYLALPERAELASL GLTQTOVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNSP QSPAVWEPQGSRSLSHHPAHPPPTSNQSPASSYLENSASWYTS AASSINSHLPPPGSLQHPLALASGTY
6050	566	1718	KGLERTCCAMEESDSEKTEKENLGPRMDPPLGEPG\GSLGWL PNTAMKKKVLMLGKSGSGKTSMRSIIFANYIARDTRRLGATILD RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW DCGGQDTFMENYFTSQRDNI FRNVEVLIYVFDVESRELEKDMHY YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQORDLIFKEREEDLR RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLMEMNLRN FAEIIIEADEVLLFERATFLVISHYQCKEQORDAHRFEKISNIIKQ FKLSCSKLAASFQSM EVRNSNFAAFIDIFTSNTYVMVMSDPSI PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6051	566	1718	KGLERTCCAMEESDSEKTEKENLGPRMDPPLGEPG\GSLGWL PNTAMKKKVLMLGKSGSGKTSMRSIIFANYIARDTRRLGATILD RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW DCGGQDTFMENYFTSQRDNI FRNVEVLIYVFDVESRELEKDMHY YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQORDLIFKEREEDLR RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLMEMNLRN FAEIIIEADEVLLFERATFLVISHYQCKEQORDAHRFEKISNIIKQ FKLSCSKLAASFQSM EVRNSNFAAFIDIFTSNTYVMVMSDPSI PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6052	566	1718	KGLERTCCAMEESDSEKTEKENLGPRMDPPLGEPG\GSLGWL PNTAMKKKVLMLGKSGSGKTSMRSIIFANYIARDTRRLGATILD RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW DCGGQDTFMENYFTSQRDNI FRNVEVLIYVFDVESRELEKDMHY YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQORDLIFKEREEDLR RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLMEMNLRN FAEIIIEADEVLLFERATFLVISHYQCKEQORDAHRFEKISNIIKQ FKLSCSKLAASFQSM EVRNSNFAAFIDIFTSNTYVMVMSDPSI PSAATLINIRNARKHFEKLERVDGPKQCLLMR
6053	201	1704	KGTEMNKSRLWQSRRRHGRSHQONPWFRRLRDSRSDSRAAQA HDSGHGDDSPSTSSGTAGTSSVPELPGFYFDEPKRYFRLLPG HNKCNPLTKESIRQKEMESKRLRLQEEEDRRKKIARMGFNASM LRKSQGLFNLVTNYCHLAHELRLSCMERKKVQIRSM DP SALASD RNLILADTNSDRFLTVDVTVGSKYGIINLQSLKTPTLKVFM HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLL PASL FVN SHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS TGLSRRVLLTNVVTGHRQSPGTNSDVLAAQFALMAPLLFNGCRS GEIFAIDLRCGNQGGWKATRLFHDSAVTSVRILQDEQYLMASD MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEGILVAVG QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLMAVGQDLYCYSYS
6054	1	1054	PPIARLQEFGTSSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYH KQSSSQRRNFRRQRDISHSIVLPAAVSSAHPVPKHIIKPKDY VTGIVPDWGDSEVKNEDQIQGLHQACQLARHVL LAGKSLKX DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIIINIDVTVYNGYHGDTSFTLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHONGFQVCPHF VGHGIGSYFHGHEIWHHANDSLPMEEGMAFTIEPIITEGSP FKVLEDAWTVVSLD/TSKVSQAQFEHTVLITSRGAQILTKLPHEA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6055	421	2364	PPYFLLSFLAWWLYGQSDRTETDISQSAGPPFGTLQCSALHHD GCANCSTRFCRDCSPACQCHTHVFPGNALNGVQPPELSRTLALI SSREPPRRKKKSQTETGKERERTSFLTQGGKRFELOHGLAGICM TLLITGDSIVSAEAVWDHVTMANRELAFAKAGDVIKVLDAKNKW WVGQIDDEEGWFPASFVRLWVNHEDVEEGPSDVQNGHLDPNSD CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKIDCEGYLKQC RKRDMFSDQELKVI FGNIEDIYRFQMGFVRDLEKQYNNDPHL SEIGPCFLEHQDGFWYSEYCNHLDACMELSKLMKDSRYQHFF EACRLLQQMIDIA\IDGFLTPVQKICKYPLQLAELLKYTAQDH SDYRYVAAALAVMRNVTTQINERKRRLNIDKIAQWQASVLDW GEDILDRSSELIYTGEMAWIYQP\YGRNQQRVFFLFDHQMVLCK KDLIRDLILYKGRIDMDKYEVDIEDGRDDDFNVSMKNAFKHL NKETEELHFFAKKLEEKIRWLRAFREERKMVQDEKIGFEISE NOKRQAAMTVRKVPKQKGVNSARSVPPSYPPPPQDPLNHGQYLVP \DGIASQVFEFTEPKRSQSPPWQNFSLRTPFKK
6056	43	3358	SGGRGPVRVRSEQLSPSAEQVSQISQISLGRRLSSLPFPSPRA LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREFNK YLAYMESKGAHRAGLAKVIPKEWKPRQCYDDIDNLLIPAPIQQ MVTGQSGFLTQYNIQKKAMTVKEFRQLANSKYCTPRYLDYEDL ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVVE EECGISIEGVNTPYLYFGMWKTFPAWHTEDMDLYSINYLHFGEP KSWYAIPEHGRRLERLAQGGFFPSSSQGCDALRHKMTLISPSV LKKYGIPTDKITQEAGEFMITFPYGYHAGFNHGFCAESTNFTAF VRWIDYGVAKLCTCRKDMVKISMDIFVRKFPQPDYQLWKQGD IYITIDTKPTASTPEVKAWLQRRRKVRKASRSFQCARSTSKRP KADEEEVSDEVDGAEPNPDVTDLLKVSEKSEAAVKLRNTEA SSEESSASRMQVEQNLSHDIKLSGNSCLSTSVTEDIKTEDDKA YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSSELSWPKSPESCS SVAESNGVLTEGEESDVESHNGLEPGEIPAVPSGERNSFKVPS IAEGENKTSKSWRHPLSRPPARSPMTLVKQAPSDEELFEVLISI EEVEETESWAKPLIHLWQTKPPNFAAEQSYNATVARMKPHCAI CTLLMPYHKPDSSNEENDARWETKLEVVVTSEGKTKPLIPEMCF IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPI ETCDGWLCAKCRNAWTAECCLCNLRGGALKQTKNNKWAHVMA VAVPEVRFTNVPERTQIDVGRIPLQRLKLCIFCRHRVXRVSGA CIQCSYGRCPASFVHTCAHAAGVL\MEPDDWPYVNIITCFRHKV NPNVSKACEKVISVQTVITKHNTRYYSRCVMAVTSQTIFYEV MFDGSGFSRDTFPEDIVSRDCLKLGPPEAEVGVQVWPDGKLYG AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF VSAGRCHLGTQVNSLSPPHVSQAQQETYLGFWINSKSKQCNI LSGTY
6057	1	853	FVARLKEQEGEGGLQPRKEKGRARGRRRRKMLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKS RPMANSTLLGALLAPGEAWGILGQPPNPNHSPPPSAKVKKIFG WGDYFSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNIS ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMWEKVE\RGRR TSLFTHDPAKICSRDHAQSSATWSQSPPFKVVCVYIAFYSTDYR LVQKVCPCDYNHSDTPYYPSPG
6058	1	986	HPLPSASLGLPSVSLGVSLCVRSALEAVVPMPLPKRRRARVGS SGDAASSTPPSTRFPGVAIYLVPRMGRSRAFLTGLARSKGFR VLDACSEATHVMEETSAAEAVSWQERRMAAAPPGCTPPALLD ISWLTESLGAGQPPVECRHRLVAGPSKGPLSPAWMPAYACQR PTPLTHNTGLSEALEILAEAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSLQGLPHFGEHSSRVVQELLEHGVCCEEVERVRSE/ RLFTQIFGVGVKTADRWRREGLRTLDDLEQPPQKLTQQKAGEP SREAGPWASLNCITLDPASSTP
6059	2	3650	QQDFESLADLTDRHARCPGDDDDPQLSWASSFSSKDVASPT QMIGDGCGLGEGEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH SKLFPKCTYCSRLFKHRSRDRHIKLTGDKKYHCECEAAFS RSDHLKIHLKTHSSKPFKCTVCKRGFSSTSSLSQSHMQAHKKNK EHLAKSEKRAKKDDFMCDYCEDTFSQTEBLEKHVLTTRHPQLSEK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ADLQCTHCPEVFVDENTLLAHIQAHANQKHKCPMCFE\QFSSV EGVYCHLDSDHRQPDSSNHSVSPDPVLGVSVMSSATPDSSASV ERGSTPDSTLKPLRGQKMRDDGQGWTKVVYSCPYCKRDFNSL AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRLKHN HAYPVMQFGNISAFHCNYCPMFADINSLQEHIRVSHCGPNANP SDGNNAFFCNQCSMGFLTSSSLTEHIQ\Q\AHCSVGSAKLESFV VQPTQSFMEVYSCPYCTNSPIFGSILKLTKHKENHKNIPLAHS KKSKEQSPVSSDDEVSSPKRQRLSASANSISNGEYPCNQCDLK PSNFESFQTHLKLHLELLLRKQACPOCKEDFDSQESLLQHLTVH YMTTSTHYVCESCDKQPSVDD\LQKH\LLDMPHPLCCTHCT\L CQEVFDS\KVIS\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ VHVKSHLGNPAKAKHCFI CGETFFSTEVELQCHITTHSKKYNCK FCSKAFHAIILLEKHLREKHCVFDAATENG TANGVPPMATKKAE PADLQGMLLKNPEAPNSHEASEDDVDASEPMYGCDCIGAAATME VLLQNHRLRDHNIRPGEDDGSRRKAEFIKGSCHKVNCVSRTPFSE NGLREHLQTHRGPAKHVMCPICGERFPSLLTLTEHKVTHSKSLD TGTCRICKMPLQSEEEPIEHQCMHPDLRNSLTGPRCVCMQTVT STLELKIHGTFHMQKLAGSSAASSPNGQGLQKLYKCALCLKEFR SKQDLVKLDVNGLPYGLCAGCMARSANGQVGLAPPEPADRCPA GLRCEPCSVKFESAEDLESHMQVDHRDLTPETSGPRKGTQTSFV PRKKTYYQCIKQMTFENEREIQIHVANHMI BEGINHECKLCNQM FDSPAKLLCHLIEHSFEGMGFTKCPVCFTVFPVQANKLQQHIFA VHGQEDKIYDCSQCPQKFFQTELOHNTMSQHAQ
6060	2145	202	SYEIVGKKNLEVNHSQKALCKSLPSRLPLGLENLPLDRGFR KEPRSRGSRERNMLHLHSHCLCFRSLWLAVALVLLSLAPSASS DISASRPNILLMADDLGIGDICYGNNTMRTPNIDRLAEDGVK LTQHISAASLCTPSRAAFLTGRIYFVRSGMVSSIGYRVLQWTGAS GGLPTNETTFAKILEEKGYATGLIGKWHGLNCESASDHCHHPL HHGFDHFYGMPSFLMGDCARWELSEKRVNLEQKLNFLFQVLAIV ALTLVAGKLTHLIPVSWMPVINSALSAVLLASSYFVGALIVHA DCFLMRNHTITEQPMCFQRTTPTLILQEVASFLLKRNKHGPFLLFV SFLHVIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV EGLSNSTLIYFTSDHGGSLNQLGNTQYGGWNGIYKGGKMGWG EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPVTVRLAGSEVP QDRVIDGQDLLPLLLGTAQHSDFELMHYCFELHAARWHQRDR GTMWKVHFVTPVFPQEGAGACYGRKVCPCFGEKVHHDPPLLLFD LSRDPSETHILTPASEPVFYQVMER\VOQAVWEHQRTLSVPVPLQ LDRLGNIWRPWLQPCCGPFPPLCWCLREDDPQ
6061	110	1330	MNIHMKRRTIKNTFENRMLMDGMPAVRVKTELLESEQGSNP VHNPDMEAVALLLNNVKGPEPDSLSVDHFQTEPVDLSINK ARTSPTAVSSSPVSMASASSPSTSTSSSSSRLASSPTVITS VSSASSSTVLTGGLVASASGVGGQQLHIIHPVPSSPMNLQ SNKLSHVHRIPVVVQSVFVYTAVRSPGNVNTIIVVPLEDGRG HGKAQMDPRGLSPRQSKSDSDDDDLNVTLDVNETGSTALSIA RAVQEVHPSVSRVRGNRMNNQKFPCSI SPFSIESTRRQRTVLN PPDSRKTAYSTDCDF\EGLQKLYTKSSSPGRVHRRTHTEKPY KCTWEGCTWKFARSDDELTRHYRKHTGVKPFKACDCRSFSSRDH LALHRRRRMLV
6062	71	1079	ETMAKNGPENCEDCHILNAAEFKSKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKAYDMEHTFYNGEKKKIYMEIDPVTR TEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKTQIKVIP BFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFKQLHNFAPILVSELQDFE BEGEDLHFPANEKKGIEQNEQWVVPQVVEKTRHARQASEEELP INDYTENGIEFDPMLDERGYCCIIYCRRGNRYCRRVCEPLLGYYP YPICYQGGRVICRVIMPCNWWVARMGRV
6063	71	1079	ETMAKNGPENCEDCHILNAAEFKSKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKAYDMEHTFYNGEKKKIYMEIDPVTR TEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKTQIKVIP EFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNSKI LEICDNVTMYW\INPTL\ISGTFKQLHNFAPILVSELQDFE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EEGEDLHFPANEEKGIEQNEQWVVPQVKVEKTRHARQASEEELP INDYTENGIEFDPMLEDERGYCCYCRGGRNRYCRRVCEPLLGYY YPYCYQGGRVICRVIMPCNWWVARMGLGRV
6064	913	311	NLPQSLPRPTEHSPFYSLEKMTDLVAVWDVALSDGVHKEIEFEHG TTSGRKVVYVDGKEEIRKEWMFKLVGKETFFVGAAKTKATINID AISGFAYEYTLINGKSLKKYMEDRSKTTNTWVLHMDGENFRIV LEKDAMDVVCNGKKLETAGEFVDDGTETHFSGTH\ACYIKAV\ SSG\KRKEGIHTLIVDNREIPEIAS
6065	1153	641	MSVRVARVAVVRGLGASYRRGASSFPVFPFGAQQVAELLRDATG AEEEAAPWAATERMPGQCSVLLFPQGQSQVVMGRGLLNPVR ELYAAARRVLGYDLLELSLHGPOETLDRTHVCQPAIFVASLA EKLHLQPSVIENCVAAGFSVGEFAALVFAGAMEFAEG
6066	68	3470	VKENMPATRKPMRYGHTEGHTEVCFFDSGSFIVTCGSDGDVRIW EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHTFPEG VPDGIILTRFTTANHVVFNGDGTIAAGSSD\FLVKIVDVMDS QOKTFRGHDAVLSLSDPKDI FLASACDGSVRVWQISDQTCA ISWPLQKCNVDINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR ESWHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLIIVNVN ETKDCMERVKHEKGAYICGLAWHPTCGRISYTDAGNGLLENV CDPSGKTSKSVSRVEKDYNDLFDGDDMSNAGDFLNDNAVEIP SFSKGIINDEDEDLMMASGRPRQRSHILEDDENSVDISMLKT GSSLLKEEEDGQEGS IHNLPVTSQRPFYDGPMPTRPKPFQS GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSIHHT HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSWSSK EWIIDLQONEDIEAICLGQGWAAATSAALLRLFTIGGVQKEVF SLAGPVVSMAGHGEQLFIVYHRTGDFDQCLGVQLLELGKKKK QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSBGIVRMLNRGLG NTWTPICNTRHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFP TLPRPAVAILSFKLPCQIATEKQMEEQFWRSVIFHNHLDYLA KNGYEYESTKNQATKEQQLLMKMLALSCKLBERFRCVELADL MTQNAVNLAIKYASRSRKLILAQKLSLAVEKAAELTATQVEEE EEEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVNPFFKVAS SKEPAMSMNSARSTNILDNMGSSKKSTALSRTTNNEKSPI IKP LIPKPKPKQASAAASYFQKRNSQTNKTEEVKEENLKNVLSPTAI CPPQNTENQRPKTGFMWLEENRNLSDNPDFSDEADI IKEGM IRFRVLSTEERKVVANKAKGETASEGTEAKRRKRVVDESDTEN QEEKAKENLNLSSKKQKPLDFSTNQKLSAFAFKQE
6067	858	321	LPWQRLGVLLSRGKMAVTGWLESRTAQKTALLQDGRKRVHYLF PDGKEMAEYDEKTSSELLVRKWRVKSALGAMQWQLEVGDPAPL GAGNLGPGLIKESNANPIFMRKDTKMSFQWRIRNLPYKDVYSV SVDQKERCIIVRTTNKKYKFKFSIPDLDRHQLPLDDALLSFA\T PTAP
6068	13	1730	GSKMADLANEEKPAIAPPVVFQDKGQKSPAEQKNLSDSGEEP RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL PPFPRELGRSAGGSSPEGGEDSDREDGNYCPCPKRETSSTLQ FPPSQSEERSGFRLPKPTLIHQAPSAGLPSQKPKQQRSVLR PAVLQAPQPKALSQTVPSSTNGVSLPADCTGAVPAASPDAAW RSPSEAADEVCALEEKEPKNESSNAEEEEACEKDPATQQA FGQNLDRVVKLINESVDEADMENAGHPSADTPTATNYFLQYISS SLENSTNSADASSNKVFGQNMSESVLSPKLENVSSDANRENA AAESGSESSQEATPEKESLAESAAAYTKATARKCLLEKVEVIT GEEAESNVLMQCKLFVFDKTSQSWVERGRGLRLNDMASTDDG TLQSRISDAGPRGSLR\LI LNTKLWQMIDKASEK\SRITAM DNEDQGVKVLISASSKDTQGVYALHHRILALRSRVEQEQA MPAPEGAAPSNEEDSDDDVLA PGATAAGAGDEGDGQTTS T
6069	583	27	PTRPGQAGSSSMAAQR LGKRVLSKLQSPSRARGPGGSFGLQK RHARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN IDELLELESEERSRKIQGLLSCGKPVEDFIQELLAKLQGLHR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QVPLRQSPSP\DGQPSAPFQGPARTASPLTLLALPPGPPER RPALLCVLSCI
6070	478	858	IRVTVDGEFLHYIFPLQFLDSPW/RFTETHRGRHF\QVTLTAE TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND RVYIGKRYHYDIRLNFYQMSPTPEIRRSPLTQHFNSSRYW
6071	2	1654	HEARTKGNMALARP\VRLFSVLTLLAPRRGLTVRSPEPLPV VRIPVALQRQLEQRQSRRLNLPVLPVLRPGLLVSARRPELNQF ARLTGLRWERAPLASQGWKSRRRARDHFSIERAQEAPAVRKLS SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSSTIPSLLR GRHVVCAAETGSGKTL SYLLPQLRLLG\HPSLDLPIAPRGL VLVPSRELAQQVRAVAQPLGRSLGLLVRLDLEGGHGMRRIRLQLS RQPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLDES FLRLVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ LLNKVASPDVTTITSSKLHCIMPHVKQTFRLKLGADKVAELVH ILKHRDRAERTGPSGTVLVFCNSSTVNWLGYILDDHKIQHLRL QGQMPALMRVGI FQSFQKSSRDILLCTDIASRGDSTGVELVN YDFPPTLQDYIHRAGRVGRVGEVPGTVISFVTHPVDVSLVQKI ELAARRRRSLPGLASSVKEPLQAT
6072	1	742	KMERTEMMPTINSQLEFKSKPFLVSSSRWLVRKGELTAYVEDT VLFSRRTSKQVYFFLNDVLIITKKKSEESYNNVNDYSLRDQLL VESCDNEELNSSPGKNSSTMLYSRQSSASHLFTLTVLSNHANEK VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT AKQPDLSLQVADVLI\YQRVSDGWYEGE\LRDGERGWFPME CAKEITQATIDKNVERMGRLLGLETNV
6073	620	860	PCRRGLARPLSRPG/SILVHCAVGVSRSATLVLAYLMYHHLT LVEAIKKVKDHGRIIPNRGFLRQLLALDRRLRQGLEA
6074	168	1110	PGARCMATELCQCPDSMPCHNQVNSASTPSPEQLRPGDLILDHA GGNRASRAKVIILLTGYAHSSLPALDSGACGSSLNSENGSGG DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE GVKFEKGNCGVS IMRSGEAMEQGLRDCRSIRIGKILIQSDEET QRAKVYYAKFPDIIYRKVLLMYPILOTG\NTVIEAVKVLIEHG VQPSVILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG QKYFGTD
6075	320	1091	PPTCQPEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSHLLGT KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV LRRPQEFVNRTFETVFIWGPSPKMQKPGQSLVRIQAGLVFP NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFMTVIA VELCDHVHVYGMVPPNYCSQRRLQRPYHYEYKGPDECVTYI QNEHSRKGNNHFRFITEKRVSSNAQLYGITFSHPSWT
6076	1721	107	HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV KKPASVSVKSCVSGYTLTELSMHWVRQAPKGLEWMAFDPED GETIYAKQKFGQVMTEDTSTDTAYMELSSLRSEDVAVYCATD HGDIYAFDIWGGQTMVTVSSAPTAPDVFPPIISGCRHPKDNSEV LACITGYHPTSV\TVTWYMGTSQA\QRTFPEIQRRDSYYMTS SQLSTPLQQRQGEYKCVVQHTASKSKEIFRWPESPKAQASSV PTAQPOAEGSLAKATTAPATRNTRGRGEEKKEKEKEEQEERE TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD AHLTWEVAGKVPTGGVEEGLLERHNSGSQSQHSRLTLPRSLWNA GTSVTCTLNHPSLPQRLMALREPAQAPVKLSLNLASSDPPE A\ASWLLCEVSGFPPNILLMWLEDHGEVNTSGFAPARPLPKP\ RSTTFWA\WSVLRVPAPSPQPATYTCVVSHEDSRTLLNASRSL EVSYVTDHGPMK
6077	3687	1268	LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ AGPNCGWCTNSTFLQEGMPTSRCDLLEALKKKGCPDDIENPR GSKDIKKNKNTNRSGTAEKLPEDITQIQPQLVLRSLRGEP QTFTLKFKRAEDYPIDLYLM\DLSSYMKDDLNVKSLGTDLMN EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS PFSYKNVLSLTKNGEVFNELVGKQRI SGNLDSPEGGDAIMQVA VCGSLIGWRNVTRLLVFSFDAGFHAGDGKLGIVLPNDGQCHL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ENMYTMSHYDYDPSIAHLVQKLSNNIQTIFAVTEEFQPVYKE LKNLIPKSAVGTLSANSSNVLIIDAYNSLSSEVILENGKLS GVTISYQSY\CKNGVNGTGNGRKCNSISIGDEVQFEISITSNK CPKDSDSFKIRPLGFTEEEVILQYICECECQSEGIPEPKCH EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCTARKENQ FQKSASNHGRVPSAGQCVCRCRDNTNEIYSGKFCECDNFNCDRS NGLICGGNGVCKCRVCECNPNYTGSAACDCSLDTSTCEASNGQIC NGRGICECGVCKCTDPKFGGQTCCEMCQTCLGVCAEHKECVQCR FNKGEKDTCTQECSEYFNITKVESRDKLPQVQDPVSHCKEKD VDDCWFFYFTYSVNGNNEVMVHVVENPECPTGPDIIPIVAGVAVAG IVLIGLALLLIWKLMI IHDRREFAKFEKEKMNKWDGTGENIY KSAVTTVVNPKEYGK
6078	1425	180	ETEDVMELLEEDLTCTPICCSLFDDPRVLPCHSHNFKCKLEGILE GSVRNSLWRPVFPKPTCRKKTFSYWELIPLQVNYSLKGIKEY NKIKISPKMPVCKGH\LGQPLNIF\CL\TDMQLDL\CGIC\ATR GEHTKHIVFCSIEDAYAQRDAFESLQSFETWRRGDALSRDLTL ETSKRKSLLTKDSDKVKEFFEKLQHTLQKKNEILSDFTMK LAVMAYDPEINKLNTILOEQRMFNIABAFKDVSEPIVFLQOM QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVVK LSLPQDTGTFISKIPWSFYKFLILLLLGLVIVFGPTMFLEWSL FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE RFKNFTLVVLNNVAEFVCKYKLL
6079	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFGLGLSP GVLDRLYGHAPATCLAVFRELPSLAKNWVMRMLFLEQLPQAABA LWVKKEFSKAQEEESTGLSGLRIWHTQLLPGLQGLILNPIFRQ NLRIALLGGGKAWSDDTSQGLPDKHARDVPSLDKYAERWEVVL HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGQFL LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLFQLSPSTLGKD YSVEGMSDLSLLNLQHLREFGLVFORKRKSRYYPT/RALAINL SSGVSAGGTVHQPGFIV\VETNYRLYAYTESELQIALIALFSE MLYPPF\NMVV\ARVTR\ESVQQAIASGITAQQIIHFLRTRAHP VMLKQTPVLPPTITDQIRLWELERDLRFTBGVLYNQFLSQVDF ELL\LAHAPKLGVLVFE/NTPAKRLMVVTPAGHSDVKRFWRQK HSS
6080	1	1199	IETIDHVGFEFAMAAQAGVSRQRAATQGLGSNQNALKYLQDQFK TLRQQLDSGLVFKDPRFPACPSALGYKDLGPGSPQTQGIWKR PTELCPSPQFIVGGATRTDQCQGLGDCWLLAAIASLTLNEELL YRVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR LPTKNGQLFLHSEQGFNFWSALLEKAYAKLNGCYEALAGGSTV EGFEDFTGGISEFYDLKKPPANLYQIIRKALCAGSLLGCSIDVY SAAEAIAITSQKLVKSHAYSVTGVEBNFQGHPEKILRLRNPWG EVEWSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFWMSLSDFVR QFSRLIICNLSPDSLSSSEEVHKWNLVLFNGHWTRGSTAGGCQNY PGSS
6081	3	865	EMLPDLLPLPLLWA/GALAQDARFRLEMPESVTQEGLCIFVHC SVFYLEYGKWDSTPAYGHWFRREGVSVDQETPVATNNSQKVQKE TQGRFHLGDPFRNNCSLSIRDARRRDNNGSYFFWVARGRTKFSY KYSPLSVYVTALTHRPDILPEFLKSGHPSNLTCSPVWVCEQGT PPIFSWMSAAPTSLGPRTLHSSVLTIIIPRQDHGTNLICQVTFP GAGVTERTIQLSVSWKSGTVEEVVVLAVGVVAVKILLCLCLI ILSFHKKKAVRAVEVEENVYAVMG
6082	283	1288	EARSFGPTQTRTAPGLAAGLAQPAALRLLSRPPSAAMDGDGD PESVGQPEEASPEEQPEEASAEERPEDQEEAAAAA\Y\LD LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL LKCCQEGLVPEGGVEEERDHWQFYFLSKRRRNLRLNPGCEEDL EGWCDVEHGGDGWRVEELPGDSGVEFTHDESVKYFASSFEWCR KAQVIDLQAEGYWEEELDTTQPAIVVKDWYSGRSDAGCLYELTV KLLSEHENVLAEFSSGQVAVPQSDSGGWMEISHTFTDYGPGVR FVRFEHGGQDSVYKGFARVTNNSVWVEP
6083	1865	309	KQWCAERRGLGMSLADELLADLEEAABEEEGGSYGEEEEPAAIE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DVQEEETQLDLSGDSVKTI AKLWDSKMPAEIMMKIEEYISKQAKA SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR FPELES LVPNALDYIRT VKELGNSLDKCKNNENLQQILT NATIM VVSVTASTTGGQQLSEEELEERLEEACDMALELNASKHRIY EYVE SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPFVSAP\DL RRKAARLVA AKCTLAARVDSFHSTEGKVGYELKDEIERKFDKW QEP PPVKQVKPLPAPLDGQRKKRGGRYRKMKERLGLTEIR\KQ ANRMSFGEIEEDAYQEDLGFSGLHGLKSGSGRVRQTQVNEATKA RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI VNPQAAEKKVAEANQKYFSSMAEFLKVKGKSGLMST
6084	1865	309	KQWCAERRGLGMSLADELLADLEAAEEEEEGSSYEEEEEPATE DVQEEETQLDLSGDSVKTI AKLWDSKMPAEIMMKIEEYISKQAKA SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR FPELES LVPNALDYIRT VKELGNSLDKCKNNENLQQILT NATIM VVSVTASTTGGQQLSEEELEERLEEACDMALELNASKHRIY EYVE SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPFVSAP\DL RRKAARLVA AKCTLAARVDSFHSTEGKVGYELKDEIERKFDKW QEP PPVKQVKPLPAPLDGQRKKRGGRYRKMKERLGLTEIR\KQ ANRMSFGEIEEDAYQEDLGFSGLHGLKSGSGRVRQTQVNEATKA RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI VNPQAAEKKVAEANQKYFSSMAEFLKVKGKSGLMST
6085	2	1456	SGPRSFQGNRAVGRISLGGKRNFEVTL LPGVSSERVRWRARV GVARVKGPNPWKPSPATQVPR/VPAQVYLPGRGPPLRGEELVM DEEAYVLYHRAQTGAPCLSFDIRDHLGDNRTLP LTLYLCAQT QAESAQSNRLMMLRMHNLHGTPPPSEGSDEEEEEDEDEEER KPQLELAMVPHYGGINRVRVSWLGEFPVAGVWSEKQVEVFALR RLLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPR VTGRLLTGDCQKNIHLWTP TDGGSWHVDQRFVGHTRSVEDLQW SPTENTVFASCSADASIRIWDIRAAPSKACMLTTATAHDGDDNVV ISWSRREPFLSGGDDGALKIWDLRQFKSGSPVATFKQHVAPVT SVEWHPQDSGVFAASGADHQITQWDLG/IVERDPEAGDVEADPG LADLPQQLLFVHQGETELKELHWHQPCPGLLVSTALSGFTIFRT ISV
6086	2419	1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGF RV YNTDPLKEKEKEQEFLEGGVGHVEMLFRCNYLALVGGGKPKYP NKVMIWDDLKKTIVIEIEFSTEVKAVKLRR\DKIVVLD SMIKV FTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSLLAFPGHTG HVQLVDLASTEKPPVDIPAHEGVLSIALNLQGTRIATASEKGT LIRIFDTSSGHLIQELRRGSQAANIYCINFNQDASLIVSSDHG TVHIFAAEDPKRNKQSSLASASFLPKYFSSKWSFSKFQVPSGSP CICAFTGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT DDKL
6087	476	1877	QNSQRTGLPITIFSRSPFLLTGSDLCENMPCTCTWRNWRQWIRP LVAVIYLVSI VVAVPLCVWELQKLEVG IHTKAWFIAGIFLLTI PISLWVILQHLVHYTQPELQKPIIRILWMPVIYSLDSWIALKYP GIAIYVDTCRECYEAYVIYNFMGFLTNLTNRYPNLVILEAKD QQKHFPPLCCPPWAMGEVLLFRCKLGVLYTTVVRPFTTIVALI CELLGIYDEGNFSPNAWTLVLIINMNSQLFAMYCLLLFYKVLK EELSPIQVPGKFLCVKL VVFSFWQAVVIALLVKGVISEKHTW EWQTV EAVATGLQDFIICIEMLAAIA\HHYTF SYKPYVQEAEE GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKLPEDQ DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFHTVTPTQTP TTA KISDEILSDTIGEKKEPSDKSVDS
6088	1684	689	GASGLVRLLOQGHRCCLLAPVAPKLVPPVRGVKKGFRAAFRQKE LERQRLLRCP PPPVRSEKPNWDYHAEIQAFGHR LQENFSLDLL KTA FVNSCYIKSEAKRQQLGIEKEAVLNLKSNQELSEQGT SF SQTCLTQFLEDEYPMPTGINKLVDFLTGEEVVCHVARNLAVE QLTLSSEFPVPPAVLQQTFFAVIGALLQSSGPRTALFIRDFLI QTMTGKELFEMWKIINPMGLLVBELKKRNVSAPE SRLTRQSG\A

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PTALPLYFVGLYCDKKLIAEGPGETVLVAEEAARVALRKLYGF TENRRPWNYSKPKETLRAEKSITAS
6089	3	3054	TRLGIPGSTISSRRLCALAAEGHFLGHSWTGSRAGAHTGAPAW PSRRLRDLPAAGMMRLRRRAVACEVCQSLVKHSSGIGKSLPLQK LHLVSRSIYHSHPTLKLQRPQLRTSQQFSSLTNPLRLKLFKS PIKYGYPQRRNFWPARLATRLLKRLYLILGSAVGGGYTAKKTFD QWKDMIPDLSEYKWIVPDIVWEIDYIDFEKIRKALPSSSEDLVK LAPDFDKIVESLSLLKDFFTSGSPTEAFRATDRGSESDEKHFKE VSDKEKIDQLQEELHHTQLKYQRIERLEKENKELRKLVLQKDD KGIPFIESLRKSLIDMYSEVLDVLSYDASINTQDHLPRVVVVG DQSAGKTSVLEMAIQAIRIFPRGSGEMMTRSPVKVTLSEGPHEVA LFKDDSSREFDLTKEEDLAALRHEIELMRKNVKEGCTVSPETIS LNVKGPGLQRMVLVDLPVINTVTSGMADPTKETIFSISKAYMQ DPNAIILCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTKVLD AEKNVASPSRIQQIIIEGLFPKALGYFAVVTGKGNSSIESIEAI REYEEFFQNSKLLKTSMLKAHQVTTRNLSLAVSDCFWKMVRES VEQQADSFKATRFNLETEWKNYPRLELDRLNELFEKAKNEILD EVISLSQVTPKHWEIILQQSLWERVSTHVIENIYLPAAQTMNSG TFNTTVDIKLKQWTDKQLPNKAVEVAVWETLQEEFSRFMTPEPKGK EHDDIFDKLKEAVKEESI KRHKWDFAEDSLRLVIQHNALEDRI SDKQQWDAAIYFMEALQARLKDTENAIENMVGPD\WKRWLYW KNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLE SRGVEVDPSLIKDTWQVYRRHFLKTALNHCNLCRRGFYYYQRH FVDSLELCNDVVLFWRIQRLAITANTLRQQLTNTVEVRLKENV KEVLEDAEDGEXKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE ALHQEK
6090	194	1560	PVFVPAPGAVLEQAS/ASPPLATQTVVPLQHKCIPQLFVQASTL FELQLFFCQIALFVHYINIKTVWVYPPSHPSHTSLNFHLID FNLLMVTITVLGRRFISIVKEASQGRKVSLSRILFLTRFTV LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHVSFAAELR P\RKTSLFNHHMAMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSML SAYYVAFVPVWFVNTHYYDKRWSCLEFLLVSISTSVILMQHLL PASVCDLLHKAHAHLGCWQKVDPALCSNVLOHPWTEECMWQGV LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFSSKPLRLILNILL LEGAVIVYQLYSLSMSSEKWHQITISLALILFSNYAFAFKLLRDL VLGKAYSYSASPQRDLDRHS
6091	3279	412	SSRTREMEKEILRRQIRLLQGLIDDYKTLHGNAAPAGTPAASG WQPPTYHSGRAFSARYPRPSRRGYSSHGSPSWRKYSLVNRPFG PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVLSQGNVVIK VKPPSKSGSASASGAQRGSLEEFEDTPWSDORPREGEGERPRGQ LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKS SVGSVGDSPRE PRRTVSESVIAVKASFPSSALPRTGVALGRKLGSHSVASCAQ LLGDRRVDAGHTDQVPVSGSVGGPARPASGPRQAREASLVVTCR TNKFRKNKYKWAASSKSPRVARRALS PRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPVAGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKT PNKGLVQVTTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPT SKVI KTRYRIVKKT PASPLSAPFFPLSLPSWRA RRLSLSRSLVNLRLRPVASGGGKAQPGSPWWSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLRTGRLDPAGSCSRSLASRAVQ RSLAIRQARORREKRKEYCMYNNRFGRCNNGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPPFSHHVSKEKMPVCSYFLKGICNSN CPYSHVYVSRKAECSDFLKGYCPLGAKCKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRAATSPAPGPSDATARSRVASASHG PRKPSASQRPTRQTPSSAALTAAVAAPPHCPGGSASPSSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL
6092	143	3190	AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ EVFKPENISLRNKLRELCVKLMFLHPVDYGRKAEELLWRKYYIE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VIQLIKTNKKHIHSRSTLECYRTHLVAGIGFYQHLLLYIQSHY QLELQCCIDWTHVTDPLIGCKKPVASAGKEMDWAQMACHRCLVY LGDLSRYQNELAGVDTELLAERFYYQALSVAQIGMFPNQLGTL AGSKYYNVEAMYCYLRICQSEVSFEGAYGNLRLDYKAAKMYHQ LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLQPKSSSVSESL TSLCQSVLEDFNLCLFYLPSNPNSLASEDEEYESGYAFPLPDL LIFQMVIICLMCVHSLERAGSKQYSAATAFTLALFSLHVNHNVI RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEDPEPPPVPT PQVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSH SARASEGSDSGDKSLEGGGTAFDAETDSEMNSQESRSDLEDME EEEGTRSPPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ MFQTKRCFRLAPTFSNLLLOPTTNPHTSASHRCPVNGDVKPSE PASEGSESESGESSGRSCRNERSIQEKLQVLMAGELLPAVKVF LDWLRTNPDLLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA LCPEVQDLLEGCELPDLPSSLLLPEDMALRNLPLRAAHRFRNF DTDRLPLSTLEESVVRICIRSFHFIA RLQGSILQFNPEVGIF VSIAQSEQESLLQQAQAQFRMAQEAEARRNRLMRDMAQLRLQLEV SQLEGSLLQPKAQSA MSPYLVPDQALCHHLPVIRQLATSGRFI VIIPRTVIDGLDLLKKEHGPARGDGI RYLEAEFKKGNRYIRCKQE VGKSFERHKLKRQDADAWTLYKILDSCKQLT\LAQGAGEEDPSG MVTIITGLPLDNPSLLSGPMQALQAAHASVDIKNVLDIFYKQW KEIG
6093	76	1002	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL PPVPCCLGCLAERWRLRPAALGLRLPGIGQRNHCAGKAAPR\ PAAGAGAAAEAPGGQWGPASTPSLYENPWTIPNMLSMTRIGLAP VLGYLIEEDFNIALGVFALAGLTDLDDGFIARNWANQRSALGS ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDMVLI AAVF YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVQLILVA ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV IKD
6094	23	1010	PFLRCLRGDQKAKMSERKVLNKKYPPDFDPSKIPKLLPKDRQY VVRLMAPFNMCRCKTCGEYIYKGGKFNARKETVQNEVYLGLPFR FYIKCTRCLAEITFKTDPENTDYMTEHGATRNFAEKLLEEBEK RVQKEREDEELNPMKVLENRTKDSKLEMEVLENLQELKDLNQR QAHVDFEAMLRQHRLSEBERRRQQQEEDQETAALLEARKRRL LEDSDSEDAAPSPLQPALRPNPTAILDEAPKPKRKVEVWEQSV GSLGSRPPLSRLVVVKKAKADPDSCNSGQPQA/APHPRSPAQEGB GQPYTPDAWRVLPPTGCI PGQ
6095	1	1599	TRGRAAERSRGRGHGFLGGGFA\SVVDYFPSEDYRCGYCKNES GSRNGMWAHSMTVQDYQDLIDRWRRSGKYVYKPMNQTCBPQ YTIRCRPLQFPQPSKSHKKVLKMLKFLAKGEVPGKSGE\DEPMD STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGKNSKKE EPQELLQSQDFVGEKLGSGEP SHS

TRADCS:1416257.1(%CSH01.DOC)

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VKVHTVPKPGKGADLSKPPCRKAKETRKBRKRLKLMQQNPAGEL EGFQAQGHPPSLFPPKAKSNQPKSLEDLIFESLPENASHKLEVR VVRSSPPSSQFKATLLESYQVYKRYQMVIHKNPPDTPTESQFTR FLCSSPLEAETPPNGPDCGYGSFHQQYWLGDGKIIAVGVIDILPN CVSSVLYLDPDYSFSLGVSALREIAFTRQLHEKTSQLSYY MGFYIHSCPKMKYKQYRPSDLLCPETYVWVPIEQCLPSLENSK YCRFNQDPEAVDEDRSTEPDRQLQVFHKAIMPYGVYKKQKQDPS EEAVALQYASLVGQKCSERMMLFRN
6096	2277	575	QRVRAALLSSAMEDSEALGFHEMGLDPRLLQAVTDLGWSRPTLI QEKAIPALLEGKDLLARARTGSGKTAAYAI PMLQLLLHRKATGP VVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVVRVANVSAA EDSVSQRAVLMEKPDVVVGTPSRILSHLQQDSLKLKRDSELLVV DEADLLFSFGFEEELKSLCHLPRIYQAFILMSATFNEDVQALKE LILHNPVTLKLQESQLPGPDQLOQFQVVCETEEDKFLLYALLK LSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGBLPLRSR CHII SQFNQGFYDCVIATDAEVLGAPVKGKRGRGPKGDKASDP EAGVARGIDFHHVSAVLNFDLPPTPEAYIHRAGRTARANNPGIV LTFVLPTQFHLGKIEBLLSGENRGPIILPYQFRMEEIEGFRYR CRDAMRSVTQAIAREARKETKEELLHSEKLTTFEDNPR\DLQ LLRHDLPHPAVVKPHLGHVDPDYLVPALRGLVRPHKK\GRSCL PLVGRPREQSPRTHCAASSTKERNSDPQSPPEVVGPLWS
6097	1673	192	APGTMSGGKKKSSSQITSVTTDYEGPGSPGASDPPTPQPTGPP RLPNGEPSDPDGGKGTFRNGSPPPGAPSSRFVRVVKLPHGLGEP YRRGRWTCVDVYERDLEPHSFGGLLEGIRGASGGAGGRSLDSRL ELASLGLGAPTPPSGLSQGPTSWLRPPPTSPGPQARSFTGGLGQ LVVPSKAKAEKPLSASSPQRPPEPETGESAGTSRAATPLPSL RVEAEAGGSGARTPPLSRRKAVDMRLRMELGAPEEMGQVPLDS RPSSPALYFTHDASLVHKSPPDFGAVAAQKFSLAHSMIAISGHL DSDDDSGSGSLVGIDNKIEQAMDVLKSHLMFAVREEVEVLKEQI RELAERNAALEQENGLLRALA\ SPEGQLGSAGPPRGVPR\LGPPA PNGPFVLSLPSLTIVPLGLPLASAAWPPPLMPALIVPVFPVG VQALSNQWSPGFLPHLLIIPSLDGGGEGFRTGRQQGAFFGEET QPPPSLPGTPQQ
6098	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETS DTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSEKCAQQRQK RLNASQRSSSLPSPNRKSSPTKREIMLTPVTVAYS PKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEVPNGVKVSVR TAWKKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALS RMPSPGGRITLQTRLNQEAFGRSFGKD
6099	168	1074	NYCLRHRSPLEKDSSPGSSSTSLLIKKQRETS DTPIMRALKELD EGKIFKNWGTQTEKEDTSNINPRQTETSVNASRSEKCAQQRQK RLNASQRSSSLPSPNRKSSPTKREIMLTPVTVAYS PKRSPKE NLSPGFSHLLSKNESSPIRFDILLDDLDTPVSTLQRTNPRKQL \QFLPLDDSEEK\TYSEKAT\DNIVNHSSCPEVPNGVKVSVR TAWKKNKSVSYEQCKPVSVTPQGNDFEYTAKIRTLAETERFF\D ELTKEKDQIEAALS RMPSPGGRITLQTRLNQEAFGRSFGKD
6100	2	713	FVEVSGYRSRADPEPRGRDTPYAYLFKYYIIIGDTGVGKSCLL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF RSITRSYYRGAAGALLVYDI TRRET FNHLTSWLEDARQHSSSNM VIMLIGNKSDLESRRDVKREGEAFARE\HGLIFMETSAXTACN VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP SASQRNSRDIGSNAGCC
6101	1	1399	FRGRAWPLREVSHWLGRRVCSWSASWGRPLPALSARLSPLLA FKMVFPLSCAVQYAWGKMGSNSEVARLLASSDPLAQIAEDKPY AELWMGTHPRGDAKILDNRISQKTL SQWIAENQDSLGSVKVDTF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NGNLPFLFKVLSVETPLSTIQAHPNKELAEKHLQAPQHYPDANH KPEMAIALTPFQGLCGFRPVVEIIVTFLKKVPEFQFLIGDEAATH LKQTMSHDSQAVASSLQSCFSLMKSEKKVVVEQLNLLVKRISQ QAAAGNNMEDIFGELLQLHQYYPGDIGCFAYFLNLLTLKPG AMFLEANVPAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE MLSYPSSSKDRFLPFRSQEDPYLSIYDPPVPDFTIMKA\BVP G\SVTEYKDLALDSASILMVQGTVIASPTPTTQTPILQRRGVL FIGANESVSLKTEPKDLLIFRACCLL
6102	70	2415	QTPQATLAANGAEDSRGGEMPLPAGEIGASPAAPCCSESGDERKN LEEKSDINVTVLIGSKQVSEGTNDGDLPSYVSFAFIEKEVGNLKL SLKKLDKLEIQRVTVMQLEEQVLTISSEIPKRIRSAKNAEES KQFLNQFLEQETHLFSAINSHLLTAQPMDDLGTMSQIEIER HLAYLKWISQIEELSDNIQOYLMNNVPEASTLVMAELDIKL QESSCTHLLGFMRAVTKFHHKILDKLTSDFEILAQHLWPFIA PPQSQTVGLSRPASAPEIYSYLETLFCQLLKLQTSHELLTEPK\ HSQKNTLFLPPLLSS/WPIQVMLTPLOKFRFHYFRGNRQTNVLS KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSVFNARLEFSRG LMMVLLEKLATDIPCLLYDDNLFCHLVDEVLPERELHSHVHGYP GTFASCMHILSEETCFQRWLTVERKFALQKMDMSLSSEAAWVSQ YKIDITDDEMKVPCDAETFMILLVITDRYKNLPTASRKLOFLE LQKDLVDDFRIRLTQVMKEETRSLGFRYCAILNAVNIYSTVLA DWADNVFFLQQAALVFAENNTLSKLQGLQASMESSVFDMM INLLERLKHDMLTRQVDHVFREVKDAKLYKKERWLSLPSQSEQ AVMSLSSSACPLLLTLRDHLLQLEQQCLCFSLFKIFWQMLVEKLD VVIYQEIILANHFNEGGAQQLQFDMTRNLFPFLSHYCKRPNFY KHIKEACIVLNLNVGSALTAGKDVLPVQLQGSFPAT
6103	207	2523	ESNSTMTTYLEFIQNEERDGVFSWNVWPSRLEATRMVVPVA ALFTPLKERPDLPPIQYEPVLCSTRTTCRAVLNPLCQVDYRAKLW ACNFCYQRNQFPSPYAGISELNQPAELLPPQFSSIEYVVLGRGPM PLIFLYVVDTCMEDELQALKESMQMSLSLLPPTALVGLITFGR MVQVHELGCBGISKSYVFRGTDLKSAKQLQEMGLSKVPVTQAT RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRPWPVPQGR PLRSSGVALSIAVGLECTFPNTGARIMMFIGGPATQGPGMVVG DELKTPIRSWHIDDKDNKYVKKGTKHFEALANRAATTGHVIDI YACALDQTLGLEMKCCPNLTGGYVMVMGDSFNTSLFKQTFQRFVT KDMHGQFKMGFGGTLEIKTPR\BIKISGAIGPCVSLNSKGPCVS ENEIGTGGTCQWKICGLSPTTTLAIYFEVNVQHNAPIPQGG\RG A\IQFVTQY\QHSSGQRRIRVTIARN\WADAQTQIQNIAASFD QEAAILMARLAIYRAETEGPDVLRWLDRQLIRLCQKFGYEHK DDPSSFRFSETFSLYPQFMFLRRSSFLQVFNNSPDESSYYRHH FMRQDLTQSLIMIPIYAYSFGPPPEPVLLDSSSILADRILLM DTFFQILYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGQES GAPILTDVSLQVFMHKLKLAUSSAA
6104	124	732	KVSEYIILSKDKILFHALAMLVLVSPWSAARGVLRNYWERLLR KLQSRPGFPSPWGPALAVQ\AQPCLOSQQMIPVEVKRI/RS LDSIFWMAAPKNRRTIEVNRERRRNPQKLKVKNNIDVCECGH LKQKHVLCAYCYEKVKETAERRQIGKQEGGPFKAPTITVVL YTGETPSEQDQGRKRIIERDRKRPSTFTQ
6105	3	989	PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAPVLLLLLFC GSQRKAATAACGRPRMLNRMVGGQDTQEGEWQVSVIQRNGSHF CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM YARVRQVESNPLYQGTASSADVALVEAPVPFTNYILPVCLPD PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR CNLLYSKDTEFGYQPKTIKNMCLCAGFEKGKDKACKGDSAGPLV CLVQGSWLQAGVISWGECCARQNRPGVYIRVTAHNNIHRIPK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6106	3	1302	LQVQPSSEVGRPEVTTPPGPGAP GRPPTAPHTGRPPTANRGDPRDLKRGCARLLTSIESRGRPAAS AGLRRDRCALRRWPLRRAPLARATRRRAGSPRRCAPRPRACPG WSRARHQPQGLCLLLLLLQCFMEDRSAQAGNCWLRQAQNGRCQV LYKTELSKEECCSTGRLLSTSWTEEDVNDNTLFKWMIFNGGAPNC IPCKETCENVDCGPGKKCRMKNKPRCVCAPDCSNITWKGVPVC GLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRDVFCPS STCV\VDQTNNAVCVTCNRICPEPASSEYQLCGNDGVTYS\SAC HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLWDFKV GRGRCSLDELCPDSKSDPEVCASDNATYASECAMKEAACSSGV LLEVHSGSCNSISEDTEEEEEDEDDQYSFPISILEW
6107	623	168	SRCSSPRPEPGRGRGK/LSPSEHRRKWVEVFKACDEHKGYSRE DFKTA VVMFLPGYKPSKIEVD SVMSSINPNTSGILLGFLNIVRK KKEAQR YRNEVRHIFTAFDTYYRGFLTLED FKKAFRQVAPKLPE RTVLEVFREV\DRDS\DGHVSF
6108	3	1348	GGSLRFSPFRVPFSCSRVFCPVPPGGCGLSPMSASRPQSPTTPW CLPRRYMKHKRDGPEKQDEAVDVTVMTCVFFVMCCSMLVLL YYFYDLLVYVYVIGIFCLASATGLYCLAPCVRRLP\SASAGESA LLAPTIPNNSLPYFHKRPQARMLLLALFCVAVSVVWGVFRNEDQ WAWVLQDALGIAFCLYMLKTI RLPTFKACTLLLLVLFYDIFV FITPPLTKSGSSIMVEVATGPSDSATREKLPMVLKVPRLNSSPL ALCDRPFSLGFGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI AYGVGLLVTFVALALMQRGQPALLYLPCTLVTS CAVALWRREL GVFWTGSFGFAKVLPPSPWAPAPADGPQPPKDSATPLSPQPPSEE PATSPWPAEQSPKSRSTSEEMGAGAPMREPGSPAESSEGRDQAQPS PVTQPGASA
6109	1	1381	CRSRAGAASGGAILGKTLRRQRVDTNKPLDPLVPSALRAAMLY LEDYLEMIEQLPMDLRDRFTEMREMDLQVQNMADQLEQRVSEFF MNAKKNKPEWREEQMASIKKDYKALEDADEKVLQANQIYDLVD RHLRLDQELAKFKMELEADNAGITEILERRSLELDTPSQPVNN HHAHSHTPVEKRYNPTSHHTTTDHIPEKKFKSEALSTLTSDA SKENTLGCRRNNNSTASSNNAYNVNSSQPLGSYNIGSLSSGTGAG GI\TMAAAQAVQATAQMKEGRTSSSLKASYEAFKNNDFQLGKEF SMARETVGYSSSSALMTTLTQNASSSAADSRGRKSNNNKSSS QQSSSSSSSSSLSSSSSSSTVVQEISQQTTVVPESDSNSQVDWT YDPNEPRYICINQVSYGEMVGCDDTQDCPIEFHYGCVGLTEAPK GKWYCPQCT\AAMKRRGSRHK
6110	77	2464	ACPSAATMSDQDHSMDMTAVVKIEKGVGGNNGGNGGGGAFSQ ARSSSTGSSSSSTGGGGQESQPSPLALLAATCSRIESPENENSNS QGSPSQSGGTGELDLTATQLSQGANGWQIISSSSGATPTSKEQSG SSTNGSNGSESSKNRTVSGGQYVVAAPNLQNNQVLTGLPGVMP NIQYQVPIPQFQTVGQQLQFAATGAQVQDQSGQIQIIPGANQQ IITNRGSGGNIIAAMPNLLQAVPLQGLANNVLSGQTQYVTVNP VALNGNITLLPVNSVSAATLTPSSQAVTISSSGSQESGSQPVTS GTTISSASLVSSQASSSSFFTNANSYSTTTTTSNMGMNFTTSG SSGINSQGTQPRVSGGLQGS DALNIQQNQTSGGSLQAGQQKBE Q\NQQTQAAAPKSLSRPQLVQGG\QALQ\AFQAAPLSGQTFTTQA ISQETLQNLQQLQAVPNSGPIIIRTPTVGPNGQVSWQTLQQLNLQ VQNPQAQTITLAPMQGVSLGQTSSSNTTLTPIASAASI PAGTVT VNAQLSSMPGLQITINLSALGTSGIQVHP IQGLPLAIANAPGDH GAQLGLHGAGGDIHDDTAGGEEGENSPDAQPQAGRRTREACT CPYCKDSEGRSGDPGKKKQHI CHIQGCGKVYKGTSHLRAHLRW HTGERPFMCTWSYCGKRFTSRDELQRHKTHTGEEKKFACPEC PK RFMRSDHLSKHIKTHQNKKGPGVALSVGTLPDLSGAGSESGT ATPSALITTNMVAMEAICPEGIARLANSGINVEKGGQFCSPINT SANGF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6111	1637	797	RVDPRVRGAMAPWGKRLAGVRGVLLDISGVLYDSGAGGGTAIAG SVEAVARLKRSRLKVRFCNTESQKSRAELVGQLQRLGFDISEQE VTAPAPAAQCILKERGLRPYLLIHGCV\ASEFDQIDTS/STPNC VVIADAGESFSYQNMNNAFQVLMLEKPVILSLGKGRYYKETSQ LMLDVGPYMKALEYACGIKAEVGGKPSPEFFKSALQAIGVEAHQ AVMIGDDIVGDVGGACQRCGMRALQVRTGKFRPSDEHHPEVKADG YVDNLAEAVDLLQHADK
6112	77	196	MSSHKSFKSKRFLAKKQKPNRPILQWILWLTGNKIRHNWK
6113	1779	567	WEGRSWAACGVNLQGAWGERSGVRASEAESPGKRAVSWWSRQL ETMVDHLANTEINSORIAAVESCFGASGQFLALPGRVLLGEGVL TKECRKKAKPRIFFLFNDILVYGSIVLNKRKYRSQHIIPLEEV TLELLPETLQAKNRMIKTAKKSFVVSAAATERQEWISHIECV RRQLRATGRPA\STEHAAPWIPDKATDTCMRCTQTRFSALTRRH HCRKCRVVVCAECRQRFLPRLSPKPVVRVCSLCYRELAAQQRK EEAEQAGVPRAAASHLARPICGRPVEMTMTPTTRRAAGTATG PAAWSSTPRGWPLPSTADPRPAEHLSPSLHCPGPGQEGSSRSC PGLRDPPIPWQVQRWGVALSGLPVFFCWTLCPYGFTAGNAFFPR KPQNTHRSW
6114	818	246	PTSRPRPSFGSPAMSWACVSAAPSSSWPSSSWPCGPRRCCTR RRRCSPRCGLAAGSMCSCSPSWRCTPVPAWSPPPP\PAEQVQC GHLPPHADRRALRLPVAAPARGPGPHGAPGAPRPARTPPASP HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTRTREDMLGRGSQVT GRPQWFLRGLVLFSL
6115	324	71	DVCGRVCAHPHLYTHIHMHCAC\IHTHAQLC/ITASHALAH SHLYTCMVMLTASHTPSHTPHPTAVHKEHRADVLRLTTLPLR
6116	595	1430	TGVMPFPGRWAA/ISSSGPVFEGARA\LQTVKKEEEDSYTPVQ AARQTLNRPGQELFRQLFRQLRYHESGPLETSLRLRELCRW LRPVLSKAQILELLVLEQFLSILPGELRVVQLHNHPESGEE\L WPCWRSCRGTLMGHPGGTRALP\EPRCALDGYRS\LRSAQIWSL ASPLRSSALGDHLEPPYEIEARDFLAGQSDTPAAQMPALFPRE GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSDQEWGLDSAQRN LYRDVMLENYRNMAISLGK
6117	1433	222	VGVSPFAPPCSWEVGPGGWTGPIIKEGQGGRRTPLLLLATRTR GLLSLFPFAAMHPAAPPFPVVAAVLWGAAPTRGLIRATSDHNA SMDFADLPALFGATLSQEGQLQGLVEAHPDNACSPIAPPPAPV NGSVFIALLRRFDCNFDLVLNAQKAGYGAADVHNVNSNELLNM VWNSEBIQQQIWIPIPSVFIGERSSEYLRALFVYKGARVLLVPDN TFPGLYYLIPFTGIVGLLVAMGAVMIARCIQHRKRLQRNRLTK \EQLKQI\PTHQYQKGDQVDVCAICLDEYEDGDKLRVLPCHAY HSRCDPWLTPQTRKTCPICKQPVHRGPGDEDEQEETQCGEEGDE GEPRDHPASERTPLLGSSPTLPTSFGLAPAPLVFFPGPSTDPPL SPPSSPVILV
6118	1044	247	STISCRACSTGATPGAQSHRSARGHAAGGKETAALGMRGKVKK KEKETQKEKIGKEGKEEKVKRKEVEQKIKQEKQEKQERRK GK EKEEKRTKQKGTNKEKEQFKGQEEKGENKDSLTTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFVSGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II
6119	1217	462	DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRVWTSAPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLNGVLTIVLEEDGTAVDSBDFQLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSDIARFTFDVYKQNPRL FGLSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ GLGHMLLGISSTLRHAVEGAEQWQKGRLSHY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6120	785	179	LERAGGGGLSSRALVGSAGCLSLVARANGKGLPRGRKEFVRAVR VRYVAFPRYRTPRAVCLRLWSCRREVIMSGRGKQGGKVRAKAKSR SSRAGLQFPVGRVHRLRLKGNVAERVGAGAPVYLAHVLEYLTAE ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLKGKVTIAQG G\VLNPIQAVLLPKKTESQKDEGANDP
6121	1612	107	FVRAQARGSRQPVRRPLLGAGSRRLCRSCGRMEPLKVEKFATAN RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE KLMRCSQCRVAKYCSAKCQKAWPDHKRECKLKSCKPRYPDS VRLGRVVKLMDGAPSESEKLYSYDLESNINKLTEDKKEGLR QLVMTFQHFMRREEIQDASQLPPAFDLPEAFKVICNSFTICNAE MQEVGVGLYPSISLNLHSCDPNCSIVFNGPHLLRAVRDIEVGE ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAISSNSERL PDINIYQLKVLDCAMDACINLGLLEALFYGTRTMEPYRIFFPG SHPVRGVQVMKVGKLQLHQGMFQAMKNLRLAFDIMRVTHGREH SLIEDLILLE/AMRRQHQSIILRERSQREIRRVSLNALLRSHT LCFVSCVNLVSYWKFCSVVF
6122	2	2324	RFRKMDGGAASQDESSAAAAAADSRMNNPSETSKPSMESGDG NTGTQTNGLDFQKQFVPVGGAISTAQAQAFGLHGHQVQLAGTSL QAAQSLNVQSKSNEESGDSQQPSQPSQQPSVQAAIPQTQLMLA GGQITGLTLTPAQOQLLQQAQAQALAAVQQHSASQQHSA GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQLNLQQFV LVHPTNLQPA\QFIISQTPQGGQGLLQA\QNLLTQLPRQSQA NLLQSQPRI\TLTSQPATPTCTIAATPIQTLPSQSTPKRIDTSL LEEP\SDLELEQFAKTFKQRRIKLGF\QGDAGLAMVKLYGND FSPTTIFRFEALNLSFKNMCKLKLPLEKWLNDENLSSDSSPSALNSPGIEGLSRRRKKRTSIEA\NIRVALEKSFLN\QKPTS BEITMIADQLNMEKGVIRVWFNRRQKEKRINPPSSGG\TSSSP IKAIFPSPTSLVATTPSLVTSAAATTLTVSPVPLTSAAVTNLS VTGSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA SSASESTTTQTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPFKG AAQLPANASLAAMAAAAGLNPSILMAPSQFAAGGALLSLNPGTSL GALSPALMSNSTLATIQALASGSLPITSLDATGNLVFANAGGA PNIVTAPLFLNPQNLSLLTSNPVSLVSAASAGNSAPVASLHA TSSTAESIQNLSLFTVASASGAASSTTTTASKAQ
6123	3	2944	HLLHRWFQTDQMNFMTTGEFQLTEACPYLGTHSEESRFGILHL HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG ARELLKVGGRLPAGGSLRFKVPESLMDCCRQLKDSKQILSIT KNFKVENIGPLPITVSSSLKINGYNCQGYGFVLDCHQFSLDPNT SRDISIVFTPDFTSSWVIRDLVTAADLEFRFTLNVTLPHHLL PLCADVVPGPSWBESEFWRLTVFFVSLSLGVILIAFQQAQYIIM EFMKTRQRQNASSSSQONNGPMDVISPHSYKSNCKNFLTDTYGPS DKGRGKNCLPVNTPQSRIQNAKRSPATYGHSSQKHKKSVMYYSK HKTSTAASSTSTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIIVFSNPSSECS MKEGIQTCMFPKETDIKTSSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQDLPETSRKNGNQQVPVKNEVDHCENLKKVDTK PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGLN QNLNWSKSRTCRKNKKRGVAPVSRPPQSCLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREABGYQKPEK KCVDFKCSDDSSDCGSSSGSVRASRGWSWSSTSSSDGDKPM VDAQHFLPAGDSVSQNDFFSEAPISLNLSHNICNPMGTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVQIESAPVHNSFIDWSATCEGQFSSAYCPLELNDYNAPP EENMNYANGFPCCADVQTDIDHNSQSTWNTPP\NMPAS\WGNA QFPSSSRPYLKSTPKACLPMGSLFGPI\WAP\QSDVYENCCPIN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAVMNLDIWT\TA NRNANFPLSRDSSYCGNV
6124	1573	236	SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL GAPLPFFRAIRVTCIGSCGVSNKANDTAWVVEGYFNSSLSLADK GSLPAGEHSFPFQFLLPATAPTSFEGPFGKIVHQVRAAIHTPRF SKDHKCSLVFYILSPLNLSIPDIEQPNVASATKKFSYKLVKTG SVVLTASTDLRGYVVGQALQLHADVENQSGKDTSPVVASLLQKV SYKAKRWIHDVRTIAEVEGAGVKAWRRRAQWHEQILVPALPQSAL PGCSLIHIDYYLQVSLKAPEATVTLVPVFIGNIAV/NPCPSBPPA RPGAASWGPTPGG\PSAPPQEEAEARAAAGGPHFLDPVFLSTKS HSQRQPLLATLSSVPGAPEPCPDGSPASHPLHPPLCISTGATV PYFAEGSGGPVPTTSTLILPPEYSSWGYPYEAAPPSEYQSCGGVE PSLTPEs
6125	1	904	KTCPKLTCAFTVSVDPSCCRVCRGDGELSWEHSDGDI FRQFANR EARHSYHRSHYDPPPSRQAGLSRFPGARSHRGALMDSQQASGT IVQIVINNKHKGQVCVSNKTYSHGESWHPNLRAPGIVECVLC TCNVTQKECKKIHCNRYPCYPQKIDGKCKVCPCG/KKAKEEL PGQSF DNKGYFCGEETMPVYESVFMEDGETTRKIALETERPPQV EVHVWTIRKGIHQHFIKISKRMFEELPHFKLVTRTTLTSLQWKI FTEGEAQISQMCSSRVCRTLEDLVKVLRLERSEKGH
6126	1224	389	RLLEAPCPRSRRRFQMNPEWQAFVHVAVAGGLCAVAVFTGIF DSVSQVGYEHYAEAPVAGLPAFLAMPFNSLVNMYTLLGLSWL HRGGAMGLGPRYLKDVFAAMALLYGPVQWLRRLWTQWRRRAVLDQ WLTLPFAWPVAVCLYLDGRWRP\WLFSLCVCVSLASVGLALLH PQGFVALGAHVVPVAVGQALRT\HRHYG/SATPSATYALGVLS CLGFVVLKLCQDLARWRLFQCLTGHFWSKVCVLDLQFHFAFLFL THFNTHPRFHPSGGKTR
6127	1335	463	VLPRRCLVFFVNTMDSREPTLGRDLAAGFWQVWRQFDEDEKGY IEEKELDAFFLHMLMKLGDDTVMKANLHKVKQFMTTQDASKD GRIRMKELAGMFLSEDENFLLLFRENPLDSSVEFMQIWRKYDA DSSGFI SAABLNRNLDLFLHKKAI SEAKLEEYTGTMKIFDR NKDGRDLNLDLARI LALQENFLQFKMDACSTEKRGDFEKFIFA YYDVSKTGALGP\EVDGFVKMMELVQPSISGVLDLDPKFEILL RHCDVNDGKIQKSELALCLGLKINP
6128	2511	843	TCRMSRRQLBRWVSSQVQARGNRVAPRLGKIAMGLEMSKSD SPGSLDGRAWEDAQKPQSAWCGGRKTRVYATSSRRAPPSEGTRR GGAARPEKTAEEGPPAAPGSLRHSGPLGPHACPTALPEPQVTS MSSQVVGIEPLYIKAEPA SPDS PKGSS ETETEPVALAPG\ PAP TRCLPGHKEEEDGEGAGPGEQGGKLVLSLPRKRLCLVCGDVAS GYHYGVASCEACKAFFKRTIQGSI EYSCPASNECEITKRRRKAC QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLFPFGP FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDEAGPD GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQS VWMEVLVLGVAQRS LTLQDELAFAYLVLDDEEGARPAGLGELG\ AALLQLVRRQLALRLEREYVLLKALALANSDSVHI EDEPRLWS SCEKLLHEALLEYEAGRAGPGGAERRRAGRLLLTPLLRQTAG KVLAFYGVKLEGVPMHKLFLMLEAMMD
6129	1764	771	ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK HPCNASMECDKQRRQKNRAFCYFCNSVQKLPICACQCGKTKCMM KSSDCVIKHAGVYSTGLAMVGAICDPCEAWVCHGRKCLSTHACA CPLTDAEC\VECERGVWDHGGRI FSCSFCHNFLCEDDQFEHQAS CQVLEAETFKVSCNRLGQHSCLRCACFCDHTRSKVFKQKAG KQPPCPKCGHETQETKDLMSSTRSLKFGRTGGEEGDGASGYDA YWNKLSDDKYGDTSYHDEEDEYEAEDEDEDEDEGRKSDSTESS DLFTNLNLGRTYASGYAHYEEQEN
6130	3	577	GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTFIEKYDPTIE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DFYRKEIEV\DSSPSVAGISWTQQTQEQF\ASMRDLYIKKGQGC ILVYSLVNQQSFQ\DIKPMRDQIRVKVSEKVPVI\LVGN\SVD LESEREVSSEGRALAEWGC PFMETS AKSKTMVDELFAEIVRQ MNVAAQPKDDPCCSACNIQ
6131	3	1811	SSPREKTS DSSHRPSRHGFLFLRLVGLSPFSYLCVPPSRPVPGS PRSLSAMRLLEPLAPGRLRRGS PRHLFSCSPALLLLVLGGCLGVF GVAAGTRRPNNVLLLTDDQDEVLGGMTP LKKT KALIGEMGMTFS SAYVPSALCCPSRASILTGYPHNHVNNNTLEGNCSKSWQKI QEPNTFPAILRSMCGYQTF\AGKYLNEYGAPDAGGLEHVPLGW SYWYALEKNSKYNYTLS IN GKARKHGENYSVDYLT DVLAVLSL DFLDYKSNFEPFFMMTATP\APHS PWTAA PQYQKAFQNVFAPRN KNFNHGTNKHWRIRQAKTPMTNSSIQFLDNAFRKRWQTLLSVD DLVEKLVKRLFTGELNNTYI FYTSDNGYHTGQFSLPIDKRQLY BFDIKVPLLVRGP GIKPNQTS KMLVANIDLGP TILDIAGYDLNK TQMDGMSLLPILRGASNLTRSDVLVEYQGEGRNVTDPTCPSLS PGVSQCFPDVCEDAYNNTYACVRTMSALWNLQYCEFDQEVFV EYVNL TADPDQITNI AKTIDPELLGKMNYRLMMLQSCSGPTCRT PGVFDPGYRFPDRMLFMSNRGSVRTRRFSKHL
6132	96	1241	AAGLLPGLVPEDPRRTNLLPFGIQGPPFALSRLPFCVESGW AWEAMEPEFLYDLLQPKGVEPPAEELS KGGKKKYL PPTSRKD PKFEELQKPA\VLMEWINATLLPEHIVVRSL EEDMFDGLILHHL FQRLAALKLEAEDIALTATSQKHKLTVLEAVNRS\CSWRSGRP SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI ESTKSGLKSEKLVQLTEYSTDKDEPPKDVDELFKLAPEKVNA VKEAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLLIGQLEGFF LHLKEFYLT PNPSPAEMLHNVT LALELL/IGRGPAQLPC/LALK/ TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN
6133	2	4256	FVHGSMADTDLFMECEEELEFPWQKISDVIEDSVVEDYNSVDKT TIVSVSQQPVSAVPVIAAHASVAGHLSTSTTVSSGAQNSDSTK KTLVTLIANNNAGNPLVQGGQPLILTQNPAPGLGTMVTPVLR PVQVMQNAHVTS SPVASQPI FITTQGFVVRNVRPVQAMNQVG IVLNVQGGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMT PVRPG STMPVRPTNTFTTVIPATLTIRSTVPQSQSQTKSTPSTSTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSPFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSAH\ GSORTSGPESSMKVTSSI PVFDLQDGGRIKCPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFFY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHVE LDQONGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESEPLFLQHKMDTHKPGEMPYVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA SRGQPRTPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST CCSRAYANHMNNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVXNMYPPPSFPTNKAATVKSAGATPABPEELLTPLAPALPSPA STATPPPTPTHQALALPPLATEGAECNLVDDQDEGSPVTQEP E LASGGGGSGGVGKKEQLSVKKLRVLFALCCNTEQAAEHFRNPQ RRIIRRLRRFQASQGENLEGKYLSEAEKLAEWLVTQREQLP VNEETLFOKATKIGRSLEGGFKISYEWAVRFMLRHHLT PHARRA VAHTLPKDVAENAGLFI DFVQRQIHNQDLPLSMIVAI DEISLFL DTEVLSSDDRKENALQTVGTGBPCDVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVQKHTACQ RSKGMLVMDCHRTHLSEEVLAMLSASSTLPVVPAGCSSKIQPL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DVCIKRTVKNFLHKKWKEQAREMADTACDSVLLQLVLVWLGEV LGVIGDCPELVQRSFLVASVLPDGNINSPTRNADMQEELIAS LEEQLKLSGEHSESTPRPRSSPEETIEPESLHQLFEGESETES FYGFEEADLDLMEI
6134	2	4256	FVHGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAFPIAAHASVAGHLSTSTTVSSSGAQNDSSTK KTLVTLIANNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR PVQVMQANANHTSSPVASQPIFITTQGFPPVRNVRPVQANMNQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPOVFSQMTFVRPG STMPVRRPTTNTFTTVPATLTIRSTVPQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSAH\ GSQRTSGPESSMKVTSSI PVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFFY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESPLFLQHMKDTHKPGEMPVVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNAGNAQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPQLEGLKPGTKVTIRA SRGQPRTPVPSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFNFHFTTYVHCSLCRYST CCSRAYANHMNNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPSPSPPTNKAATVKSAGATPAEPEELLTPLAPALPSPA STATPPPTPTHQALALPLATEGAELNVDQDEGSPVTQEPE LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ RRIRRLRRFQASQGENLEGKYLSEAEKLAEWLVTQREQQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFLMRHHLTPHARRA VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPLVIFY RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ RSKGMVMDCHRTLSSEVLAMLSASSTLPVVPAGCSSKIQLPL DVCIKRTVKNFLHKKWKEQAREMADTACDSVLLQLVLVWLGEV LGVIGDCPELVQRSFLVASVLPDGNINSPTRNADMQEELIAS LEEQLKLSGEHSESTPRPRSSPEETIEPESLHQLFEGESETES FYGFEEADLDLMEI
6135	2	4256	FVHGSMADTDLFMECEEELEPWQKISDVIEDSVVEDYNSVDKT TTVSVSQQPVSAFPIAAHASVAGHLSTSTTVSSSGAQNDSSTK KTLVTLIANNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR PVQVMQANANHTSSPVASQPIFITTQGFPPVRNVRPVQANMNQVG IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPOVFSQMTFVRPG STMPVRRPTTNTFTTVPATLTIRSTVPQSQQTKSTPSTSTTP TATQPTSLGQLAVQSPGQSNQTTNPKLAPSPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSAH\ GSQRTSGPESSMKVTSSI PVFDLQDGGRKICPRCNAQFRVTEAL RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFFY GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC KICEWAFESPLFLQHMKDTHKPGEMPVVCQVCQYRSSLYSEVD VHFRMIHEDTRHLLCPYCLKVFKNAGNAQQHYMRHQKR\NVYH\ CNKCRVQFLFAKDKIEHKLQHHKTFRKPQLEGLKPGTKVTIRA SRGQPRTPVPSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS IQKRAVRKMSVMGRQTCLECSFEIPDFNFHFTTYVHCSLCRYST CCSRAYANHMNNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR NVKNMYPSPSPFNKAATVKSAGATPAEPEELLTP LAPALPSPA STATPPPTPTHQALALPLATEGAECNLVDDQDEGSPVTQEP E LASGGGSGGGVKGKQLSVKKLRVVLFCNCNTEQAAEHFRNPQ RRIIRWLRRFQASQGENLEGKYLSEAEKLAEWLVTQREQLP VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA VAHTLPKDVAENAGLFDVQVQRIHNQDLPLSMIVAIDEISLFL DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY RGQMDQPANMPDSILLEAKESGYSDDIMELWSTRVWQKHTACQ RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL DVCIKRTVKNFLLHKKWKEQAREMADTACDSDVLLQLVLVWLGVE LGVIGDCPELVQRSFLVASVLPDPGNINSPTNRADMQEELIAS LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES FYGFEEADLDLMEI
6136	1704	539	FGVRMALEGMSKRKRKRSVQEGENPDDGVRGSPPEYRLGQVAS SLFRGEHHSRGGTGRLASLFSLEPQIQPVYVPVK\ESALASA DLEEEIHQKQGGKRNKNSQPGVKVADRKILDDTETVVSQRKKIQ INQEEERLKNERTVFGNLPVTCNKKLKSFFKEYGQIESVFRF SLIPAEGTLSKKLAAIKRKIHDPQKNINAYVVFKEESAATQALK RGAQIADGFRIRVDLASETSSRDKRSVFGNLPYKVEESAIEK HFLDCGSSIMAVRIVRDKMTGIGKGFYVLPENTDSVHLALKLNN SELMGRKLRVMSVSNKEKFKQNSNPRLNKNSKPKQGLNFTSKT AEGHPKSLFIGEKAVLLKTKKGQKKSGRPKQKQKQK
6137	141	2656	RALRKRRCCPGRGALGSGGPGPQRRPGRVPEERPAPEERKHFG MWNMLIVAMCLA\LLGLPGKAQELQGHVS\IILAGEQLGLDAKK YLWQ\LFQLYLDEAGRGHSFSFHGAALTAPKQGGELMAKALLES LSCPKDMAPSHCAEHKQFLQLSQYRQLKTAEDYQALNKDIEAQ LQHAGLREAGGIIFYFSVPPFAYEDIARNINSSCRPGGAWLRVV LEKPPFGHDHPSAQQLATELGTFFQBEEMYRVDHYLKQAVAQIL PFRDQNRKALDGLWNRHIVERVEIIMKETVDABGRTSFYEEYGV IRDLQNLHTEVLTIVAMELPHNVSSAEAVLRHKLQVQALRGL QRGSVAVGQYQSYSEQVRRELQKPDSPHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCQSEKHMAAAS QCLPRQLVFHIGHGDGSPAVLVSRNLFPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLSELAHKAPRLYPGAENGRLLDFEFSGRFFFS QQQPEQLVPGPGPGMPSPDFQVLRKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVP LSPDFESNFOGLQAHLLQHVRIPIYNIH\AM PVHLQORLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPGTGLDGEQLVVLTTPSPSQPHRRMSLSLPLINRAKVV AVLVMGMRMKREITTLVSRVGHFKKWPISGVLPHSGQLVWYMDY DAFIG
6138	4587	934	EFSKLTDRWQNAVQGVQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTDLTKTESVGRRISQLQDSWKMPEQLAEMIQQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHROWEDLCRLVAIRKQEIIRDLNTWVVFNEKNKELCAWLQVM ENKVLQTADISIEEMIEKLQKDCMEINLFSENKILQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFIFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDQEQIQRRLAEQQD LQRDIEQHSAGVESVFNICDVLHSDACANETECDSIQQTTRS LDRWRNICALMSERRMKIETWRLWQKFLDDYSRFEDWLKSAB RTAACPNSSSEVLYTSAKEELKRFEAFQRQIHERLTQLELINKQY RRLARENRTDTASRLKQMVHEGNQRWDNLQRRVTAVLRLRLHFT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NQREEFEGTRESILVNLTEMDLQLTNVEHFSSESDADDKMRQLNG FQQEITLNTNKIDQLIVFGEQLIQKSEP\LDVLIIEDELELHR YCOEVFGRVSRFHRRLTSCTPGLEDEKEASENETDMEDPREIQT DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETFPVSVDS\IPLE WDHTGRRGGPSSSH\EEDEBAQYY\SALSGKSISDGHSHWVPDS PSCPEHHYKQMEGDRNVPPVPASSTPYKPPYKLLLPPTDGG KEGPRVLNGNPQQEDGGLAGITEQQSGAFDRWEMIAQEL\HNK LKIKQNLQQLNSDISAITTWLKKTEAELEMLKMAKPPSDIQIE LRVKRLQEILKAFDTYKALVSVNVSSKEFLQTESPESTELQSR LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLLWLA SAKNRRQKAHVTDPKADPRALLECRRELMQLEKELVERQGPQVDM LQETSNLSLLIKGHGEDCIEAEKVVHI\EKKLKQLREQVSDML ALQQTQNPASPLPSFDEVDSDGQPPATSVPAAPRAKQFRAVRTTE GEEETESRVPGSTRPQRSFLSRVRAALPLQLLLLLLLLLLACL PSSSEEDYSCTQANNF\ARSFYPMRLRYTNGPPPT
6139	52	1131	LGDNVWSRTCGVLETPTSVLRRARARGPCPTDSKWLPRLEGE TERRPWEASSWKT/LAGWIGGAASVIVGHPDVTVTRLQAGVG YGNLSCIRVVYRRESMFGEFKGMSFPLASIAVYNSVVFVGSN TQRFSLQHRCEPEASPPRTLSDLLASLVAGVSVGLGGPVDL IKIRLQMOTPPVSGRQPRFEVQSGSGCG\EPAYQGVHCITITIV RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACT PSPCAVWLAGGMAGAIISWGTATPMDVVKSRQLQADGVYLNKYKV LDCISQSYQKEGLKVFFRGITVNAVGRGFMSAAMFLGYELSLQA IRGDHAVTSP
6140	694	136	RPELELWRLRSRWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASAALEPLGPAPV SVAPQAEAEARSTFGPAGSRLGPETFRQRFRQFRYQDAAGPREA FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR ARRIRRRTDVIRITG
6141	2	984	AQVGPRSRPCKMPLKLRGKKAKSKETAGLVEGEPTGAGGGSLS ASRAPARRLVFHAQLAGHSATGRVEGFSSIQELYAQIAGAFEIS PSEILYCTLNTPKIDMERLLGGQLGLEDIFAHVKGIEKEVNVI KSEDSLGLTITDNGVGYAFIKRIKDGVIDSVKTCVGDHIESI NGENIVGWRHYDAKKLKEELFTMKLIEPKKAFEIELRSK AGKSSGEKIGCGRATLRLRSKGPATVEEMPSKAK\AIEKIDD VLELYMGIRDIDLATTNFEAGKDKVNPDEFAVALDETLDGFAFP DEFVFDVWGVIGDAKRRGL
6142	116	602	EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRR FRVRQPIQYRWIDIMHRLGEPQARMREENMERIGEVRQLMEKL REKQLSHSLRAVSTDPHHDHDEFC\LMP
6143	2802	270	FRMRIFLHCPWNQMWKIWNLLTSLSCAKHLSIQKLLKER/Q QLPVFKHRDSIVETLKRHRVVVAGET\GSGKSTQVPHFLLED LLLENEWASKCNIVCTQPRRISAVSLANRVCDLGCENGPGGRN SLCGYQIRMESRACESTRLLYCTTGVLRLKLQEDGLLSNV/S/HM FIVDEV\HER\SVQSDFLIILKEILQKRSOLHLILMSATVDSE KFSTYFTHCPILRISGRSYVPEVFHLEDIEETGFVLEKDSYC QKFLSEEEVTVINVTSKAGGIKKYQEIYIPVQTGAHADLNPYQK YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI FLPGLAHIQQLYDLSNDRRFYSERYKVALHSILSTQDQAAAF TLPPPVGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS QMSSIVETFVSKASALQROGRAGRVRDGFCEFRMYTRERFEGFMD YSVPEILRVPLEELCLHIMKCNLGSBDFLSKALDPPQLQVINS AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTESPFPTTIGRKDEADLAKSALAMADSDHL TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LIKLVKAAGFSSSTTSTSWEGNRASQTLSFOEIALLKAVLVAGL YDNVKGKIIYTKSVDTVTEKLACIVETAQGKAQVHPSSVNRDLQTH GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIQVHRERLLS IDGWIYFQAPVKIAVIFKQLRVLIDSVLRRKKLENPKMSLENDKI LQIITELIKTENN
6144	1289	568	SGPGSMGQQRVDVKVVMGKEYVGKTSLSVERYVHDRFLVGPYQN VSASGGARHGGRSGGVPVICTYGPDLFPPLVA\TIGAAFVAKVMS VGDRTVTLGWDTAGSERYEAMSRIYYRGAKAAIVCYDLTSSS FERAKFWVKELRSLSEEGCQIYLCGTKSDLEEEDRRRRRVDFHDV QDYADNIKAQLFETSSKTQSVDLFPQKVAEDVVSAAAFQVMT E DKGVDLGQKPNPYFYSCCHH
6145	1109	196	GGMDLSELERDNTGRCLSSPVPVAVCRKEPCVLGVDEAGRGPVL GPMVYAIYCPLPRLADLEALKVADSKTLESERERLFAKMETD DFGWALDVLSPNLISTSMGLRVKYNLNSLSDTATGLIQYALD QGVNVTQVFVDVTGMPETYQARLQSSFPGIEVTVKAKADALYPV \VSAASICAKVARDOAVKKWQFVEKLQDLDTDYG\SGYPNDPQD /TKAWLKEHVEPVF\GFP\QFVRF\SWRTAQTI\LEKEAEDVIR EDSASENQEGLRKITSYFLNEGSQARPRSSHYFLERGLESTTS L
6146	428	781	LKKKGKEKAEAAQQVEALPGPSLDQWHSAGEEEDGPVLTDEQKS R/YPGHEAHDQGG\WDARQSIIRKVVDPEPTRRLIKGDGEVLE EIVTKERHREINKQATRGDCCLAFQMRAGLLP
6147	1	2304	GTRQLPPPSPGSGPGDSPEGPEGEAPERRRKAHGMKLKLYGLSE GEAAGRPAGPDPLDPTDLNGAHFDEPVYLDKLRRECPLAQLMDS ETDVMVRQIRALDSMQTLVYENYNKFISATDTIRKMKNDFRKME DEMDRLATNMAVITDPSARISATLQDRHERITKLAGVHALLRKL QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSFRA IQDDCQVITARLAQQLRQRFREGGSGAPEQAECVELLLALGEP A EELCEEFLAHARGRLEKELRNLEAELGSPPPADVLEFTDHG\ S SGFVGGLCQVAAAYQELFAAQGPAGAELKLAFAARQLGSRYFALV ERRLAQEQGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYPFRGEF CSQVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA RRLLTHTYVKVQGLVISQMLRKSVEPTRDNLSTLEPRNVRAVMKRV VEDTATIDVQVLPRLAGVALTQAGGTVPSPRGAGAAEDHWQSLPG GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS CSFSAQDYDIPAPILPVEKQRLRVTVQEVRAGLVLVLKIRPQTNS CILPLPHSTGSINSDHVPTK
6148	3056	353	VPAVGGETFADGAMGEAEKFHYIYSCDLIDINVQLKIGSLEGKREQ KSYKAVLEDEPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT SYKAFSTRWNNEWLKLVPKYPDLP RNAQVALTIWDVYGP GKAV PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT SSTLSAQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES VKRSSNFMYLMGGFRVCKCDDKEYGIVYIEKDGDESSPILTSFE LVKVPDPQMSLENLVESKHNLPRSLRSGPSDHDLPKYPSPRPDQ LKNIVSYPPSKPPTYEEQDLVWEFRYLTNQDKALTILTSVIW DLPQGAQALALGKWKPMVDVEDSLELLSSHYTNPTVRRYAVAR LRQADDEDLLMYLLQVLQALKYENFDDIKNGLEPTKKDSSQSSVS ENVNSNGINSABIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG ENLEQDLCTFLISRASKNSTLANLYLYWYVIVECEDQDTQQRDPK THEMYLNVMRFRSQALLKGDKSVRVMRSLAAQQTFFVDRVLHLM KAVQRESGNRKKNERLQALLGDNEKMNLSDELIPLEPQVK IRGIIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLQD QLIQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PVAEVLDTGSIQNFPRKYAPSENGPENGISAEMDTYVVKSCAGY CVITYILGVGDRHLDNLLTKTKGLFHDIFGYILGRDPKPLPPP MKLNKEMVEGMMGTQSEYQEFKQCYTAFHLRLRYSNLILNLF SLMVDANIPDIALEPDKTIVKKVQDKFRDLSDDEAVHYMQSLID ESHALFAAVVEQIHKFAQYWRK
6149	1	1413	RVDPVRRENGTANPIKNGKTSFASKDQRTGKKTSSVQGVQKQND ESESDPESDPPSPKSEEEEDDEVLQGEQGFNDDDTEPENL GHRPLLMDSDEEEEEKHSSDSYEQAKAKYSDMSSVYRDRSGS GPTQDLNTILLTSAQLSSDVAVETPKQEFDFVGAVPFFAVRAQQ PQQEKNEKNLPQHRFPAAGLEQEEFDVFTKAPFSKKVNVQECH VGPAAHTIPGYPKSVDFVGSSTPFQPFLLTSTSKSESNEDLFGLVP FDEITGSQQQKVKQSLQKLSSRQRRTKQDMKSNKGRHHTPT STKTKLTKPTYRTPERARRHKKVGRDRSQSSNEFLTISDSKENIS VALTDGKDRGNVLQPEESLDDPFGAKPFHSPD\LSWHPP\HQGL S\DIRADHNT\VLPGR\PRQNSLHGSFHSADVLMDDFGAVP/F LTELVVQSITPHQSQQSQPV\ELDPFGAAPPFSKQ
6150	372	37	MSNKKYIIDYDWKASTETETIDHDMTEEKLHQINNFWSDSEYR LNKHGSVLNAVLIQLAHALLIAISSDLNAYGVVCEFDWNDGNG QEGWPPMDGSEGRITDIDTSGIF
6151	1555	521	DSNQSVSGTAASTLLHSFKATIIYQGTGHVQQFYGVTS PYSQT TPPIVQSYAQPSLQYIQGQIIFTAHPQGVVQPAAAVTTIVAPG QPQLQPSSEMVVNTNLLDLPSPSPKPTIVLPPNWKATARDPEG KIYYHYHVTIRQTQWDPPTWESPGDDASLEHEAEMDLGTPPYDEN PMK\ASKKPKTAEADTSSSELAKKSKVFRKMSQFIVQCLNPYR KPDCVG\RTITTEDFKHLARKLTHGVMNKELKYCKNPE\DLCE NENVKHKTKEYIKKYMQKFGAVYKPKEDTEFRVTGPGWEDGWS GKTDSSRERKSCGPFCSPTPVSTVLLMIHHPGBFNPADVN
6152	1366	648	NRTWSTPSTWGMVALPFLCSTGFWPVTROITARTTCGAVPAKCP PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC GPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRPC KCEHHCPDCKPTGNCSVSRVKQLQPPPEATLRAGELSFPFRTAW LALTLALAFLLLISTAANLSLLSRAERNRRLHGDYAYHPLQEM NGEPLAAEKEQPGGAHNPFKD
6153	2	3368	GRVGARSPGRAYALLLLICFNVGSGHLHLQVLSTRNENKLLPKH PHLVRQKRAWITAPVALLEGEDLSKKNP IAKIHSDLAEERGLKI TYKYTGKGITPPFGIFVFNKDTGELNVTSILDRBETPPFLLTG YALDARGNNVEKPLELR IKVLDINDNEPVFTQDVFGSVEELSA AHTLVMKINATDAEPNTLNSKISYRIVSLEPAYPPVFYLNKDT GEIYTTSVTLDRHESSYTLTVEARDGNGEVTDKPVKQAQVQIR ILVDNDNIPVVENKVLEGMVEENQVNVETRIKVFDADEIGSDN WLANFTFASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEMKNLD FSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGIFHKSSVI SIYVSSEMDRSSKQIIIGNFQAFDEDTGLPAHARYVKLEDRDNW ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDPKRTI TGTVLINVEDINDNCPTLIEPVQTI CHDAEYVNVTAEDLDGHPN SGPFPSFVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQ FLISDNQGFSCPRKQVLTITVCEVLHGS\GCREAQHDSYVGLGP AALALMILAFLLLLLVPLLLLMCHCGKAGKFTPIPGTIEMLHP WNEGAPPEDKVVPSFLPVDQGGSLVGRNGVGGMAKEATMKGSS SASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAI\MTTE TTITARATGASRDVAGAQAVALNEEFKNYFTDKAASYTED ENHTAKDCLLVYSQEETESLNASIGCCSPIEGELDDRFLDDLGL KFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTM VNSENTYSSGSSFPVPSLQEAANAQKVTQEVTERSVSRRQAQK VATPLPDPMASRNVIAETSTVVTGSTMPTTIVLGPSPQSLIV TERVYAPASTLVDPQPYANEGTVVVTERTVQPHGGGNSPLEGTQH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL APASTLQSSYQIPTENSMTARNITVSGAGVPGPLPDFGLEESGH SNSTITTSSTRVTKHSTVQHSYS
6154	3660	2146	KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLQMVSKDLDTDAKN SDTAHIKSIETISILNGLQAESESAEDSEQDERGAQDMNNGK EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADLVISKPVSK SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDITDKSSKPQIK RGKRRYCNTEELKTGSPGKKEEKAKNKESELCMENSSNSSSDED EETKAKMTPTKKYNGLEEKRSRLRTTGFYSGFSEVAEKRIKLL NNSDERLQNSRAKDRKDVWSSIQQGWPKKTLKELFSDSDTEAAA SPHPAPEEGVAEESLQTVAEESCSPSVELEKPPPVNVDSKPI EKTVEVNDRAEFPSSSGSNFSA*IPLPYLHLNRLHQSL*QKGS RQSSSVTVSEPLAPNQEEVRSIKSETDSTIEVDSVAGELQDLQS ERE*LASRF*QCELEQ**SARTRTS*KSLYRSEKSEKSGRRK FIKKAEEKP*SNSGKQKEGK
6155	869	121	HLLPELRGKSWITMKYVFLGVLAGTFFADSSVQKEDFAPYLV YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMGNFKSRVRDG TEQTNPIQIVRYWNYSHSAPQDDMLIKLAKPAMLNPKVQALN P/PTTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLAPVMSDRE CQKTEQKSHRNSLCVKFVKVFSRIFGEVAVATVICKDLQGTIE VGHEMGDVGIIYTNVYKYVSWIENTAKDK
6156	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNQDTRKLLMTWALEVAV VMKSETYAPLFCPLPSFHKFCCKGLLADTLVEDVNICLQACSSHL ALSSSLPDDLLQRCVDVCRVQLVHRGTICIRQAFGKLLKSIPLGV FLSNNNHTEIQEISLALRSHMSKAPSNTFFHPQDFSD/VISFIFY GNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRNLKTDVAVLWQW AIWEAAQFTVLSKLRTPLGRAQDTFQTEGIIIRSLAGHTLNPDQ DVSQWTTADNDEGHGNNQLRLVLLQYLENLEKLMYNAYEGCAN ALTSPPKIVIRTFLYTNRQTCQDWLIRLSIMRVGLLAGQPAVT VRHGFDDLTEMKTTLSQGNELVSIIMMVVEALCELHCPEAIOG IAVWSSSIYVGHLLWINSVAQQAEGRFKASVEYQEHLCAMTGV DCCISSFDKSVLTLASAGCKSASLKHCLNGESRKSIVLSKPTDSS PEVINYLGNKACECYISTADWAAVQEWQNAIHDLLKSTSTSLN LKADFNYIKSLSSPESGKFVECTEQLELLPGENINLLAGGSKEK IDMKLLRNM
6157	946	329	MANRGPSTYGLSREVQEKEIEQKYDADLENKLVDWIIILQCAEDIEH PPGGRAHFQKWLMDGTVLCKLINSLYPPGQEPPIPKISESKMAFK QMEQISQFLKAAETYGVRTTDIFQTVDLWEGKDMAAVQRTLMAL GSVAVTKDDGCVRGEPSPFHRKAQONRRGFSEBQLRQGNVIGL QMGSNKGASQAGMTGYGMPRQIM*DAASCP
6158	441	1482	LGSILVLSLHCKVIFSSQSLERAMKEKAVDLVPILAQNPGLAQN PILEGKDHQNTGVDPPIIDHVQDRKTD/SRSKSPHKRSKSRER RKSRSRSHSRDKRDKTREKIKERKERVKEKREKEREREKEKE KERGNKDRDKEREKREKDKEREREREKEHEKDRDKEKEKE QDKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSRE RRRRSRSSSRSPRTSKTIKRKSSRSPSPSRNKKDKREKERD HISERERERERSTMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD SSVSKEVDDKAPRTEENKIQHNGNCQLNEENLSTKTEAV
6159	53	84	AVIAPLHISLGDRAAPYLKNTKSSSTTCSSRRRNQSFPPVMSLTH RLHLCKYWGCAVSNVCRFWEGRPPLPLMIVVPYTLVPSLVPGSCV IITGTPILTFFVKDPQLEVNFYTGMDSDSDIAFQFRHLHFGHPAIM NSCVFGIWRYEKCYLLPFEDGKPFELCIYVRHKEYKVMVNGQR IYNFAHRFPASVKMLQVFRDISLTVLISD*GRCVRITAVQEF DVSVSCDCTTAYQPG
6160	1626	1790	AGAKFFP*F*KVADAQPTSEKEIYNQNVVLKDAEGILEDLQS YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGLKPKFYFSQR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LEAALRGLLGALTSTPYSPTOHLEREQALAKQFAEILHFTLRFDELKMTNPAIQNDFSYYRRTLSRMRIINNVPAGEGENEVNNEANRMSLFYAEATPMLKTLSDATTKFVSENKNLPIENTDCLSTMASVC RVMLETPEYRSRFTNEETVSPCLRVVMGVII LYDHVHPVGAFAK TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQIKSM LQ*QLLTLVNKG
6161	455	1569	PVSGSESLRRASILRLMLGPRVAVSILCEDGISH*LLEKH* KSHVLEPLSSSLALEBQCLALSLDWSGTGKTGRAGDQPLKI ISSDS TGQLHLLMVNETRPRLOKVASWOAHQFEAWIAAFNYWHPPIVYS GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT GSYDEHILLWDTRNMKQPLADTPVQGGVRIKWHPFHHLHLLAA CMHSGFKILNCQKAMEERQEATVLTSHLTPDSL VYGADWSWLLP RSLQRAPSWSPFNLTGKTADLKGASELPTPCHECREDNDGEGH ARPQSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEADSAFSL LATCSFYDHALHLWEWEGN
6162	1	586	RTIHATGRAGASPMHRLITVWRLAEANKQHVRCQKCLEFGHWTYE CTGKRKYLRHPSRTAELKKALKEKENRLLQQSIGETNVERKAK KKRKSVTSSSSSSSDSSASDSSSESEETSTSSSSSDSDTDESS SSSSSASSTSSSSSDSDSSSSSKQ*HQHR*QL*R*TTKEE EKETELLSYWTGDLKTL M
6163	1081	785	RIRSTTEGCAVRLHPTONTGKARIMILLSVSLGRHWAFTYKFFL TPVVFVFFFFFHRKE*VMQKNPMKSREDEWMEKLNHLHVQRAD MNRLLMNVLTGEGFKEAAEKFRMESGIEPSVDLETDERIKIRE MILKGQIQEAIALINSLHPELDDTNRVLYFHLQQQHLELIRQR ETRAALFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPFGDLLHMTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKLLWAQN ELDQKKVKYPKMTDLSKGVIEEPK
6164	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKRR SCISRTAPRLLCTLEPGVDTKLKFLEPSLGQNGFQQWYDALK A VARLSTGIPKEWRRKVWLTADHYLHSLAIDWDKTMRTFNERS NPDDDSMGIQIVKDLHRTGCSSYCGQAEQDRVVLKRVLLAYAR WNKTVGYCQGFNLAALILEVMEGNEGDAKIMYILDKVLPES YFVNNLRALSVDMAVFRDLLRMKLPESLQHLDTLQRTANKESGG GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE LMQTVYSMAFPFPQLAELREKYTYNITPFPATVKPTS SVSGRHS KARDSDEENDPDEDAVVNAVGC L GPFSGFLAPELQYKQIKE PNEEQSLRSNNIAELSPGAINS CRSEYHAAFNSMMERM TTDIN ALKRQYSRIKKKQQQVHVYIRADKGPVTSILPSQVNSSPVIN HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVYEDLKTCLNS PWRTHIRVHKKNMPTKSHPGCGDTVGLIDEQNEASKTNGLGAA EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEVPFGDADVDVSA VQAKLGALELNQRDAAAE TELRVHPPCQRHCPEPPSAPEENKAT SKAPQGSNSKTPIFSPFPVKPLRKSATARNLGLYGP TERTPTV HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEQYQRN GGERFG
6165	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKRR SCISRTAPRLLCTLEPGVDTKLKFLEPSLGQNGFQQWYDALK A VARLSTGIPKEWRRKVWLTADHYLHSLAIDWDKTMRTFNERS NPDDDSMGIQIVKDLHRTGCSSYCGQAEQDRVVLKRVLLAYAR WNKTVGYCQGFNLAALILEVMEGNEGDAKIMYILDKVLPES YFVNNLRALSVDMAVFRDLLRMKLPESLQHLDTLQRTANKESGG GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE LMQTVYSMAFPFPQLAELREKYTYNITPFPATVKPTS SVSGRHS KARDSDEENDPDEDAVVNAVGC L GPFSGFLAPELQYKQIKE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTDIN ALKRQYSRIKKKQQQVHVQYIRADKGPVTSILPSQVNSSPVIN HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVYEDLTKTKLNS PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDBQNEASKTNGLGAA EAPPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA VQAKLGALELNQRDAAETELRVHPPCQRHCPEPPSAPBENKAT SKAPQGSNSKTPIFSPPFSVKFLRKSATARNLGLYGPTERTPTV HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEQYQRN GGERFG
6166	2	1206	HKLWRTVAMAGAEWKSL EECLEKHLPLPDLQEVKRVLYGKELRK LDLPREAFEAASREDFELQYAFRAAEQLRRPRIVHVGVLQVNR IPLPANAPVAEQVSALHRRRIKAIVEVAMCGVNIICFQEAWTMP FAPCTREKLPWTEFAESAEDGPTTRFCQKLAKNHDMMVVSPILE RDSEHGDVLWNTAVVISNSGAVLGKTRKNHPIRVGDFNESTYTM EGNLGHPVFQTFGRIVAVNICYGRHHPNLWLMYSINGAEIIFNP SATIGALSESLEWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS GDGKKAHQDFGYFYGSSVVAAPDSSRTPGLSRSRDGLLVAKLDL NLCCQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE*PAS VPALG
6167	1220	1844	YGI V T G P S L C A G D K Q P K K Q E K N P V L S P E F V D E A L C A C E E Y L S N L A H M D I D K D L E A P L Y L T P E G W S L F L Q R Y Y Q V V H E G A E L R H L D T Q V Q R C E D I L Q Q L Q A V V P Q I D M E G D R N I W I V K P G A K S R G R G I M C M D H L E E M L K L V N G N P V V M K D G K W V V Q K Y I E R P L L I F G T K F D L R Q W F L V T D W N P L T V W F Y R D S Y I R F S T Q P P S L K N L D K * A P L Y L T P E G W S L F L Q R Y Y Q V V H E G A E L R H L D T Q V Q R C E D I L Q Q L Q A V V P Q I D M E G D R N I W I V K P G A K S R G R G I M C M D H L E E M L K L V N G N P V V M K D G K W V V Q K Y I E R P L L I F G T K F D L R Q W F L V T D W N P L T V W F Y R D S Y I R F S T Q P P S L K N L D K
6168	84	1392	VWPVPSVSAMPFKKQAQAGGSKKAEQKKKEKIIEDKTFGLKNKK GAKQQKFIKAVTHQVKGQONPRQVAQSEAEKKLKKDDKKKELQ ELNELFKPVVAAQKISKGADPKSVVCAFFKQGCQTKGDKCKFSH DLTLERKCEKRSVYIDARDEELEKDTMDNWEKKLEVVNKKHG EAEKKKPKTQIVCKHFLEAIENNKYGFVWVCPGGGDCMYRHAL PPGFVLKKKKKKKKKDEISL*DLIERERSALGNVTKITLESF LAWKKRKRQEKIDKLEQDMERRKADFAGKALVISGREVFEEFRP ELVNDDEEADDDTRYTQGTGGDEVDDSVSVDIDLSLYIFRDVD ETGITVASLERFSTYTSKDKENKLSASGGRAENGERSDLLEDN EREGTENGADAVPVDENLFTGEDLDELEBELNTLDLEE
6169	112	662	APAAAMAERPEDLNLNPAVITRIIKEALPDGVNISKEARSAISR AASVFVLYATSCANNFAMKGRKTLNASDVLASAMEEMEFQRFVT PLKEALEAYRREBQGGKEASEQKKDKDKKTDSBEQDKSRDEBN DEDEBRLEEEBQNEEEVDN*KGRETVAPWKVPLEMRRATCFCE AFPCWAE
6170	62	667	STKVMLEPNTGRLAGCTVFITGASRGIGKAIKAAKDGANIVIA AKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVDVRDEQQISAA VEKAIKFGGIDILVNNASAI SLTNTLDTPTKRLDLMNVNTRG TYLASKACIPYLKKSVAHNPINISPPNLNPNVWFQKHCGRW*VV G*GDGLCLICFELNLCMSDVITICT
6171	382	941	HFMQSDVELDCDIEFCGHTKFPPTLPLSTTVIVCSCHPVATAST MAEAFSKTTSEEDQSIQEPKEANSMTAQKQK*GLRGSRRRHAN SGGDI PGDSFAAYFPRVLKQVHQALSLSQEAHSVMDSMVRDILD RIATEAGHLAHYSKCVTTISRDIRMAVCLLPKMGKLAESQGT NATLRYTKSK
6172	651	54	GLCRAGGAHRFSRTHVEAALKMLRREALRREYLYRKAREEAQR SAQERKERLRRALEENRLIPTELRREALAQSGSLEFDDAGGEGV TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMFALBLKLVFPGA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QRMNRRGHEVGALVRACKANGVTDLLVVEHRGTPVGLIVSHLP FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV SDILRYLFFVPKDDSHRVITFANQDDYISFRHHVYKKTDRHNVE LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYNTARKRVF LSTE*AAPRPLGQLL
6173	3	288	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL LQHQRIHTGEKPYVCSVCGKAFSSQSSVLSKHRTIHTGEKPYECN ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAPTQLSHLIQHQ RIHTGERPYVCPCLCGKAFNHSTVLRSHQVRHTGEKPHRCNECGK TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHNNVHT GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVQ HSHLIHQHKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
6174	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMVGLQLARRLGVAESWT RDRHCAADLALAPLGDALVLRPRRLMNANGRSVARAAELFGL TAEVYLVDDELDPGLRLALKLGGSARGHNGVRSCISCLNSNA MPRLRVGIGRPAHPEAVQAHVLCGCFSPAQEQLPLLLDRATDLI LDHIRERSQGPSLGP*H*WFSKKA
6175	2204	334	RYFRADPRSRSGQPRAEGLGAFAGPLRAMAAPVKGNRKQSTEG DALDPPASPKPAGKQNGIQNPISLEDSPAEGEREEBQEREEBQ AFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE LVTGRRLWKNVYNELGSGSPGSTGATCTRRHY*RLVL PYVRHLK GEDDKPLFTSKPRQYKMAKENRGDDGATERPKKAKEERRMDQM MPGKTADAADPAPLPSQEPNRNSTEQQLASGSSVSFVGASGC PEAYKRLLSFYCKGTHGIMSPPLAKKKLLAQVSKVEALQCQEEG CRHGAEPQASPAVHLPESPQSPKGLTENSRRHLTPQEGLOAPGG SLREEAQAGPCPAAPIFKGCFTYHTPEVLKPVSQHPRDFFSRLK DQVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGRKGLIYP KPKACWVSPMAKVPAESPTLPPTFPSPGLGSKRSLEEBGAHS GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPEA YRGTMHLHCLNFTGTGPGPLKGQAALPFSPLVIPAFPAHFLATAG PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF FHLNTKL
6176	1040	402	PLSALRAMAEVHVIGQIIIGASGFSESSLFCWKGIHTGAAWKLLS GVREGQTQVDTPOIGDMAYWHPIDLHFATKGLQGWPRLHFQVW SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWRBQLAR AFVGGGPQLLHGDITISGADRYRLHTAAGGTVHLEIGLLLRNFD RYGVEC*GTLPTSPSTPRTPSDGGGWHSGQEHRL
6177	1400	992	VPIESLVGKVHNFPLIAFYCCEKGRQPHKSLHRCFCGEALDPN CSHCYLDQIKRSDPLGFGSGYSPHFVAISTNSEHKMQPSSMQQAL PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPLPGTSGCSDRPP VCPI
6178	1027	254	STQRGGIKGVARAASLVGRRRAGTGMALLCLVCLTAALAHGCL HCHSNFSKKFSFYRHHVNFKSWWVDIPVSGALLTDWSDDTMKE LHLAIPAKITREKLDQVATAVYQMDQLYQGMYPFGYFPNELR NIFREQVHLIQNAIIESRIDCQHRCGIFQYETISCNCTDSHVA CFGYNCESSAQWKS AVQGLLNYINNWHKQDTSMRPRSSAFSWPG THRAAPAFVLVLPALRCLEPPHLANLSLEDA*CLKQH
6179	806	276	RGETREMAGNLLSGAGRRLWDVPLACRSFSLGVPRLIGIRLTL PPPKVVDWRNEKRAMFGVYDNIIGLGNFEKHPKELIRGPIWLRG WKGNELQRCIRKRMVGSRMFADDLHNLNKRIRYLYKHFNHCK FR*KRKLRTSEKAHLSPWRRVETVLPVVRKRLCIFSVIKWGFPGI
6180	156	1833	DHHILKAASTTHVCARGNIFATPNTRCLEC*ATATPSSLEQCN* SHLSLCLPATTSGLTNSMIPEKERQNIARLLRVMCADLAL SVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLAKHLPR MYNQVKVKTCAIGSNACLGIGVTCHSQSVGPDSCYILTAYQAE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GNHIKSYVLGVKGADIRDSGLVHHVQNVLSBFVMSEIRTVYV TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE VIELNVCELAGSTGLAKETFGSLEETSPPPCWNSVTDSELLV HERYEQICEFYSSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE LSNESQPTLQLVLPYVRLEKLF TAKANDAGTVSKLCHLFLEAL KENFKVHPAHKVMILDPQQLRPVPPYQHEEIIIGKVCelinev KESWAEADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN MCEQALLIKRRRLSPEDMKNLMLFLKSNML
6181	169	1032	TRTLSPVLLPGPRWKPWRRRPMGLALPAWLQPRYRNAYLFI YYLIQFCGHSWIFTNMTVRRFSGKDSMVDTFYAGLVMRLCQS VSLLELLHIYVGIBSNHLLPRFLQLTERIIILFVVISQEEVQE KYVVCVLFVFNLLDMVRYTYSMLSVIGISYAVLTWLSQTLWMP IYPLCVLAEAFIYQSLPYFESFGTYSTKLFPDLISYFPYVLKI YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKM*STAFQCDTR KDRLWQCSK*NTGSILVEKFLVF
6182	1769	1224	AS*IDYQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI VRPFGSSVNTFGKLGCDLDMFLDDETRNLNSAHKISGNFLMEFQ VKNVPSEIATQKILSVLGECLDHFGPGCVGVQKILNARCPILVR FSHQASGFQCDLTNNRIALTSSSELLYIYGALDSRVRALVFSVR CWARAHSLTSSIPGAWITNFSLTMMVIFPLQRSPPIPLTLDL KTLADAEDKCVIEGNNCTFVRDLRSRIKPSQNTETLELLLEFFE YFGNFAFDKNSINIRQGREQNKPDSSPLYIQNPFTSLNISKNV SQSLQKQFVDLARESAILQVEDTDRPSSSNRPWGLVSLLLPS APNRKSFTKKKSNKFAIETVKQLLESKGNRTENFTKTSKRTI STQT
6183	1118	452	HLDRYIKSPGSGSSTPAPPSHLLLYLLHPQSTRMTGCCGCSRG GSGCGGCGSSCGGCGSGCGGCGSGRGGCGSGCGGCGSSCGGCGS RCYVPVCCCKPVCWVPACSTSCGSCGSGKGGCGSGCGSKGC GSCGCSQSSCCKPCCSSGCGSSCCQSSCCKPCCQSSCCVPVC CQSSCCKPCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM VP
6184	1	2191	IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGSGGGGARGAE EPPPPQLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTL FLTATGQVETFFVCCWAAQIKEHLLKSKWCRPTSLNVRIITS ELYRSLGDVLRDVKALVRSDFLLVYGDVISNINITRALEHR LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVAVDSTTNRL HFQKTQGLRRFAFPLSLFQGSDDGEVRYDLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRAAGAIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGNITLPEGSVISLHPPDAEDEDDEGFSDDSGADQEK DKVKMGYNPAEVGAAGKGYLWKAAGMNMEEEELQQLNLWGLKI NMEESESESEQSMDSSEEDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVLEPPLQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAEID FFLEHEALGISMALVMAFYQLEILAEETILSWFSQRDITDKGQ QLRKNQQLQRFIQWLKEABEESDD
6185	791	44	PCTSCVLWATLHLPASTRKAPQAECEMISITWQKIGVIGITGFG IFFILFGTLLYFDSVLLAFGNLLPLTGLSLIIGLRKTFWFFQR HKLKGTSLGGLGVVIVLLRWPLLMFLETYGFPSLFGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTESSNLNLDHWLKGAK REEWEPPQSPALTHSPTYPGPPQVQKERNGAELTSNPQVDSR GCQEAEMQTPRLGLGWYHTLTLYLWBEK
6186	569	238	VYGDSSNTNTHGAERNRKLKKHWKLCHAQSRDLVNGLALKMA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KERKVKNKVRNKADTEEVFNNSPTNQEKMPSTAILPDFSGSVIS NIRNQMETLHSQPHQEENLCFENSFSLINLLPINAVEPTSSQOI PNRETSEANKERRKMTSKSSESNIYSPITSFITADSELHDIKD LEDCLMVGLHTCGDLAPNLTIRIFTSNSEIKGVCSVGCCVHLLSE EFENQHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV AAGQGLPTESLFYRAVLQDIKDCCYGITKCDRHVGKIYSKCSSF LDYVRRSLKKGLEDKLPBKIIIMNYEYKYPKPMNELEAFNMLK VVLAPCIETLILLDRCLCYLKBQEDIAWSALVKLFDPVKSPRCYA VIALKKQ*FPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP PSGRVGSRYD
6187	1701	771	DAWGPETRLARILNPDSFIEPRPGRLLPELEATRPHMEPKASCPA AAPLMERKFHVLVGVGTGSVAALKPLLVSKLLDIPGLEVAVVTT ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDDPVLHIDLRRLWDL LLVAPLDANTLGKVASGICDNLCTVMRAWDRSKPLLFPCAMNT AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG TIVDKVKEVLFOHSGFQQS*PGISVMGVPLYSEWVQAKSVKMDV GKIGGYPHLLNGGPALS LPRGQACSRLNWTGPGLSFFQPGEEAA A
6188	238	1534	KGFVNAGPLMAELQVSPQWKAPEMSQICLSCGHPSA*GPRWASW NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCMQEMG NGKANRLYEAYLPETFRRPQIDPAVEGFIRDYKYEKKYMDRSLD INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKMPQKKEDPQLP RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDLLASV PSPSSSGSRKVVGSMPTAGSAGSVPENLNFPEPGSKSEBIGKK QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG VPNGMMTTQQAGYMGMAAMPQTVYGVQPAQQLQWNLTQMTQQM AGMNFYGGANGMMNYGQSMGSGNBQANQTLSPQMWK
6189	1297	793	LGEPLGDLCELI PGDQQQLQMGVEHPGTGAQGSAAQSVAGEVQL TQLSHARQRPSCQGSQILALDLQHMDISRQPRWQHVPVARQVQ RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGGVFAANACDL VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR RVRAFMIHNLQITGIGREDFATTYFLEELNLSYNRITSPOVHRD AFRLRLRLSLDLSGNRLHMLPPGLPRNVHVLKVKRNLALALAR GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQ LTEIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN KLAVGSVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE EEEEDEVEEBETR
6190	66	1309	ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTGQCECRPGYQ GLHCETCKEGFYLNYSGLCQPCDCSPHGALSIPCNSSGKCQCK VGVIGSICDRCDGYGFSKNGCLPCQCNRSASCDALTGAELN CQENSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK SSELEPECDQCKDGYIGPNCNKCEGYYNFDSICRKCQCHGHVY PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLBGNCIK KVILPTPEGSTILVSNASLTTSVPTVINSTFTPTTLQTFVSVS TSENSTALADVSWTQFNIIILTVIIIVVLLMGFVGAVMYRE YQNRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLEDDGNE VAPNGQLTLTTPIHNYKA
6191	1212	1511	VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFPHLTPQPKCPS MIDWIKKIWIYITMEYYATIKRNEIMFFAGTWEMEAIIILSKLM QDYMFSLISGS
6192	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPSDGEAGIEAVGSAEE KGGLVSDAYGEDDFSRLGGDEGDEEEDENSQSEDDDSSETEK PEADDPKDNTEAKRDPQRLVASFSERVNMSFDEIKIPPEPPG RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI QFCAIDELGTNYPKDMFDPHGWSEDSYEEALAKAQKIEMDKLEK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AKKERTKIEFVTGTTKGGTTTATSTTTTASTAVADAQKRKSKW DSAIPTVTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ
6193	3	950	TRGCGNKMGAKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAE KGGLVSDAYGEDDFSRLLGGDEEDGYEEEDENSQRQSEDDDDSETEK PEADDPKDNTEAEKRDPOELVASFSEVRNMSPPDEIKIPPEPPG RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI QFCAIDELGTNYPKDMFDPHGWSSEDSYIEALAKAQKIEMDKLEK AKKERTKIEFVTGTTKGGTTTATSTTTTASTAVADAQKRKSKW DSAIPTVTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ
6194	3	950	TRGCGNKMGAKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAE KGGLVSDAYGEDDFSRLLGGDEEDGYEEEDENSQRQSEDDDDSETEK PEADDPKDNTEAEKRDPOELVASFSEVRNMSPPDEIKIPPEPPG RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI QFCAIDELGTNYPKDMFDPHGWSSEDSYIEALAKAQKIEMDKLEK AKKERTKIEFVTGTTKGGTTTATSTTTTASTAVADAQKRKSKW DSAIPTVTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT IVKKAKQ
6195	736	235	VANGLQSNMPPKFCYCDYCTYLTHDSPSVRKTHCSGRKHKENVKD YYQKWMEEQAQSLIDKTTAAFOQGIPTPTFSAAPPAGAMIPPP PSLPGPPRPGMMPAPHMGGPPMMPMMPGPPGMPMPVGPAPGMRP PMGGHMPMMPGPPMMPRPPARPMMPVTRPGMTTRPDR
6196	1512	623	KTGKRSAAYVRNILDNAEQVISNLEARNLGPRLTPLLQEDSH QRLMLGLMVSELKDHFLRLHQQGVEKKIEQMVLDIYSKLLDLIC HIVETNWRKHNLSWVLFHNSRGSAAEFVAFHIMTRILEATNSL FLPLPPGFHTLHTILGVQCLPLHNLHCIDSGVLLLTETAVIRL MKDLNTEKNEKLKFSIIIVRLPPLIGQKICRLWDHPMSSNIISR NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS NQALYPFEGHDNVDAEFVBEAALKHTAMLLGL
6197	3	819	ADPEGTEEAVMSRYTRPNTSLFIRNVADATRPEDLRREFGRYG PIVDVYIPLDFYTRRPRGFAYVQFEDVDAEDALYNLRKWCVG RQIEIQFAQGRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS RSSWGRNRRRSDSLKESRHRFRFSYSQSKSRKSLPRRSTARSQ SRTPRNFGSRGRSRKSLQKRKSKSIGKSQSSSPQKQTSSGTSK RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSR YRHKNSW
6198	111	1912	SEAAALSPSFISPACFLRLKLPALDGTLPHPDTLGMNYEGARSE RENHAADDSEGGALDMCCSRLPGLPQPIVMEALDEAGLQDSQ REMPPPPPPSPSDPAQKPPPRGAGSHSLTVRSLSLCLFAASQFL LACGVLFWSGYGHIWSQATNLVSSLLTLKQLEPTAWLDSGTW GVPSLLLVFLSGGLVLTTLVWHLRTPEPPTPLPPEDRRQSV SRQPSFTYSEWMBEKIEDDFLDLPVPBTPVFCVMDIKPEADP TSLTVKSMGLQERRGSNVSLTDMCTPGCNEEGFGYLMSPREES AREYLLSASRVLQAEELHEKALDPFLQAEFFEIPMNFVDPKEY DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDLSSYINANYIRG YGEEKVYIATQGPVSTVADFWRMVWQEHPIIVMITNIEEMN EKCTEYWPEEQVAYDGEVITVQKVIHTEDYRLRLISLKSGETER GLKHYWFTSWPDQKTPDRAPLLHLVREVEEAQQEGPHCAPII VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCCQLRQDRGG MIQHCEQYQFVHHVMSLYEKQLSHQSPE
6199	144	1211	MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEKA TGKLPVAVKCIKKALKGKESSIEIEIAVLRIKHENIVALEDIY BSPNHLVLMQLVSGGELFDRIVEKGFYTEKDASTLIROVLDAV YYLHRMGIVHRDLKPENLLYSQDEESKIMISDFGLSKMEGKG VMSTACGTPGYVAPEVLAQKPYSAVDCWSIGVIAYILLCGYPP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FYDENDSKLFEQILKAIEYFDSFYWDDISDSAKDFIRNLMKDDP NKRYTCEQAARHPWIAAGDTALNKNIHESVSAQIRKNFAKSKWRQ AFNATAVVRHMRKLHLGSSSLDSSNASVSSLSLASQKDCASGTF HAL*
6200	702	96	LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAFFDLDTLWPF WVDTHVDPFPHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL QOKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTL QGLETFAKAQTGPLRSSLEESPFEA
6201	2809	2383	GQTPRVVRWMMRRSLRAGKRRQTAGRKSKSPKVPVPIQDDSLPA GPPQIRILKRPTSNVGVSSPNSTRPTLPVKSQAQREAEYAEA RKRLGSSASPEEQEKPIILDRPTRISQPEDSRQPNVIRQLPGP DGSQGFQKRR
6202	2	426	INADRAAVASSLLSRPTRKMAPQKDRKPKRSTWRFLDLTHPVE DGIFDSGNFEQFLREKVKVNGKTGNLGNVHIERFKNKITVVSE KQFSKRYLKYLTKKYLKKNLRDLRVVASDKETYLRYFQISQ DEDESESED
6203	419	2550	RCPRPPATAGAAASRPDRSPFSGISGSEAAAGAGAAAPASQHPA TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDYQERMNKG LNQDQLDAVSKYQEVNTNNLEFAKELQRSFMALSQDIQKTIKTA RREQLMREEAEQKRLKTVLELQYVLDKLGDDDEVRTDLKQGLNGV FILSEELSLDEFYKLVDPERDMSLRLEQYEHASIHLDLLE GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNGHQLCEEEAA SAPAVEDQVPEAEPEAEYETEQSEVESTRYVNRQFMAETQFTS GEKEQVDEWTVETVEVNSLQQPQAASPSVPEPHSLTPVAQAD PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPVISAQPM NPTQNMMPQLVCPVHSESRLAQPNQVQVPEATQVPLVSSTS EGYTASQPLYQPSHATEQRPKQEPIDQIQATISLNTDQTASS LPAASQPVQFQAGTSKPLHSSGINVNAAPFQSMQTVFNMAFPV PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQEQELQTVVG TYHGPSQDQSHQVTGNHQPPQONTGFPRSNQPYNSRGVSRGGS RGARGLMNGYRGPANGFRGGYDGYRPSFNTPNSGYTQSQFSAP RDYSGYQRDGYQONFKRGSQSGPRGAPRGRGPPRPNRGMPQM NTQQVN
6204	2933	787	CTHNLISLGGRALIHFNRLNLKIQEGEAHNI FCPAYDCFLV PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV RLTKQGSNTSGSDTSLFPLLRAPAVDCGKHLFCWECLGEAHEP CDCQTWNWLOKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC ANCKSPIQKNEGCNMQCAKCKYDFCWLCEEWKHSFVHWEVI YRCTRYEVIQHVVEEQSKEMTVEAEKKHFRQELDRFMHYITRFK NHEHSYQLEQRLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV HVLKTRRLKCSYPYGFLEPKSTKKEIFELMQTDLEMTEDL AQKVNRPYLRTPRIHKIKAACLVQCKRQEFASVARGVAFADSP EAPRRSFAGGTWDWEYLGFASPEEYAEFYRRRRHRQRRRGDVHS LLSNPPDPDEPSESTLDIPEGGSSRRPGTSVVSSASMSVLHSS SLRDYTPASRSNQSLQALSSLEDDPNILLAIQLSLQESGLA LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE LLELGDLSMLRGAENDPFSTDTLSSHPLSEARSDFCPSSDPDS AGQDPNINDNLLGNIMAWFDMNPQSIALIPATTEISADSQLP CIKDGSEGVKDELVLPEDSMFEDASVSEGRGTQIEENPLEBNI PGGGKQHPQAW
6205	1	1200	RAHRGKMALEVGDMDGQLSDSDMTVAPSDRPLQLPKVLGGD SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDSCLWKR KRQKCFNPPPKPEPFQFGSSQKPPVAGGKKINNIWGAVLQEQN QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLKESQEHKTD LDKELDEYMHGKKMGSKKEENGQGHLLKRRPVKDRLLGNRPEMN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			YKGRYEITAEDSQEKVADEISFRLQEPKKDLIARVVRRIIGNKKA IELLMETAEEVQNGGLFIMNGSRRTPGGVFLNLLKNTPSISEE QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAISLNFQED DDTSRETFASDTNEALASLDESQEGHAEAKLEAEEAIEVDHSHD LDIF
6206	10	1442	IIISERRERSCLHLVCIRCSCDVVEMGSLGLCSMASNIPCLCGS APCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ LNKIPGFCENEKGVPNCNVLGVYKAVYRLCFGLAMPYLLLSLLM IKVKSSSDPRAAVHNGFWFFKPAIAIAIIGAFFIPEGTFTTW FYVGMAGAFPCILILVLLIDFAHSWNESWVEKMEEGNSRCWYA ALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLC VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPE TNCNPSLLSIIGYNTTSTVPKEGQSVQWHAQGIIGLILFLLCV FYSSIRTSNNSQVKNLTLSDESTLIEDGGARSDGSLEDGDDVH RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWYRYEPSREM KSQWTAUVVKISSSWIGIVLVVTLVAPLVLTNDRFD
6207	2924	1471	TVMAEAAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG GGGGGSDGGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDFY SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA SSSLSSIVGVLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA VGECRYGENCVYLHGSDSCDMCGLQVLHPMDAAQORSQHIKSCIEA HEKDMELSAVQSRKDMVCGICMEVVYKANKPSERRFGILSNCN HTYCLKCIRKWSAKQFESKIIKSCPECRITSNFVIPSEYWVEE KEEKQKILKYKEAMSNKACRYFDEGRGSCPPFGNCFYKHAYPD GRREPPQRQKVGTSRRYRAQRNHFWELEERENSFPDNDDEE VVTFFELGEMLLMLLAAGGDELTDSEDEWDLFHDELEDFYDLDL
6208	2924	1471	TVMAEAAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG GGGGGSDGGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDFY SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA SSSLSSIVGVLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA VGECRYGENCVYLHGSDSCDMCGLQVLHPMDAAQORSQHIKSCIEA HEKDMELSAVQSRKDMVCGICMEVVYKANKPSERRFGILSNCN HTYCLKCIRKWSAKQFESKIIKSCPECRITSNFVIPSEYWVEE KEEKQKILKYKEAMSNKACRYFDEGRGSCPPFGNCFYKHAYPD GRREPPQRQKVGTSRRYRAQRNHFWELEERENSFPDNDDEE VVTFFELGEMLLMLLAAGGDELTDSEDEWDLFHDELEDFYDLDL
6209	1758	829	ERLCFPCMQSKIYSYMSPNKCSGMRFPLOEQRNSVTHHEVKCQK PLAGIYRKREKRNAGNAVRSAKSEEQIKDKARKGPLVFPFNQ KSEAAEPPKTPSSCDSTNAIAKQALKKPIKQKQAPRKAQKQ TQQRNKLTDFFPVRRSSRSKAELOEERKRIDELIESGKEEGM KIDLIDGKGRVIATKQFSRGDFVVEYHGLDIEITDAKKREALY AQDPSTGCMYFYQYLSKTYCVDATRETNRLGRLINHSKCGNCQ TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH
6210	3761	387	IFGMSKLRMLLEDGSGSADFRHFVNLSFFTITVVLLLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEWGTVCNNGWSMEAV SVICNQLGCPATAKAPGWANSAGSGRIWMDHVS CRGNESALWD CKHDGWSKHSNCTHQDAGVTCSDGSLNEMRLTRGGNMCSGRIE IKFQGRWGTCDNFDHASVICRQLECGSAVSFSGSSNFEGEG SGPIWFDDLICNGNESALWNCKHQGWGKXNCDHAEDAGVICSKG ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK QLGCPTAVTAIGRVNASKGFGHIWLDVSVCQGEPAVWQCKHHE WGKHYCNHNEDAGVTCSDGSDLELRLRGGSRCAGTVEVEIQRL LGKVCDRGWGLKEADVVCRLGCGSALKTSYQVYSKIQTANTWL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FLSSCNGNETSLWDCKNWQWGGGLTCDHYEEAKITCSAHREPRLV GGDIPCSGRVEVKHGDWGSICDSDFSLEAASVLCRELQCGTVV SILGGAHFEGEGNGQIWAEFQCEGHESHLSLCPVAPRPEGTCSH SRDVGVCSTRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD IEDAHVLCQQLKCGVALSTPGGARFGKNGQIWRHMFHCTGTETQ HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSGWTICD DSWDLSDAHVVCRLGCGEAINATGSAHFEGGTGPIWLDKCN GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE ACAGRLEVFYNGAWGTGKSSMSETTVGVVCRQLGCDKKGKINP ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET WITCDNKIRLQEGPTSCSGRVEIWHGGSGWTVCDSDWLDLDAQV VCQQLGCGPALKAFKEAFGQGTGPIWLNVEVKCKGNESSLWDCP ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFFIA VGILGVVLLAIFVALFLLTKRRRQRLAVSSRGENLVHQIQYR EMNSCLNADDLDMNSSGGHSEPH
6211	3761	387	IFGMSKLRMLVEDSGSADFRRHFNLSPTITVVLILLSACFVT SSLGGTDKELRLVDGENKCSGRVEVKVQEBWGTVCNNGWSMEAV SVICNQLGCPATAIKAPGWANSSAGSGRIWMDHVS CRGNESALWD CKHDGWGKHSNCTHQDAGVTCSDGSNLEMLRTRGGNMCSGRIE IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFEGEG SGPIWFDDLICNGNESALWNCKHQGWGKHNCDAEDAGVICSKG ADLSRLRLVDGVTECSGRLEVRFGQEWGTICDDGWDSYDAAVACK QLGCPATAIGRVNASKFGHIWLDVSVCQGHEPAVWQCKHHE WGKHYCNHNEADAGVTCSDGSLELRRLRGGGSRCAGTVEVEIQRL LGKVCDRGWGLKEADVCRQLGCGSALKTSYQVYSKIQTATNWL FLSSCNGNETSLWDCKNWQWGGGLTCDHYEEAKITCSAHREPRLV GGDIPCSGRVEVKHGDWGSICDSDFSLEAASVLCRELQCGTVV SILGGAHFEGEGNGQIWAEFQCEGHESHLSLCPVAPRPEGTCSH SRDVGVCSTRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD IEDAHVLCQQLKCGVALSTPGGARFGKNGQIWRHMFHCTGTETQ HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSGWTICD DSWDLSDAHVVCRLGCGEAINATGSAHFEGGTGPIWLDKCN GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE ACAGRLEVFYNGAWGTGKSSMSETTVGVVCRQLGCDKKGKINP ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET WITCDNKIRLQEGPTSCSGRVEIWHGGSGWTVCDSDWLDLDAQV VCQQLGCGPALKAFKEAFGQGTGPIWLNVEVKCKGNESSLWDCP ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFFIA VGILGVVLLAIFVALFLLTKRRRQRLAVSSRGENLVHQIQYR EMNSCLNADDLDMNSSGGHSEPH
6212	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFR RELFPFACHEIGLGAEGSGPPAPAPARESRSRAMEEASSPGL GCSKPHLEKLTGLITRILESSPGVTEVTIIIEKPPAERHMISSWE QKNCVMPEDVKNFYLMINGFHMVTSVKLDEHIIPLGSMAINS I SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS VIFELDCNGSGKVCLVYKSGKPALAEDTEIWFDRALYWHFLT DTFTAYYRLLITHLGLPWQYAFTSYGISPQAKQRVSMYKPTTY NTNLLTEETDSPVNKLDPSKVFKSKNKIVIPKKKGVPQAGGQK GPSGSPGPTSSTSKSSSGGNPTRK
6213	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFR RELFPFACHEIGLGAEGSGPPAPAPARESRSRAMEEASSPGL GCSKPHLEKLTGLITRILESSPGVTEVTIIIEKPPAERHMISSWE QKNCVMPEDVKNFYLMINGFHMVTSVKLDEHIIPLGSMAINS I SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VIFELDCSCNGSGKVCIVYKSGKPALAEDTEIWFLLDRALYWHFLTDTFTAYYRLLITHLGLPQWQYAFSTSYGISPAKQQRVSMYKPITYNTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGFPVQAGGQKGPSPGSPGSTSTSSSSSGSGNPTRK
6214	2	460	HELAPSAIRRAARLGLGPARWQSRAAAFYFVRGFRGTGWSFVGWVVLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRRESKRFSAYNYRTYAVRRIRDAFRENKVNKDPVEIQTLVNKAKRDLGVIRRQVHIGQLYSTDKLIIENRDMPT
6215	2	1849	FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVSIAGKNVMLDCGMHMGFNDRRFPDFSYITQNGRLTDFLDCVISHFHLDCGALPYFSEMVGVDGFIYMTHTPTQAIICPILLEDRKIAVDKKGANFFTSQMIKDCMKKVAVHLHCTVQVDDELBIKAYYAGHVLGAAMFQIKVGSSESVYTGDNMTDPDRHLGAAWIDKCRPNLLITESTYATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGRAQELCILLETFWERNMLKVPIYFSTGLTEKANHYKLFIPWTNQKIRKTFVQRNMFEFKHIKAFDRAFDNPGPMVVFATPGMLHAGQSLQIFRKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRQVLEVQMVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKMEFLKQLIEQELRVNCYMPANGETVTLPTSPIPVGISLGLKREMAQGLLPEAKKPRLLHGTLMKDSNFRVLSSEQALKELGLAEHQLRFTCRVHLHDTRKQETALRVYSHLKSVLKDHCVQHLPGDSVTVESVLLQAAAPSEDPGTVKLLVSWTYQDEELGSLTSLKKGLPQAPS
6216	11	393	QTTREPEPRNSALRQSRKMAVGVSSVSRLLGRSRPQLGRPMSSGAHGEEGSARMWKTTLTFFVALPGVAVSMLNVYLKSHHGEHERPEFIAYPHLRIRTKFPFPGDGNHTLFHNPHVNPLPTGYEDE
6217	9	1178	TRVGRGESGLKMEVKPFPGRFPQDSGRRRRRRGEEGHDPKEPEQLRKLFIGGLSFETDDSLREHFEKWTTLTDCVVMRDPQTKRSRPGFVTYSCVEEVDAAACARPHKVDGRVVEPKRAVSREDSVKPGAHLTVKKIFVGGIKEDTEEYNLRDYFEKYKIEETIEVMEDRQSGKRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSQEMQSGSQRGRGGGSGNFMGRGNGFGGGGNGFGRGNGFGGSGGGGGGSGRGSYGGGDDGNGFGGDDGNGGGGPGYSSRGGYGGGPGYGNQGGGYGGGGYDGYNEGGNFGGGNYGGGNYNDFGNYSQQQS NYGPMKGSFGRSSSGSPYGGGYGGGGSGGYGSRFP
6218	1305	906	SCERRGFIMADDLKRFLYKLLPSVEGLHAIVVSDRDGVFVIVKANONAPEHALRPGFLSTFALATDQGSKLGLSKNKSIIICYNTYQVQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELRQVVEVS
6219	2	890	AGPGEAGAGAGTRCAGAEAEASAGGEDCESPAPEADRPHQRPFLLIGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVILSQDRFYKVLTAEQKAKALKQYNFDHPDAFDNDLMHRTLKNIVEGKTVEPVTYDFVTHSRLEPETTVVPADVLFEGILVFYSQEIRDMFHLRLFVDTSDVRLSRRVLRDVRGRDLQILTQYTFVVKPAFEEFCLPTKKYADVIIIPRGVDNMVAIHLIVQHIQDILNGDICKWHRRGSGNSRSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH
6220	227	764	EQNISLEMSCTIEKALADAKALVERLRDHDAAESLIEQTALNKRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQOENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMKLKEQHSKIDMVHRNKSEGFPLDASRHILEAPQHGLERRHLEANQNVH
6221	98	916	RNIWDLNFPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTPNIWAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAEAGAMTLCITNPLWVTKTRMLQYDAVNSPHRQYKGMFDTLVKIYKYEGVRGLYKGFVPGFPGTSHGALQFMAYELLKLKYNQHINRLPEAQLSTVEYISVAALS KIFAVAATYPYQVVRARLQDQHM FYSGVIDVITKTWRKEGVGGFYKGIAPNLI RVT PACCTFVVYENVSHFLDLREKRK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6222	2	2116	MARELRALLLWQRRRLRPLLRAPALAAVPGGKPLCPRRRTTAQLG PRRNPAWSLQAGRLFTQTAEDEKPELHSIISSSTESVQGSTSKH EFOAETKKLLDIVARSLYSEKEVFIRELISNASDALEKLRHKL SDGQALPEMEIHLQTNAEKGTITITQDTGIGMTQEEVLVSNLGTIA RSGSKAFLDALQNAEASSKIIGQFGVGFYSAFMVADRVEVYSR SAAPGSLGYQWLSDGSGVFEIAEASGVRTGTKIIHLKSDCKEF SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIWMDPKDQVRE WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPMKPSM FVDSRELGSVALYSRKVLITKATDILPKNLRIRGVVDSEDI PLNLSRELLQESALIRKLRDVLQQRLLIKFFIDQSKKDAEKYAKF FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSL EYASRMRASTRNIYYLCAPNRHLAEHSYYEAMKKDTEVLFCE EQFDELTLHLREFDKKKLISVETDIVVDHYKEEFEDRSFAAE CLSEKETEEELMAWMNRVLGSRVTNVKVTLRDLTHPAMVTVLEMG AARHFLRMQQLAKTQBERAQLLQPTLEINPRHALIKKLNQLRS EPGLAQLLVDQIYENAMIAAGLVDDPRAMVGRNLNELLVKALERH
6223	3	715	DAWARTMAGMVDQDEEQVKSFLNMEVECNVHCYHEKDPDGCY RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDCYKLGAYVVTGK GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAHDGQVND GQPDLGKARDYYTRACDGGYTSSCFNLSAMFLQAGPGFPKMDL ACKYSMKACDLGHIWACANASRMVYKLGQDGVKVEAKAEVLKNRA QQVHKEQQKGVQPLTFG
6224	1	133	LRTISSMAWGPILLTLHAHCTGSAQSVLTQPPSVSGARIPHEK
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPPQAGARRQAFLEFGDVTVDFT QKEWRLLSPAQRALYREVLTENYSHLVSLGLHLSKPELIRLEQ GEVWPGEERRRRRPGPCAGIYAEHVLRPKNLGLAHQROOQLQFSD QSPQSDTAEGQEKEKSTKPMASFSPPLRHAVSSRRRNSVVEIES SQGQRENPTIDKVLKGIENSRWGAFCABRGQDFSRKMMVIH KKAHSRQKLFTRCHQGFREDSEALLLHQNTHTEKSYVCSVCG RGFSLKANLLRHQRTSHGEKPFCKVCGRGYTSKSYLTVHERTH TGEKPYECQECGRFRNDKSSYNKHLKAHSGEKPFVCKECCGRGYT NKSYFVHVHRIHSGEKPYRCQECGRGFNSKSHLITHQRTSHGEK PFACRQCKQSFVKGSLLRHQRTSHGEKPFVCKDCERSFSQKST LVYHQRTSHGEKPFVCRECGGFIQKSTLVKHQITHSEKPFVFC KDCGRGFQKSTFTLHQRTSHSEKPYGCREGRRFRDKSSYNKH LRAHLGEKRFRCDCGRGFTLKPNTLTHQRTSHGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFIKSTLLFHQKTH SGEKPFICSECGGFIWKSNLVXQLAHSGKQPFVCKECCGRGFN WKGNNLTHQRTSHGEKPFVNCVCGGFSWKRSLTRHHWRHHSKE KPFVQCQCKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS
6226	29	266	TKVSELLGGSQRLFFPLWRRLCRCGLGRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA
6227	2581	890	MSASSLLEQRPKGQGNKVQNGSVHQKDGNDLDDDFEPYLSQARP NNAYTAMSDSYLPSYSPSIGFSYSLGEAAWSTGGDTAMPYLT YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFPPSGIDFS AWGNSSQGSTQSSGYSSNYAYAPSSLGAMIDGQSAFANETL NKAPGMNTIDQMAALKLGSTEVASNVKVVGSVAVSGSITSNI VASNSLPPATIAPPKASWADIASKPAKQPKLKTNGIAGSSL PPPPIKHNDIGTWDNKGPAKAPSQALVQNIQPTQGSQPQVQ QWANNPPVAQASVGGQTQLPPPPPPQAQLSVQQQAAQPTRV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHVLEKLSIN NYPKDFDWNLKHGRVFIKSYSEDDIHRSIKYNICWSTBHGK RLDAAYRSMNGKPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG VWSQDKWKGRFDVRWIFVKDVPNSQLRHLRLNENKPVNTSRD TQEVPLEKAKQVLKIIASYKHTTSIFDDFSHYEKRQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6228	47	1978	<p> GRRCRRRGAVMELAQEARELGCWAVEEMGVPVAAARPESTLRRL CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDSPOVRRKL ELEAAVTRLRAEIQELDQSLERMDTEAQDTAMEQARQHTQDT QRRALLLRAQAGAMRRQOHTLRDPMQRLQNLRLQDMERKAKV DVTFGSLTSAALGLEPVVLRDVRTACTLRAQFLQNLPLPQAKRG SLPTPHDDHFGTSYQQWLLSSVETLLTNHPPGHVLALEHLAAER EAEIRSLCSGDLGDTISRPQAPDQSDSSQTLPMSVHLIQEGW RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL ILGLRRCCLTWELKALHDQSQELQDAAGHRQLLLRELQAKQQR LHWRQLVEETQEQVRLIKGNSASKTRLCRSPGEVLALVQRKVP PTFEAVAPQSRELLRCLLEEVRLHPLHILLTLLRHRPGELKPLP TVLPSIHQLHPASPRGSSFIASHKLGLPPGKASELLPAAASL RQDLLLLQDQSLWCWDLHMKTSLLPGLPTQELLQIQASQEKQ QKENLGQALKRLEKLLKQALERIPELQGIQVGDWWEQPGQAALSE ELCQGLSLPQWRLRWVQAQGLQKLC </p>
6229	1571	560	<p> GPSLLGTRGTPNPARTLQIFFLIIGRRITGRMAAVDDLQFEFEG NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREEDDELLG NDDSDKTELLAGQKKSSPFWTFEYYQTFDVTYQVFDRIKGS LPIPGKNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLSNFI HLGEKTYHYVPEFRKVSIAATIIYAWLVPLALWGLMWRNSK VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIPHKAVRWILVMI ALGISGSLAMTFWPAVREDNRVALATIVITIVLLHMLLSVGCL AYFFDAPENDHLPTTTATPNQTVAANKSS </p>
6230	1723	600	<p> SKMSGRSGKKKMSKLSRSARAGVIFPVGRMLMYLKKGTFKYRIS VGAPVYMAAVIEYLAEILELAGNAARDNKKARIAPRHILLAVA NADELNQLLKGVTIASGGVLPRIHPELLAKKRGTKGKSETILSP PPEKRGRKATSGKKGGKSKAAKPRTSKSKKPKKDSKKEGTSNST SEDGPGDGFILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP TTAIEDLKBIDIGALEKAGGKBFLETVKELRKSQGPLEVAEAAV SQSSGLAAKFVHCHIPQWGSCKCEEQLEETIKNCLSAEDKKL KSVAFPPFPSSGRNCFPKQTAQVTLKAISAHFDDSSASSLKNVY FLLFDSSEIGIYQEMAKLDAK </p>
6231	149	870	<p> LIFSSSTMDRSLRNVLVVSFGFLLLFAYGGLQSLQSSLYSEEG LGVTALSTLYGGMLLSSMFLPPLLIERLGCKGTIILSMCGYVAF SVGNFFASWYTLIPTSILLGLGAAPLWSAQCTYLTITGNTHAEK AGKRKDMVNQYFGIFFLIFQSSGVWGNLISLTVFGQTPSQETL PEEQLTSCGASDCLMATTTTNTSTQRPSSQLVYTLGIYTGSGVL AVLMIAAFLQPIRDVQRESE </p>
6232	3679	1476	<p> FVAGTTMAGFWGTAPLVAAGRGRWPPQQLMLSAALRTLKHVL YYSRQCLMVSRNLGSGVYDPNEKTFDKILVANRGEIACRVIRTC KKMGIKTVAIHSVDVASSVHVKMADEAVCVGPAPTSSKSYLNMDA IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA IQAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEAVRIAREIGY PVMIKASAGGGGKGMRIAWDDEETRDGFRLLSSQEAASSFGDDRL LIEKFIDNPRHIEIQVLGDKHGNALWLNRECSIQRRNQKVVEE APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHQADIR INGWAVERVYAEADPYKSFGLPSIGRLSQYQEPHLPLGVRVDSG IQPGSDISIIYDPMISKLITYGSDRTEALKRMADALDNYVIRGV THNIALLEVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK NQLLAIASSLFVAFQLRAQHFQENSRMPVVKPDIANWELSVKLH DKVHTVVASNNGSVFSVEVDGSKLNVSTWNLASPLLSVSDVGT QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV TEDTSVLSRPMGPVVVAVSVKPGDAVAEGQECVIEAMKMQNS MTAGTGTVKSVCQAGDTVGEGLLVELE </p>
6233	1	2654	HSTRENLNAGNPNFPSEGHVLRSTGPGGSFAKHMVAQCVPSPKGP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LACSRITYFFGATHVPYLGGSKLPPKTEQIRLLSQIYAAVIEAV LAGIACYAKTSSLTAKAEVAEQTLGSGLDSEFELIPFKAALRSKM TFHIHAVNNQGRIVPLDSEDSLSFVKACMAVYDIPDLLGGNGC LGSVVFSEFSLTSQILVKEKDGTVTTETSSSVLTAAPRFCSWL VEDNEVKLSEKTHQAVRGDESFLGTLYLTGGEGAYLYSSNLQSWP EEGNVHFFSSGLLFSHCRHGSIIISKDHMSISFYDGDSTSTVA ALLIDFKSSLLPHLPVHFHGSNNFLMIALFPKSKIYQAFYSEVF SLWKQDQNSGILSKVIQEDGLSVEQKRLHSSAQKLSALSQAPAG EKRSSLLKLSAKLPELDWFLOHFAISSISQEPVMRTHLPVLLQQ AEINTTHRIESDKVIIISIVTGLPGCHASELCAFLVTLHKECGRW MVYRQIMDSSECFHAAHFQRYLSSALEAQNRARSARQSAIRKKT RLLVVLQGYTDVIDVQALQTHPDSNVKASFTIGAITACVEPMS CYMEHRFLFPKCLDQCSQGLVSNVFTSHTTEQRHPLLVLQQLS IRANPAAAFILAENGIVTRNEDIELILSENSESSPEMLRSRYL MYPGWYEGKLNAGSVYPIVMVQICVWFGRLPKEKTRFVAKCKAIQS SIKPSPPSGNIYHILGKVKFSDSERTMEVCYNTLANSLSIMPVL EGPTPPPSKSVSQDSSGQCECYLVFICGSLKEDSIKDWLRQSA KQKPQRKALKTRGMLTQOEIRS IHVKRHLEPLPAGYFYNGTQFV NFFGDKTDFHPLMDQFMNDYVEEANREIEKYNQLEQEQEYHDLF ELKP
6234	1731	404	PRVREDMDHKSPGNKGLSVYAGIKSIVKSSLSGMVESSRHNSGL DKQSDIQNLNEERILALQLCGWIKKGTDDVGVFPFLNSLVQEGEW ERAAVALFNLDIRRAIQILNEGASSEKGDNLNLVAMALSGYT DEKNSLWREMCSTLRQLQNNPYLCVMFAFLTSETGSYDGVLYEN KVAVRDRVAFACKFLSDTQLNRYIEKLTNEMKEAGNLEGILLTG LTKDGVDLMESYVDRTDGVDQTASYCMLQGSPLDVLKDERVQYWI ENYRNLLDAWRFWHKRAEFDIHRSKLDPSSKPLAQFVSCNFCG KSI SYSCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC ALCLINMGTFVSSCPGGTKSDEKVDLSKDKKLAQFNNWFTWCHN CRHGGHAGHMLS WFRDHAECVPVSACTCKCMQLDTTGNLVPETV QP
6235	1	571	EKRDRHRLPSWPRAALKVPGRGGRVGTTPELAAGGIMATRNPPPO DYESDDDSYEVLDTLEYARRHQWNRVFGHSSGPMVEKYSVATQ IVMGGVTGWCAGFLQKVGKLAATAVGGGFLLLQIASHSGYVQI DWKRVEKDVNKAQRQIKKRANKAAPEINNLIEATEFIKQNI SSGFVGGFLGLAS
6236	1	703	WDQNKGAAGSGTLPLSLPSARFSAGPPTQSRPTMSNMEKHLF NLKFAAKELSRSAKCDKEEAKAKIKKAIQKGNMEVARIAE NAIRQKNQAVNFLRMSARVDAAARVQTAVTMGKVTKSMAGVVK SMDATLKTMLNLEKISALMDKFBHQFETLDVQTQMEDTMSSTTT LTPQONQVDMLLQEMADEAGLDLNMELPQGQTSVGTSVASAEQ DELSQRLARLRDQV
6237	312	720	PTAMABEGIAAGGVMDVNTALQEVLTALIHDLARGIREAAKA LDKRQAHLCVLANCDEPMYVKLVEALCAEHQINLIKVDNKKL GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIIEYFK CKK
6238	2	4666	EEVPTQESVKWEINVIKNPEIVFVADMTKNDAAPALVITTQCEI CYKGNLENSTMTAAIKDLQVRACPLPVRRKGKITTVLQPCDLF YQTTQKGTDPQVIDMSVKSLLTKVSPVIINTMITITSALYTTKE TIPEETASSTAHLWEKKDKTKLMWFLEESNETEKIAPTTELVP KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL INLHCQLELEVHYNNEMFGVWEPLLEPLEIDQTEDFRPNWLGK MKKKAKMAIVESDPEENYKVPEYKTVISFHSKDQLNITLSKCG LVMLNNLVKAFTEAATGSSADFVKDLAPFMIINSLGLTISVSPS DSFVSLNIPMAKSYVLKNGESLSMDYIRTKDNDFNAMTSLSSK LFFILLTPVNHSTADKIPLTKVGRRLYTVRHRESGVERSIVCQI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDITLGTASPENEFN IPLGSYRSFIFLKPEDENYQCEGIDFBEIKNKGALLKKKCRS KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL RNLLPYKIAYYIEGIESVFTLSEGHSAQICTAQLGKARLHLKL LDYLNHDWKSEYHIKPNQQDISFVSFTCTVTEMEKTDLDIAVHMT YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPNPKPVLP FSFQPNHFNNNKVQLMVTDSLSNQFSIDTVGSHGAVKCKGLK MDYQVGVITDLSFNITRIVTFTPFYMIKNKSKYHISVAEENGD KWLSDLLEQCIFFWPEYASSKLLIQVERSEDPPKRIYFNKQENC ILLRLDNELGGIIAEVNLAESTVITFLDYHDGAATFLLINHTK NELVQYNQSSLSSEIEDSLPPGKAVFYTWADPVGSRRLKWRCKRS HGEVTKQKDDMMMPIDLGEKTIYLVSFEEGLQRIILFTEDPRVFK VTYSEKAELAEQEI AVALQDVGISLVNNYTKQEVAYIGITSSD VVWETPKPKKARWKPMVKHTEKLEREFKBYTESSPSEDKVIQL DTNVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQ SFRIQIYRIQIQNIHGAFFPVFPVKPPKSVTMSAPKPFDT VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMT AEVTENTVELPHKIDIEAFKEEYKTASLDVQSQVSLYEYFHSIP IKLHLSVLSLSSGREEAKDSKQNGGLIPVHSLNLLKLSIGATLTD VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL GLDLVGNPFGLIREFSEGEAFPEPYQCAIQGPEEFVEGMALG LKALVGGAVGGLAGAASKITGAMAKGVAAMTDEDYQQRREAM NKQPAFGREGITRGGKGLVSGFVSGITGIVTKPIKGAQKGAAG FFKGVGKGLVGAVARPTGGIIDMASTFGIKRATETSEVESLR PPRFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDESDLNH
6239	2108	634	KPGMAGKSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNQA THDLLYHWQDLEQYDHFEPGVVPRTFGLPVVIAVFPSSPAVYVL SLEMSKFYSQLIVRGVLGLGVI FGLWTLQKEVRRHFGAMVATM FCWVTAMQPHLMFYCTRTPNLVLPVLLALAAWLRHEWARFI WLSAFATVFRVELCLFLGLLLALLAGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRLTWPEGVLYWNTVLNKSNNWGTSPILL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVALGFMALYSLL PHKELRFIIYAFPMNLITAARGCSYLLNNYKKSXWLYKAGSLLVI GHLVUNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAGTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLLNLTLQPLPPFNVLQTKLVLL ERLPRPS
6240	2202	1176	HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPFTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSYSKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREARHPRLVPTGPTRHREPSVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLPKDEVQLKTTYKSNQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV
6241	3	1341	RNAEKKRLSLQREKI IARVSIDNRTRALVQALRRITDPKLCIT RVEBLTFHLLFEPFGKGVAVKERIIPYLLRLRQIKDETLOAAVR EILALIGYVDPVKGRGIRILSIDGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSVD FSQNVIVGTVMKSWSHAFYDSQIWNILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGCGQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLNNPSALAMHECKK LWPDVPLECIVSLGTGRYESDVNTVTYTSKTKLSNVINSATD TEEVHIMLDGLLPDITYFRFNPVMCENIPLDESRENEKLDQLQLE GLKYIERNEQMKKVKAKILSQEKTTLQKINDWIKLKTDMYEGLP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6242	198	1310	FFSKL QHFLPGAETWSPGAHVCTARRFPGRSLAAPPRAAPRAVEMGE SSEDIDQMFTLLGEMDLLTQSLGVDTLPPDPNPRAEFNYSV GFKDLNESLNALEDQDLDMADLVADISEAQRTIQAKESLQ NQHHSASLQASIFSGAASLGYGTNVAATGISQYEDDLPPPADP VLDLPLPPPPPEPLSQEEEEAAKADKIKLALEKLKBAKVKKLV VKVHMNDNSTKSLMVDRLQARDVLDNLFKETHCDENVWCLYE IYPQLQIERFFEDHENVVVELSDWTRDTENKILFLEKEEKYAVF KNPQNFYLDNRGKESKETNEKMNKNKESLLEVRLILQSGRKE KDVCSIFKSFASENNGKI
6243	1509	614	RSASRFSGCWSRDSTCCCCPSTCWSRSSASCPRARWPPSSAPAT TSRASSRRLACGPQTRAGAETRTAMIRANSARDTRRATCRSA AGTPSPPTMTCLTDVPTGCAAVEPTARLPAAAWASTITTGCCPA MGQAGAGPAGRKGEAGGGPGRHAHPSPLPREPRVRTGPPAH SPTPGSIDPSPELSWGSAGVTQESPLLDVDFLLFRTRAVDPLR RVFFFFYQHLTFFSIQPQPPCHAFHPRDPPAGTKRQLILVPLK GPPIILAPILSLTPILSRWSCYFPRSRILAQGWHL
6244	2119	1745	FEHAYASQFGTFLGNNESECKLKLQKQTMLSWVWNPSELSK FTNPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDEAYE EMVNIIEYNKELQAKVNILRRQLAELETEDEGMQESP
6245	81	1148	LSLRNAKYSFPQELISLFSMTDLNDNICKRYIKMITNIVILSLI ICISLAFWIISMTASTYYGNLRPISPRWLFVSVVPLIVSNGL KKKSLDHSGALGGLVVGFIILTIANFSFSTLMMFFLSSSKLTKW KGEVKKRLDSEYKEGGQRNWWQVFCNGAVPTBELALLYMIENGP EIPVDFSKQYSASWMLSLAALACSAGDTWASEVGPVLSKSSP RLITTWKVPVGTNGGVTVVGLVSSLLGGTFVGIAYELTQLIFV NDLDISAPQWPIIAGGLAGLLGSIVDSYLGATMQYTGLDESTG MVVNSPTNKARHLAGKPILDNNAVNLFSSVLIALLPTAAWGF PRG
6246	1177	359	SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV QATHRGAVNSNMLCILKLASQMPLENTTVQQMVFMLLSNLALS HDCKGVIOKSNFLQNLFLSLALPKGKNKLSNLTILWLKLLNLS SGEDGQOMILRLDGLDCLLTEMISKYKHKSSPLPLIFHNVCFS PANKPKILANEKIVITVLAACLESENQNAQRIGAAALWALIYNYQ KAKTALKSPSVKRRVDEAYSIAKKTFFPNSEANPLNAYYKCLE LVQLNLS
6247	3	1678	NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFSSFL YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLLWSVT SIFAIGGLVGTILVKMIGKVLGRKHTLLANNGFAISAALLMACS LQAGAFEMLIIVGRFIMGIDGGVALSVLPHYLSBISPKIIRGSLG QVTAIFICIGVFTGQLLGLPELLGKESTWYPLFGVIVVPAVQL LSLPLPDSPRYLLEKHNEARAVKAFQTLGKAHVSEVEBEVL AESRVQRSIRLVSVLELLRAPYVRWQVTVIVTMACYQLCGLNA IWFYTNISIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI IASFCSGPGGIPFILTGEFFQSQRPAAFIAGTVNWSNFAVG LLFPFIQKSLDTCFLVFATICITGAIYLYFVLPETKNRTYAEI SQAFSKRNKAYPPEEKIDSAVTDGKINGRP
6248	56	1773	VPPPRMAAVPPGLEPNNRVRIPKAGNRSVTVQNPAAALDLICI AAVIKECHLVILSLKSLTDAETDVLCAVLYSNHNRMRHKLPHL ALKQVEQCLKRLKNMNLGSIQDLFELFSSNENQPLTTKVCVVP SQPVVLEVLKVLGACKLLRLDCCCKTFLTLVKHLGLQBFII LNLVMVGLVSRWLWLYKGVKRLILLYEPLFGLLQEVARIQMP YFKDFTFPSDITEFLGQPYFEAFKKMPIAFAAKGINKLLNKL LINEQSPRASEETLLGISKKAKQMKINQNNVDLGQPVKNKRVF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KESSEFDVRAFCNQLKHKATQETSFDKCSQSRLKTTYSSQK VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCSSKLLKAQAI FLGNKLLKSNRLKHLEAAGTSLPKKLECIKTSICNHLRLRSGGIK TSKHHLRQRRSQNKFLRRQRPQRKLQSTLLREIQQFSQGRKS ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPIVQTKEKMI HENLGIHENETDSWTVMQINKNSTSGTIKETDDDDIPALMGV
6249	56	1773	VPPPRMMAAVPPGLEPWNVRIPKAGNRSVAVTQNPGAALDLCT AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGHKKPHL ALKQVEQCLKRLKNNMLEGSIQDLFELPSSNENQPLTTKVCVVP SQPVVLEVLKVLGACKLLRLDCCCKTFLTLVKHLGLQEFII LNLVMVGLVSRLLWVLYKGVLRLLIILYBPLFGLLQEVARIQMP YFKDFTFPSDI TEFLGQPYFEAFKKMPIAFAAGINKLLNKL LINEQSPRAEETLLGISKKAKQMKNVQNNVDLGQPVKNKRVF KESSEFDVRAFCNQLKHKATQETSFDKCSQSRLKTTYSSQK VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCSSKLLKAQAI FLGNKLLKSNRLKHLEAAGTSLPKKLECIKTSICNHLRLRSGGIK TSKHHLRQRRSQNKFLRRQRPQRKLQSTLLREIQQFSQGRKS ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPIVQTKEKMI HENLGIHENETDSWTVMQINKNSTSGTIKETDDDDIPALMGV
6250	232	1306	LAALHIMALPFRKDEKYKDLDEDELLGNLSETELKQLETVLDD LDPENALLPAGFRQKNQTSKSTTGPFDRHLLSYLEKEALEHKD REDYVPYTGKKGKIFIPKQKPVQTFTEEKVSLDPELEALISA SDTELCDLAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG EKILPVFDEPPNPTNVEESLKRTKENDAHLEVENLNNIKNIPI TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK SLNVESNFTIGVILALIDALRDNETLAELKIDNQRQQLGTAVE LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVKRKR VEGDHQ
6251	62	972	TPGSGPMSAWAAASLSRAAACLLARGPGVRAAPPRDPRPSHPE PRGCGAAPGRTLHFTAAPAGHNKWSKVRHIKGPKDVERSRI KLCLNIRLAVKEGGFNPENHNSNLNILEVCRSKHMPKSTIETAL KMEKSKDTYLLYEGRPGGSSLLIEALSNSSHKQADIRHILNK NGGVMAVGARHSFDKGVIVVEVEDREKKAVNLERALEMAIEAG AEDVKETEDDEERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL EFIPNSKVQLAEPDLEQAAHLIQAALSNHEDVIHVYDNIE
6252	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPKDKLQTKRKKPRRYWEE ETVPTTAGASPGPPRNKNRRLRPQRPKNAYILKKSRIKSKPQV PKKPREWKNPESQRLSGAQDPFPGPAPVPVEVVQKFCRIDKSR KLPHSKAKTRSRLVAAEAEETSIKAARSELLAAEPPGLEGE DGEDTAKICQADIVEAVDIASAACHFDLNLRFQGPYRLNYSRTG RHLAFGGRGRGHVAALDWVTKKLMCEINVMCAVRDIRFLHSEALL AVAQNRWLHIYDNQGIELHCIRRCRDVTRLEFLPFHLLATASE TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVILHGHSG TVSLWSPAMKEPLAKILCHRGVRAVAVDSTGYMATSGLDHQL KIFDLRGTYQPLSTRILPHGAGHLAFSQRGLLVAGMGDVVNIWA GGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT SMLVPGAGEENFDGLESNPYRSRQKQEWKALLEKVPABLIC LDPRALAEVDVISLEQKKEQIERLGYDPQAKAPFQPKPKQKGR SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS ALDRFVR
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPKDKLQTKRKKPRRYWEE ETVPTTAGASPGPPRNKNRRLRPQRPKNAYILKKSRIKSKPQV PKKPREWKNPESQRLSGAQDPFPGPAPVPVEVVQKFCRIDKSR KLPHSKAKTRSRLVAAEAEETSIKAARSELLAAEPPGLEGE DGEDTAKICQADIVEAVDIASAACHFDLNLRFQGPYRLNYSRTG RHLAFGGRGRGHVAALDWVTKKLMCEINVMCAVRDIRFLHSEALL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AVAQNRWLHIYDNOGIELHCIRRCDRVTRLEFLPPHFLLATASE TGFLTLYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG TVSLWSPAMKEPLAKILCHRGGRVAVAVDSTGYMATSGLDHQL KIFDLRGTYQPLSTRTPHAGHLAFSQRGLLVAGMGDVVNIWA GQKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT SMLVPGAGEPNFDGLESNPYRSRKQRQEWVKALLEKVPALIC LDPRALAEVDVISLEQKGKEQIERLGYDPQAKAPFQPKPKQKGR SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS ALDRFVR
6254	155	1139	HAIGRRGGSQELSAACGCFALRLRAPGSGRPALAPGAAAFAGL GGAPRFPPRGSAAGRMTLLKBYRICMPLTVDEYKIQQLYMISKH SHEQSDRGEGVEVVQNEPFDPHHNGQPTKEKRVYLNKLPWSWA RAVVPKIFYVTEKAWNYPPYTITEYTCFPLPKFSIHETKYEDN KGSNDTIFDNEAKDVEREVCFIDIADEIPERYKESDEPKHFK SEKTGRGQLREGWRDASHQIMCSYKLVTVKFEVWGLQTRVEQFV HKVVRDILLIGHRQAFAWVDEWYDMTMDDVREYKMKHEQTNIK VCNQHSPPVDDIESHAQTST
6255	1	1444	PTRPQQLLVSLATVIFVASQKALSVEKAVIKQQLSVSNGWT VYRIARQASRMGNHDMAKELYQSLLTQVASKHFYFWLNSLKEFS HAEQCLTGLQEENYSSALSCLAESLKFYHKGIALSTAASTPLNP LSFQCFVFKLRIDLLQAQFSLICTCNLSKTSPPPAIATTIAMTL GNDLQRCGRISNQMQSMEEFRSLASRYGDLQASFDADSATLR NVELQQQSCLLISHAIEALILDPEASAFQEYGSTGTAHADSEYE RRMMSVYNHVLVEEVSLNGKYTPVSYMHTACLCAIALLKVP SFQRYFFQKLQSTS IKLALSPSPRNPAEPIAVQNNQQLALKVEG VVQHGSKPGLFRKIQSVCLNVSTLQSKSGQDYKIPIDNMTNEM EQRVEPHNDYFSTQFLNPAILGTHNITVSSSVKDANGIVWKTG PRTTIFVKSLDEPYSQQIRLQQQQAQQPLQQQQQRNAYTRF
6256	1	1542	CRGAGAEPAANPRSPRSLVPSLESTSTSVPPAPGTMATDSWALA VDEQEAASLSNLHLKEEKIKPDTNGAVVKTNANAECTDEEEK EDRAAQSLNKLIRSNLVDNTNQVEVLQORDPNSPLYSVKSFEEL RLKPQLLQGVYAMGFNRPSKIENALPLMLAEPQNLIAQSQSG TGKTAAFVLAMLSQVEPANKYPQCLCLSPTEYELALQTKGVIEQM GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPTGTVLDWCSKLK FIDPKKIKVFLDEADVMATQGHQDQSIIRQMLPRNCQMLLF SATFEDSVWKFAQKVVPDPNVIKLRKEETLDTIKQYVLCSSR DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAELSKEGHQVA LLSGEMMVQRAAVIERFREGKEKVLVTNVCARGIDVEQVSVV INFDLPVDKGNPDNETYLHRIGRGTGRFGKRGGLAVNMVDSKHS NILNRIQEHFNKKIERLDTDDLDEIEKIAN
6257	210	615	AFIPAMAEIQQKLQGEVEKYQQQLQKDLKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRET LAQLQQEFQRAQAAGAPG KA
6258	210	615	AFIPAMAEIQQKLQGEVEKYQQQLQKDLKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRET LAQLQQEFQRAQAAGAPG KA
6259	2	1540	ILEKGFPSQCHPERKWKVDVLESSQENEDHFWELLFHNNKTV SVENGDRGSKTFNLGTDVPSLRNYPYKICDSCENMLKNISGLII SKKNC SRKKPDEFNVC EKLLLDIRHEKIPIGESYKYDQKRNAI NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNRKSQIGETVCK YNECGRTFIESLKLNIQRPHLEMEPYGCSICGKSFCMNLRFHG QRALTKDNPYEYNEYGEIFCDNSAFI HQGAYTRKILREYKVS DTWEKSALLKHQIVHMGGSYDYNENGSNFSKSHLTQLRAHT GEKTFECGEGKTFWEKSNLTQHQRHTGKPYECTBCGKAFQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KPHLTNHQRTHTGKPYECKQCGKTFVCVSNLTHQRTHTGKPYECNACGKSFCHRSALTVHQRTHTGKPFICNECGKSFVCVSNLTVHQRTHTGKPYKCNCEGKTFCEKSALTKHQRTHTGKPYECNACGKTFQSQRSVLTKHQRITHRVKALSTS
6260	2081	1436	GTGPEIHACAHASARAPGSRAMALRELKVCLLGDTGVGKSSIVWRFVEDSFDPNINPTIGASFMKTQVQYQNELHKFLIWDTAGQERFRALAPMYRGSAAAIIVYDITKEETFSTLKNWVKELRQHGPPIVVAIAGNKCGLIDVREVMERDAKDYADSIHAFVETSAKNAININELFIEISRRIIPSTDANLPSGGKGFKLRRQPSEPKRSCC
6261	3	1188	FWYRLGPGTRSRWRPRRGSWAASLVPRGFSAPALVTSPCPDPLRSPACEPCRPDFAPRPALLLRSGPRSAFAVTKGPKALKGQPGWPWGMAEVSIDQSLPGVKEVCRDFAVLEDHTLAHSLQEQEIEHHLASNVQRNRLVQHDQLQAKQLQEEDLKAQAQLQKRYKDLEQQDCEIAQEIQEKLAIEAERRRIQEKDEDIARLLQEKELQEEKRKKHFPFEPATRAYADSYVYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDAETARKLQEBELLATQVDMRAAQVAQDEEIAARLLMAEEKKAYKKAKEKESSLDKRKQDFEWKPKTAKAANSKSKESDEPHSKNERPARPPPIIMTDGEDADYTHFTNQSSSTRHFSKSESSHKGPHYKH
6262	2	1759	FECHSQGLCSVHRPGKVPQARMSGLVLGQDEFPAGHRLSQEELLGSTRLVSQGLEALRSEHQAVLQSLSQTIETCLOQGGHEEGLVHEKARQLRRSMENIELGLSEAQVMLALASHLSTVESEKQKLRAQVRLCQENQWLRDELQQLQRLQSEQAQAQLEBEKKHLEFLGQLRQYDEGHTSEKEGDKDLSLDLFPNEEEDPSNGLSRGQGFATAAQGGGYEIPARLRLTHNLVIQYAAQGRYEVAVPLCKQALEDLERTSGRGHPDVATMLNILALVYRDQNKYKEAAHLNDALSIRESTLGPDPHVAATLNNLAVLYGKRGKYKEAEPQCORALEIREKVLGTNHPDVAKQLNNLALLCQNGKYEAVERYQRALAIYEGQLGPDNPVARTKNNLASCYLKQGYAEARTLYKEILTRAHVQEPGSDVDHKKPIWMHAEEREEMSKSRHHEGGTPYAEYGGWYKACKVSSPTVNTLRNLGALYRRQKLEAAETLEECALRSRRQGTDPISQTKVAELLGESDGRRTSQEGPGDSVKFEGGEDASVAVEWSGDGGSTLQRRSGSLGKIRDVLRR
6263	1	2408	RELDLSLADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPTIEVRRCSMPFSVCEHTKQFQTISEESNQGSLLTVPGDTSFSPKPEVFSNVPERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNTAPVNTVMDSPVHLEPSSQGVVIQNKSWEMPVDRLETSTRDFICPNSNIPDQESSLQSFCSNENKVLKENADFLSLRQTELPNGNSCAQDPASFMPQQPCSFPSQSLSDAESISKHMSLSYVANQEPGILQQKNAVQIISSALDTDNESKDTENTFVLGDVQKTDAPVVPVSDSTIQEASPNFEKAYTLPLVPSEKDFNGSDASTQLNTHYAFSKLTYKSSSGHEVENSTTDQVISHEKENKLESVLVTHLSRCDSDLCENMAGMPKGNLNEQDPKHCPSEKCLLSIEDEESQQSILSSLENHSQOSTQPEMHKYQLVKVELEENAEEDDKTENQIPQRMTRNKANTMANQSKQILASCTLLSEKDESSSTPRGIRLTEDDDPQIHHPRKRVSRVPQPVQVSPSLQAKEKTQQSLAAIVDSLKLDEIQPYSSERANPYFEYLHIRKKIEEKRKLCSVIPAQAPQYDEYVTFNGSYLLDGNPLSKICIPTITPPFSLSDPLKELFRQQEVVRMKRLQHSIEREKLIVSNEQEVLRVHYRAARTLANQTLFPFSACTVLLDAEVYVPLDSQSDSKTSVRDRFNARQFMSWLQDVDDKFDKLTCLLMRQQHEAAALNAVQRLEWQLKLQELDPATYKISISYIEIQEFYVPLVDVNDDFELTPI
6264	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAKGNKGFSLGSTVKSHTKGIWMWCVPHPKPEHTLVLLDTEGLGDVKKGDNDNDWIPTLAVLLSSTLVYNSMGTINQAMDQLYVTELTHIRIRSKSPDENENEDSADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SQKDKNFNLPRLCIRKFFPKKKCFVFDLPiHRRKLAQLEKLQDE ELDPFVQVQVADFCSYIFSNSTKTLGGIKVNGPRLESVLVTY INAI SRGDLPCMENAVLALAQIENSAAVQKAI AHYDQMGQKQV LPAETLQELLDLHRVSEAREATEVYMKNFSKDVHLPQKKLAAQ DKKRDDFCQKQNEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG YCLFIQKLQDLEKKYEEPRKGIQAEIILQTYLKSRESVTDAIL QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6265	143	1960	KHRQENNALDAPBIHMTGPMCLIENTNGELVANPEALKILSAI TQPVVVAIVGLYRTGKSYLMNKLAKNGKFSLSGTVKSHTKGI WMCVPHPKPEHTLVLLDTEGLGDVKKGDNDQNSWIFTLAVLL SSTLVYNSMGITINQAMQDLYYVTELTHRIRSKSSPDENENEDS ADPVSPFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT SQKDKNFNLPRLCIRKFFPKKKCFVFDLPiHRRKLAQLEKLQDE ELDPFVQVQVADFCSYIFSNSTKTLGGIKVNGPRLESVLVTY INAI SRGDLPCMENAVLALAQIENSAAVQKAI AHYDQMGQKQV LPAETLQELLDLHRVSEAREATEVYMKNFSKDVHLPQKKLAAQ DKKRDDFCQKQNEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG YCLFIQKLQDLEKKYEEPRKGIQAEIILQTYLKSRESVTDAIL QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6266	276	1421	GS HQKQMLVPCFLYSLQNRKPSLYGSLTCQGI GLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSI TCLD ISSRGGLGVSSSTDGTMKI WQASNGELRRVLEGHVFDVNCRRFF PSGLVVLSSGGMDAQLKIWSAEDASCVVTFKGHKG GILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGLVADCGSSINGVAVGAADN SINLGSPFQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIA SQDGS CFIVQQDL DYVTETGADCD PVYKVATWEKQIYTCCRDLVRRYQLSDL
6267	3	622	LGMKKNNNSAKRGPQDGNQPPAPEKVGWVRKFCGKGI FREITWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYKCEELRKS RSKKNHSKFTLAHSKQPGNTAPNLI FLAVSPEEKESWINALNSA ITRAKNRILDEVTVEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC
6268	160	1368	HRELQNLPAGLSSALIDNPLTLLSIDTYVMLQEPVTFQDVAV DPSREEWGLLGPTQRTYRDVMLETFGHLVSVGWETTLLENKELA PNSDIPEEPAPSLKVQESSRDCALSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSALDTNQVSLQKIDNPE SQANSALDTNQVLLHKIPPRKRLRKRDSQVSKMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSTRSTQITFIRIHKGSQVCRCECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKG FVQSSSLTQHQRVHS GERPFECQBCGRTFNDRSAISQHLRTHTGAKPYKCQDCGKA FRQ SSHILIRHQRTHTGERPYACNCKGKAFTQSSHLIGHQRTNRTKR KKKQPTS
6269	2886	1449	HASAPTRRNMAAASPLRDC HAWKDARLPLSTTSNEACKLFDATL TQYVKNWTKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTMVEISRTQPLTRREQHLVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSDAYFYLGYQEQRMSVAR IYPFWTPDIPLSYVKG IYSFGLMETNFYDQAEKLAKELASINP TDAWSVHTVAHIHEMKAEIKDGLFEMQHSETLWKDSMDLACHNY WHWALYIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSCSML YRLQMEGVSVGQRWQDVLVPARKHSRDHILLFNDAHFLMASLGA HDPQTTELLETTLRDASESPGENCQHLLARDVGLPLCQALVEAE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DGNPDRVLELLLPYRIRIVQLGGSSNAQRDVFNQLLIHAALNCTS SVHKVARSLLMERDALKPNSPLTERLIRKAATVHLMQ
6270	23	2086	SVTVTLGSEGDGRPTTYHLEEMEQEPQNGEPAETIKIIREAYKKA FLFVNKGLNTDELGQKEEAKNYKQGIGHLLRGISISSKESEHT GPWESARQMQQMKMETLQNVTRLEILEKGLATSLQNDLQEVF KLYPEFPKDMCKLPEPQSFSSAPQHAENVGNTSTPSAGAVAA PASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSEFSSVGE EFYRNHSQPPPLETLGLDADELILIPNGVQIFFVNPAGEVSAPS YPGYLRIVRFLDNSLDTVLNRPFGFLQVCDWLYPLVPDRSPVLK CTAGAYMFPDTMLQAGCFVGVVLSSELPEDDRELFEDELLRQMS DLRLQANWNRAEEENEFPQIPGRTRPSSDQLKEASGTDVKQLDQG NKDVRHKGKRGKRAKDTSSSEEVNLSHIVPCEPVPEKPKELPEW SEKVAHNILSGASWVSWGLVKGAETGKAIQKGASKLRERIQPE EKPVEVSPAVTKGLYIAKQATGGAAKVSQFLVDGVCTVANCVGK ELAPHVKKHGSKLVPESLKKDKGKSLDGMVVAASSVQGFST VWQGLECAAKCIVNNVSAETVQTVRYKYGYNAGEATHHAVDASV NVGVTAYNINNIGIKAMVKKATATQTGHTLLEDYQIVDNSQRENQ EGAANVNVRGEKDEQTEKVEKAKKKDK
6271	32	1058	GCGVKTAGMVGREKELSIHFVPGSCRLVBEENVINPNRRLVTGA TGLLGRAVHKEFQQNNWHAVGCGFRARPKEQVNLDSNAVHH I IHDFFQPHVIVHCAEERRPDVVENQPDAAASQLNVDASGNLAKEA AAVGAFLIYISSDYVFDGTNPPYREEDIPAPLNLYGKTKLDGEK AVLENNLGAAVLRIPILYGEVEKLEESAVTMFDKVQFSNKSAN MDHWQORFPTHVKDVATVCRQLAEKRLMDPSIKGTFHWSGNEQM TKYEMACAIADAFNLPSSHLRPIITDSPVLGAQRPRNAQLDCSKL ETLGIGQRTPPFRIGIKESLWPFLLDKRWQRTVFH
6272	1136	528	GAVMEDAAAPGRTEGVLERQGAAPAGQGGALVELTPTPGGLAL VSPYHTRAGDPLDLVALAEQVQKADEFIRANATNKLTIVIAEQI QHLQEQAQKVLDAHRDANLHHVACNIVKKPGNIYLYKRESGQ QYFSIISPKEWGTSCPHDFLGAYKLQHDLSWTPYEDIEKQDAKI SMMDTLLSQSVALPPCTEPNFQGLTH
6273	256	843	SCPRVSPCECRSLGCVMFSLPLNCSPDHIRRGSWCWRPQDLKIA SAAWNSKCHPGAGAAMARQHARTLWYDRPVVFMFCVBDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKKEVAVPRLTKEDIKPVWLSVDFDNWRDWEDEEME LAHVEHYAEVRDNTYCVLPT
6274	56	1142	AAAAAAAAGGAGAAARSLRFRGCLAGALLGDCVGSFYEAHDT VDLTSVLRHVQSLPEDPGTPGSETEALYTTDDTAMARALVQSL LAKEAFDEVDMAHRFAQYKQDPDRGYGAGVTVFVKLLNPKCR DVFEPARAQFNGKGSYNGGAMRVAGISLAYSSVDVQKPARLS AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED LEGDAQSVLDARELGMEEPRYSSRLKKIGELLDQASVTREEVVS ELGNIGIAAFESVPTAIYCFLRCEPDPEIPSAFNSLQRTLIYSI SLGGDTDTIATMAGALAGAYYGMQVPEWSQQSCGEYEETDILA QSLHRVVFQKS
6275	20	565	SRRGRARCLARGSRPVPFRPAKTMAFMVKTMVGGQLKNLTGSLG GGEDKGDGDKSAAEAQGMSREEYEEYQQLVEEKMERDAQFTQR KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI EEDTEEEEEKASVLGQLASLPGLNLGSLKDKAQTALGDLKQSAE KCHVM
6276	797	97	TLLPLPLPDTEGMILLNTGLEGTVAENPWPVHTPSGNILTLE SCLQQLATHPGHWGHLQIAEPALRPSLALLARLSSLGLLHWP VWVGAKISHGSFVPGHVAGRELLTAVAEVFPHTVAPGWFEV LGSGYREQLLTDMLELCQGLWQPVSFQMAMLLGHSTAGAI GRL LASSFRATVTVEHNPAGGDYASVRTALLAARAVDRTRVYRLPQ GYHKDLLAHVGRN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6277	4600	2744	MAFRTEMGLYYSYFKTIVEAPSFNLGVMMIMNDKLTETPLVINT LKRFNLYPBVILASWYRIYTKIMDLIGIQTKICWTVTIGEGLSPTESCEGLGDPACFYVAVIFILNGLMMALFFIYGYLSSGSRLLGGLVTVLCFFFNHGECTRVMWTPPLRESFSYFVLVQLMLLVTHILRA TKLYRGSIALCISNVFFMLPWQFAQFVLLTQIASLFAVYVVG YIDICKLRKIIYIHMISLALCFVLMFGNSMLLTSYASSLVIIWG ILAMKPHFLKINVSELSLWVIQGCFLWFGTVILKYLTSTKIFGIA NDAHIGNLLTSKFFSYKDFDTLLYTCAAEFDFMEKETPLRYTKT LLLPVVLVGFVAIVRKIISDMWGVLAQQTHVRKHQFDHGLVY HALQLLAYTALGILIMRLKFLTPHMCVMASLICSRLFGWLFC KVHPGAIVFALLAAMSIOGSANLQTQWNIVGEFSNLQPEELIEW IKYSTKPDVAFAGAMPTMASVKSALRPVNHPHYEDAGLRART KIVYSMYSRKAAEEVKRELKIKVNVYILEESWCVRRSKPGCSM PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLV EVV KE
6278	3	823	ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL IRIILEYCGVDNIPSVITDMLTRLSDLLKYFNSRSQCLVLAGG ALQVVGKLTITTKNALSSRCLQLIVHYIPVIRAHFEARLPPKQ YSMLRHFHDITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVA PVPSACFRNICKQMTKMHEAIFDLLPEEQTQMLFLRINASYKLH LKKQLSHLNVINDGGPQNGLVTAADVFTGNLQALKGLKDLDLN MAEIEWEQKR
6279	127	1687	GGAMASDGARKQFWKRSNSKLPQSIQHVYGAQHPPFDPLHGLT LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGEDDDDELLAMA AESLNSSEVVMETANRVLNRHSQRQGRPTLQEGPGLQKPRPEAE PPSPPSGDLRLVKSVSEHTSCPAESASDAAPLQRSQSLPHSAT VTLLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR LSWSGIPKVPVPMTWKLLSGYLPANVDRRPTLQKQKQYFAP I EHYDYSRNDVHQDTYRQIHIDIIPMSPEALILQPKVTEIFERI LFIWAIRHPASGYVQGINDLVTPFFVVFICEYIEAEVDTV DVS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR LWDTYQSEPDGFSHFHLYVCAAFVVRWKEILEEKDFQELLLFL QNLPTAHWDDEDISLLLAAYRLKFAFADAPNHYKK
6280	857	2515	ECCDQKMGSRNSSAGSGSDPSEGLPRRGAGLRSEEEEEDEE DDLAQVLAYLLRRGQVRLVQGGGANLQFIQALLDSEENDRA WDGRGLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQREGLCHRGFSLSGEQSRVISHFLPNLGF TDS YSQKAFCGIYSKDGQIFMSACQDQTI RLYDCRYGRFRKFSIKA RDVGWSVLDAFTPDGNHFLYSSWSDYIHCNIYEGEDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRR TLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQVPPKAWRKLKLPDSSLMTYRGH GVLHTLIRCFSPHISTGQQFIYSGCSTGKVVDLLSGHIVVK LTNHKACVRDVSWHFPEEKIVSSWDGNLRLWQYRQABYFQDDM PESEECASAPAPVPSSTPFSSPQ
6281	857	2515	ECCDQKMGSRNSSAGSGSDPSEGLPRRGAGLRSEEEEEDEE DDLAQVLAYLLRRGQVRLVQGGGANLQFIQALLDSEENDRA WDGRGLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQREGLCHRGFSLSGEQSRVISHFLPNLGF TDS YSQKAFCGIYSKDGQIFMSACQDQTI RLYDCRYGRFRKFSIKA RDVGWSVLDAFTPDGNHFLYSSWSDYIHCNIYEGEDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRR TLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EGMEASRQAATQONWDYRWQQVPPKAWRKLKLPDSSSLMTYRGH GVLHTLIRCRFSPHSTGQQFIYSGCSTGKVVVDLLSGHIVVK LTNHKACVRDVSWHPFEEKIVSSSWDGNLRWQYRQAEYFQDDM PESEECASAPAPVPQSSSTPFSSPQ
6282	125	906	RMAACRALKAVLVDLSGTLHIEDAAVPGAQEQALKRLRGASVIIR FVTNTTKESQKDLLERLRKLEFDISEDEIFTSLTAARSLERKQ VRPMLLVDDRALPDFKGIQTSDFNAVVMGLAPEHFHYQILNQAF RLLLDGLPIAIHKARYYKRKDGALGPGPFVTALEYATDTKAT VVGKPEKTFLEALRGTCGPEEAVMIGDDCRDDVGGAQDVGML GILVKTGKYRASDEEKINPPPYLTCEFPFAVDHILQHL
6283	140	1043	LSLFGIHVMNPFWSMSTSSVRKRSEGEKTLTGDKVTSPPRTAP KKQLPSIPKNALPITKTPSPAPAAQSTNGTHASYGPFYLEYSL AEFTLVVVKQLPGVYVQPSYRSALMWFGVIFIRHGLYQDGVKFK TVYIPDNYPDGDCPRLVFDIPVFHPLVDPTSGELDVKRAFAKWR RNHNHIWQVLMYARRVYKIDTASPLNPEAAVLYEKDIQLFKSK VVDVSKVCTARLFDQPKIEDPYAISFPWNPSVHDEAREKMLTQ KKKPEEQHNKSVHAGLSWVKPGSVQPFSSKEEKTAT
6284	1	2879	RSVIPGSTISSRWPEGLSRPRFMAAHEWDWFQREELIGQISDIRV QNLQVERENVQKRTFTRWINLHLEKCNPPLEVKDLFVDIQDGKI LMALLEVLSGRLLHEYKSSSHRIFRLNNIAKALKFLEDSSNVKL VSDIAAEIADGNPSLVGLIWNIIFFQIKELTGNLSRNSPSS LAPSGSGTSDSSFPPTPTAERSVAISVKDQKAIKALLANVOR KTRKYGVAVQDFAGSWRSGLAFLAVIKADPSLVDMKQALENST RENLEKAFSIAQDALHIPRLEPEDIMVDTPEQSIMTYVAQFL ERFPELEAEDI FDSDEKVP IESTFVRIKETPSEQESKVFVLTE GERTYTVNHETSHPPSKVFCVKPESMKFRLDGVSSHLSDS STEFMHQIIDQVLQGGFGKTSIDSEPSPESSILSSRKENGRSNS LPIKKTVEADTYKDFPFCNKLSLCEFGSPRVAKESLRQDGHV LAVEVAEEKEQKQESSKIPESSSDKVAGDIFLVEGTNNNSQSS CNGALESTARHDEESHSLSPPGENTVMADSFQIKVNLMTVEALE EGDYFEAIPLKASKFNSDLIDFASTSQAFNKVPSPHETKPDEDA EAFENHAEKLGKRSIKSAHKKKDSPEPQVKMDKHEPHQDSGEEA EGCFSAPEETPVDKKPEVHEKAKRKSTRPHYEEGEDDDQLQGVG EELSSSPSSCVSLETLGSHSEGLDFKPSPLSKVSVIPHDLF YFPHYEVPLAAVLEAYVEDPEDLKNEEMDLEEPGYMPDLDSRE EADGSGSSSSSSVPGESLPASDQVLYLSRGGVGTTPASEPAP LAPHEDHQRETENDPMDSHQSOESPNLENIANPLEENVTKES ISSKKKEKRKHVDHVESSLFVAPGSVQSSDDLEEDSSDYISPSR TSHSDSSIYLRHRHTRSSSDHFLCSVEERSRSG
6285	2157	1331	SKTENLLEMMWFQQLSFLPSALVIWTSAAFIYSYITAVTLHH IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATYVRYKQVH ALSPEENVIIKLNKAGLVGLISCLGLSIVANFQKTTLFAAHVS GAVLTFGMGSYMFVQTILSYQMOPKIHGKQVFWIRLLLVICG VSALSMILTSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTA EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTAPCPIN NERTRLLSRDI
6286	1619	276	KAGASCCGSANPYVSVGKSCVLLAMAQLQTRFYTDNKKYAVDDV PFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDLIKQQLRM PLDKHMEMENISSREVVEIYVEKYTAPQPEQCMFHDDWISSIK GAEEWILTGSYDKTSRIWSLEGKSIIMTVGHTDVVKDVAVWKD SLSCLLLSASMDQITLLWEWNVERNKVKALHCCRGHAGSVDSIA VDGSGTKFCGSGWDKMLKIWSTVPTDEEDEMEESTNRPRKKQKT EQLGLTRTPIVTLSCGHMEAVSVLWSDAEIICSAWDHTIRVVD VESGSLKSTLTGNKVFNCSISYPLCKRLASGSTDRHIRLWDPRT KDGSLVLSLTSHTGWTSVKWSPTHEQQLISGSLDNIVKLWDT RSCKAPLYDLAAHEDKVLVSDWTDGILLSSGGADNKLYSYRSP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6287	278	1482	TTSHVGA MQFFNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF APAKLQVQKILCDLLLPENLKEGLKESWSLPCCTKNRPDFHS VMEESQSLNEPSPKQSEEIPEVTSEPVKGSINRAQSAQSINSTE MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLEQDVIIVNEDGR NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMLRPFPE PVTTPCGHSFCKNCLERCLDHAFYCPCKESLKEYLADRRYCVT QLLEELIVKYLPELSEKKIYDEETAELSHLTKNVPIFVCTMA YPTVPCPLHVFEPYRRLMIRRSIQGTGKQFGMVCSDTQNSFADY GCMLQIRNVHFLPDGRSVVDVTVGKGRFVLKRGMKDGYCTADIE YLEDV
6288	1	743	VTLYPCRGLVGNLLLGASGMASGCKTGPSILNSDLANLGAECRL MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM HMMVSKPEQVWKPMVAVAGANQYTFHLEATENPGALIKDIRENGM KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM PKVHWLRTQFPPLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPKRSVINLLRNVCSAAQKRS�DR
6289	1	743	VTLYPCRGLVGNLLLGASGMASGCKTGPSILNSDLANLGAECRL MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM HMMVSKPEQVWKPMVAVAGANQYTFHLEATENPGALIKDIRENGM KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM PKVHWLRTQFPPLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM RSEDPKRSVINLLRNVCSAAQKRS�DR
6290	3	1856	TLGRWLLGVYETVAPTILACLPRPRLRRRRRRRRRMRISRYTRKA VPQSLLELKGITKHALNHPPPKLEEISPTSDSHEKDTSSQSXS DITRESSPTSADTGNLSAFPSYTGAGISTEGSSDFSNGYGEELD QNATEKVQMTFTAIDELLYEQKLSVHTKSLQEECQQTASFPHL RILGRQIITPSEGYRLYPRSPSAVSASYETTLSEQERDSTIFGIR GKKLHFSSSYAHKASSIAKSSSFCSMERDEEDSIIVSEGIIEEY LAFDHIDIEEGPHGKKSEAAATEKQKLGYPPIAPFYCMKEDVLAY VFDSVWCKVVSCEQLTRSHWEGFASDDESNVAVTRPDSESSCV LSELHPLVLPVQSKVLYITSNPMSCQASRHQPNVNDLLVHG MPLQPRNLSLMDKLLDLDKLLMRPGSSTILSTRNWPNAVFEFS TSSLSYTVQSTRRRNPPPTLHP ISTSHSCAETPRSVEEILRGA RVPVAPDSLSSPSPTPLSRNLLPPIGTAEVEHVSTVGPQRQMK PHGDSRSRAQSAVDEPNYQQPQERLLLDPFFPRPNTTQSFLLD QYRRSCAVEYPHQARPGRGSGAGPQLHGSTKSQSGGRPVSRTRQG P
6291	1732	602	LVAKMASSASARTPAGKRVINQEELRLMKEKQRLSTSRKRIES PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHKREKVAELKG AKEASQSSASSAPQSVKRKAPDADDQDVKRAKATLVQVQVQST SAWTTNFDKIGREFIRATPSKPSGLSLLPDYEDEEEEEEEEEGD GERKRGDASKPLSDAQKEHSVSSSREVTSVLPNDFFSTNPPK APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV RKVDAPKQMDKEWDEFQKAMRQVNTISEAIVAEDEEGRDRQ IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKBEEN ADSDDEGELQDLLSQDWRVKGALL
6292	1835	1142	TCPGAMKMPVAPWTRFYNSNCCCLCHVRTGTILLGVWYLIINAVV LLILLSALADPDQYNFSSSELGGDFEFMDANMCIAIAISLLMI LICAMATYGAYQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN SIQEIYRQLPPNPPYRDDVMSVNPTCLVLIILFISIIILTFKGY LISCVWNCYRYINGRNSDVLVYVTSNDTTLVLPYDDATVNGA AKEPPPPYVSA
6293	2382	1035	FWCTLGTVDVHPIGWCAINSKILVPPRTIHAFTDWKGYLMKRL VGSRTLVPDFHIKMVESMKYPFRQGMRLVVDKSVQVSRTRMAVV DTVIGGRLRLLYEDGSDDDDFWCHMWSPLIHPVGSRRRVGHGKIK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MSERRSDMAHHTFRKIYCDVPPYLFKKVRAVYTEGGWFEEGMK LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCY HASSHAIFPATFCQKNDIELTPKGYEAQTFNWNYLEKTKSKA APSRLEFNMDCPNHGFVGMKLEAVDLMEPRLICVATVKRVVHRL LSIHFDGWDSEYDQWVDCSPDIYPVGWCELTGYQLQPPVAAEP ATPLKAKEATKKKKKQFGKKRKRIPTKTRPLRQGSKKPLEDD PQGARKISSEPVGEIIAVRVKEEHLDVASPDKASSPELFPVSVE NIKQETDD
6294	354	1814	AQLTTRGRTVAGGVWRWIPSPFPDLELYSCCLGTDRGFPELSHHC KNVIATASDYDMAEITNIRPSFDVSPVAGLIGASVLVVCSVT VFVWSCCHQQAEEKHKNPYPKFIHMLKGISYIPETLSNKKKIIK VRRDKDGPREGGRNLLVDAEAGLLSRDKDPRGFPSSGSCIDQ LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV DYNFPKKALVVTTIQEAHGLPVMDQDQGSDFYIKMTILPDKRHR VKTRVLRKTLDPVDETFYFGIPYSQQLDLVHLVLSFDRFS RDDVIGEVMPVLAGVDPSTGKVLTRDIIKRNQKICSRGELQV SLSYQPVQARMTVVVLKARHLQKMDIAGLSGNPVVKNVYGRK RIAKKKTTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD RTTKNEVVRLLILGAHVSVTASGAHWRREVCSPRKPVAKWHSLS EY
6295	2795	617	VSSALLTGATSGSDAAKSEGASAPLSCTNAVAMDRPDEGPPAK TRRLSSSESPQRDP PPPPPPPPLRLPLPPQQRRLQEETEA QVLADMRGVGLGALPPPPYVILEEGIRAYFTLGAECPGWDS TIESGYGEAPPPTESLEALPTPEASGGSLEIDFQVQSSSFGGE GALETCSAVGWAPQRLVDPKSKEAIIIVEDEDEDERESMRSSR RRRRRRRRKQKVKRESRERNAERMESILQALEDIQLDLAEVNI KAGKAFLRLKRRFIQMRPFLERRDLIIQHIPGFVWKAFLNHPR ISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFTQTNPYFT NMVIVKEFQRNRSGRVLSHSTPIRWHRGQEPQARRHGNQDASHS FFSWFSNHSLEADRIAEIIKNDLWVNPRLYYLRERGSRIKRRK QEMKKRKTGRCEVVIMEDAPDYAVEDI FSEISDIDETIHDIK ISDFMETTDYFETDNEITDINENICDSENPDHNEVPNNETDN NESADDHETTDNNEADDNNENPEDNNKNTDDNEENPNNNENTD GNNFFKGGFWGSHGNNQDSSDSNEADEASDDEDNDGNEGDNEG SDDDGNEGDNEGSDDDRDI EYEEKVIEDFDKDQADYEDVIEII SDESVEEGIEEGIQQDEDIYEENYEEBGSSEDVWEEGEDSDDS DLEDVLQVPNGWANPGKRGKTG
6296	727	1199	RHCGCDAQGACDSLPTGTSSPVTARNAIPEARCCVWLLDGTTV EAVRPARERLARKELRQKRMQQFSRDSAYSSNKDSTCLLTBRDT LGTSLOFPSPFSGTISFGSFSDSGIFPLGSQCCLGFGQFSGK KVALIHKRVRLSVFGARWGRIYFGK
6297	1	922	QRAAAASPSSCGPRGAEYGAALMAMEGYWRFLALLGSAALLVGFLS VIFALVWVLHYREGLGWDSALEFNWHPVLMVTGFFVFIQGI VYRLPWTWKCSKLLMKSIHAGLNAVAAILAISVVAVFENHNVN NIANMYSLSHWSVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFL MPIHVYSGIVIFGTVIATAMGLTEKLI FSLRDPAYSTFPPEGV FVNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTILHPNGGTQ GARGSMPAYSGNNMDKSDSELNNEVAARKRNALDEAGQRSTM
6298	3	985	SVPLRRLSLSGTLQAGTTTKMAVARLAAVAANVPCRSWGWAAV PFGPHRGLSVLLARIPQAPRWLPACRQKTSLSFLNRPDLNLA YKLLKGKSPGIIFIPGYLSYMNKTKALAEIEFCKSLGHACIRFD YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPQILVGSLSGG WMLHAAIARPEKVVVALIGVATAADTLVTKFNQLPVLLKKEVEM KGVWSMPSKYSEGVYVNVQYSFIKEAEHCHLHSPIPVNCPIRL LHGMKDDIVPWHTSMQVADRVLSSTDVDVILRKHSDHRMREKADI QLLVYTTIDDLIDKLSTIVN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6299	512	814	ECDEGIMPVNTISLSLPTNGSPLODILVHPCVTSLSAILTSSSIDAMDDSAFSGPYKFPPTPPLESFNLCPYTSQVVPVPPILGFYQMKEEEVQLRNNH
6300	121	692	AAPSCWSQQRGVPAAAGTPSSPRLVSRRAAPSAGPWGAWRQGARA AQSPFSPINSSSVYPGSDSVHSSPEDGGGGRDRPVGGSPGGPR LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLMCLTKPR ITYNEDVLSKDAGECAICLBELQOGDTIARLPCLCIYHKGCIIDE WFEVNRSCPEHPSD
6301	616	284	GKFPVPVNWEPQPLPPFKYLRCYRCLLETKELGCLLGSIDICLTP AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW IFSQYCFDLDFCNDPQNRGLYTP
6302	490	745	IFGFLHLFHEHSFLLVLCALFAHVFFSSSCGSSVALHSDPCLLS PVLNCLPGDLRPLDELYAQKLKYKAISEELDHALNDMTSL
6303	2	1961	YWNYYGGGLWQSWQEKHPGQALSSPEWNPFDTKEEWQHYSQYL YWYYLEQFYWEAQGWTFDASQSCDDTYTSKTEADDKNDEKCM KVDLVSLSSPIMGDNDSSTGSDKHSEILDGINSIKLNSEEVTS QSLDSCSTSHDGHQQLSEVSSKRECPASGQSEPRNGGTNEESNS SGNNTDPPAEDSQSSGANTSKDRPHASGTGDDESEEDPPEHK PSKLKRSHELDIDENPASDFDDSGSLGFKYSGQKYGGIPNFS HRQVRYLEKNVKLKSKYLDMRRQIKMKNNKHIFFTKSEKPFKK SKILSKVEKFLTWVNKPMDEEASQSSSHDNGHDASTSCDSEEQ DMSVKKGDDLETNNPEPEKCSQSVSSAGELETENYERDSLATV PDEQDCVTQEVDPDSRQAEAEVKKKKKKKKKKVNGLPPEIAA VPBLAKYWAQRYRLFSRPDDGIKLDREGWFSVTPEKIAEHIAGR VSQSFKCDVVVDAFCGVGGNTIQFALTGMRIAIDIDPVKIALA RNNAEYVGIADKIEFICGDFLLLASFLKADVFLSPWGGPDYA TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS LAGPGGQVEIEQNFNNKLKITAYFGDLIRRPASET
6304	1	1438	HRARVDRSRESPGDLRHPGRVRRDITLSGHPRLSTQHVLLRE DEVDPGTGKDLGHPQHGSP IQETQSEVVTLVSLPGSDMAALPA WRATSGTLWPHTAEGRDLLGAENRALTGQQAEDPTLASGAYQ WPGSVEKLQGSVWCDAETLLSSRTGGQAPPWLTLDHVDQMLRL AQGEVVDKARVPAHQVQLQVGFSTEALQDLSSPRLSQLCSQGL CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLPYRY TDGGARPVIIWWAPDVQHLSDPDEDQNSLALGWLQYQALLAHSCN WPGQAPCPGIIHTEWARIALDFLLQVHDLDRYCCGFEPPEPSD PCVEERLREKCRNPALRLVHILVRSSDPShLVYIDNAGNLQHP EDKLNFRLLLEGIDGFESAVKVLASGCLQNMLLKSLQMDPVFWE SQGGAQGLKQVLQTLERQGVLLGHIQKHNLTLFRDED
6305	99	420	NMIWRGRSTYRFRFRSVPPPELIGFMLEPGDEEPQEEPTES RDPAPQGEREDQGAETQVPDLEADLQELSQSKTGDECGDGP VQGKILTKSEQPKMEGR
6306	1	1874	PTRPSKVVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLEALINGDVPMEETDFSEADKSALMD ESEDGVIIPGSHSENALHASEEEEGEGGKAQSSLGYPIMLRVVQ SVRHTTRKSSTTLREGVWVHYSNKDTRLKRHYWRLDCKCITLPQ NNTNRYKIEIPLSEILTVESAQNPSLVPPGTPNPHCFEIVTANA TYFVGEMPGGTPGGPSGQGAARAAGWETAIRQALMPVILQDAPS APGHAFHRQASLSISVNSQIQENVDIATVYQIFPDEVLSGGQF GVVYGGKHKRKTGRDVAVKVIDKLPPTKQESQLRNEVAILQSLR HPGIVNLECMFETPEKVFFVMEKLHGDMLEMLSSSEKGRLEPRL TKFLITQIILVALRHLHFKNIVHCDLKPENVLLASADPPQVKLC DPGFARIIGEKSFRRSVVGTAYLAPEVLLNQGYNRLDMWSVG VIMYVLSLGTFFNEDEDINDQIQNAAFMYPASPWSHISAGAI LNNLLQVKMRKRYSDVKSLSHPWLQEVQTLWLDLRELEGKMER YITHESDDARWEQFAAEHPLPGSGLPTDRDLGACFPQDHMQG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6307	2136	589	LAERISVL CFLLPGRDPEPPEAGAAAPCAPGAPDMSFRKVVQRQSKFRHVFG QPVNQDCYEDIRVSRVTWSTFCAVNPKFLAVIVEASGGGAPL VLPLSKTGRIDKAYPTVCGHTGPVLDDIDWCPHNDEVIASGSEDC TVMVWQIPENGLTSLTEPVVVLBGHTKRVGI IAWHPTARNVLL SAGCDNVVLIWNVGTAEELVRLDSLHPDLIYNVSWNHGSLFCS ACKDKSVRIIDPRRGLVAEREKAHEGARPMAIFLADGKVFTT GFSRMSERQLALWDPENLEBPALQELDSSNGALLPFYDPDTSV VYVCGKGDSSIRYFEITEEPYIHFLLNTFTSKEPQRMGSMMPKR GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPD TAG PEAALEAEWVSGRDADPILISLREAYVPSKQDRLKISRNVLS DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEV QELRALRALVKEQGDRI CRLEEQLGRMENGDA
6308	2	1118	GRTRPEKMLLSLVLTYSMRYLLPSVVLLGTAPTYYVLAWGVWR LLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVIILLYGDL PKNKENI IYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLK WPLYGWYFAQHGGIYVVRSAKNEKEMRNKLQSYVDAGTPMYL VIFPEGTRYNEQTKVLSASQAFAAQRLAVLKHVLTPIKATH VAPDCMKNYLDIYDVTVVYEGKDDGGQRRRESPTTEFLCKECP KIHIIHIDRIDKKDVPEEQEHMRRLHERFEIKDKMLIEFYESPD PERRRKFPKSVNSKLSIKTLPSMLILSGLTAGMLMTDAGRKL YVNTWIYGTLLGCLWVTIKA
6309	220	563	LVAEVKEPCSLPMLSVDMENKENGSGVGVKNMENGRRPPDPADWA VMDVVNYFRTVGFEEQASAFQEQEIDGKSLLLMTRNDVLTGLQL KLGPALKIYEHVKPLQTKHLKNSS
6310	36	979	GPRCWFLLI LSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE AQRGSLAEELNVAAGLWADCDQPLYDCPMGLICTNYHILQEHV DLHLEENSFQQGMDRVQCSGDLQALHQLQEQEDRKRSEESRQE IEEFQKLQRQYGLDNSGGYKQQQLRNMEIEVNRGRMPPEFHR KADMMESLALGFDDGKTKTSGIIEALHRYQNAATDVRVWLSS VVDHFHSSSLGDKGWGCGYRNFQMLLSLLQNDAYNDCLKGMLIP CIPKIQSMIEDAWKEGFDPPQASQLIIRIQGTAKWIGACEVYIL LTSLRV
6311	1	675	PVWVNSCEGPRLAAAARTGHGVRRRLACLGEPRVKAAMVMTL ASKLKRDGDKGSRTAATASDSTRVSVRDKLLVKEVAELEANL PCTCKVHFDPNKLHCFQLTVPDEGYQQGKFQFETEVDPDAYN MVPKVKCLTKIWHFNI TETGEICLSLLREHSIDGTGWAPTRL KDVVWGLNSLFTDLLNFDDPLNIEAABHHLRDKEDFRNKVDDYI KRYAR
6312	213	1400	GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVLVCISIPPLT RQISVKALGIGKNVCEKAATSVDAFRMVTASRYYPQLMSLVGN VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLSPSYGWIC DELMGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFFVRQNA IRGIRHVTSDDFCFQMLMGGGVCSTVTILNFMMPGAFVHEVMV GSAGRLVARGADLYGQKNSATQEEILLRDSLAVGAGLPEQGPQD VPLLYLKGVMYVQALRQSFQGGDRRTWDRTPVSMASFEEDGL YMQSVVDAIKRSSRSGEWEAVEVLTEPDTNQNLCALQRNNL
6313	2	2071	QRSGAARLALPSFFSPACVHRSPLSFHGCWFYFVVVFMPFLGVL FHRRAHGC TLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHFKAHKAVLAACSKFFYKFPQEP TOEPLVEIGVSKMAFRHLIEFTYAKLMIQGEENAVWKAEE FLQMLEAIAKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI TESLPSAESEPVIEVEIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDSA LALLADITSKYRQGRKQIKEDGCPSPDPTSK QVEGIEIVELQLSHVKDLFHCEKCNRSFKLPYHFKEHMKSHSTE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
			SFKCEICNKRYLRESAWKQHLNLCYHLEEGGVSKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGKPFCEPCNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNWDQPKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNI SERLVTEEVLSVETRVQ TEPVTSMTTIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSRLPEQVQVSYLEVGRITTEEGTEVHVEELHVERVNO MPVEVQTELEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAKAENEDRTALPVLE
6314	2	2071	QRSGAARLAFPLSPFSPACVHRSPLSFHGCWFYFVVVPMPLGLV FRRRAHGCTLSCSSFVEQPTAMEAETMECLQEFPEHHKMILD RLNEQREQDRFTDITLIVDGHFKAHKAVLAACSKFFYKFFQEF TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEENADVWKAEE FLQMLEAIKALEVRNKEN SAPLEENTTGKNEAKKRKIARTSNVI TESLPSAESEPVIEVIAEGTIEVEDEGIETLEEVASAKQSVK YIQSTGSSDDALALLADITSKYRQGDGRKQIKEDGCPDPTSK QVEGIEIVELQLSHVKDLFHCCKNRSFKLFYHFKHEMKSHSTE SFKCEICNKRYLRESAWKQHLNLCYHLEEGGVSKQRTGKKIHVC QYCEKQFDHFGHFKEHLRKHTGKPFCEPCNCHERFARNSTLKCH LTACQTGVGAKKGRKKLYECQVCNSVFNWDQPKDHLVIHTGDK PNHCTLCDLWFMQGNELRRHLSDAHNI SERLVTEEVLSVETRVQ TEPVTSMTTIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS QVHDSHMSRLPEQVQVSYLEVGRITTEEGTEVHVEELHVERVNO MPVEVQTELEADLDHVTPEIMNQBERESSQADAAEAAREDHED AEDLETKPTVDSEAKAENEDRTALPVLE
6315	1	1015	LGIAVNVVTLVLISYCPATEEAPYWTYLLCALGLFIYQSLDA IDGQARRTNSCSPGLGELFDHGCDLSLTVFMAVGASIAARLGT PDWFFSCSFIGMFVYCAHWQTYVSGMLRFGKVDVTEIQIALVI VFVLSAFGATMWDYTIPILEIKLILPVLGFLGGVIFSCSNYF HVILHGGVGKNGSTIAGTSLVSPGLHIGLIIILAIMIYKKSATD VFEKHPCLYILMFGCVFAKVSQKLVAHMTKSELYLQDVTFLGP GLLFLDQYFNNFIDEYVVLWMAVISSFDMVIYFSALCLQISRH LHLNIFKTACHQAPEQVQLSSKSHQNNMD
6316	1503	792	VSAGAGTGIMGGTSTRVTFEADENENITVVKGIRLSENVDR MKESSPSGSKSQRYSGAYGASVDEELKRRVAEBLALQAKKES EDQKRLKQAKELDRERAANEQLTRAILRERICSEERAKAKHL ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTQYQKAA EEVEAKFKRYESHPCADLQAKILQCYRENTHOTLKCSALATQY MHCNVHAKQSMLEKGG
6317	102	839	PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSDDQN FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG QHLGEQLGFEFFETSAKDNINVQTFERLVDIICDKMSSELET PAITAAKQNTRLKETPPPPQPNAC
6318	1765	733	PWHPLRTLPLHHPHPRPPRAEGREGADSMHLPGLRLREAPPL LGPLLSPPPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI LAPVRRDRVLAEPLQCLRKEAALHGHKDFHPRVTCACQEHRTGT VGPKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIVFNLN DVASLEHTKQWLADALKENDPSSVLLFLVSGSKDLSTPAQYALM EKDALQVAQEMKAENAVSSLTGENVREFFRVAALTFEANVLA ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
6319	88	717	AATRLNQNTLLGKKVVLVPYTSSEHVPSRYHEWMKSEELQRLT ASEPLTLEQYAMQCSWQEDADKCTFIVLDAEKWQAPGATEES CMVGDVNLFLTLEDLTLGIEVMIAPSCRGKGLGTEAVLAML SYGVTTLLGLTKFEAKIGQGNEPSIRMFQKLHFEQVATSSVFQEV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TLRLTVSESEHQWLEQTSHEVEKPYRDGSAEPC
6320	90	1111	RPRGTGREKVMAMAVDSFYLLYREIARSCNCEALALVGAWYTA RKSITVICDFYSLIRLHFIPRLGSRADLIQYGRNAVVSQATDG IGKAYAEELASRGLNIILISRNEEKLVVAKDIADTYKVETDII VADFSSGREIYLPREALKDKDVGILVNNVGVFPYPQYFTQLS BDKLWDIINVNIAAASLMVHVLPVGMVERKKAIVTISGSCCK PTPQLAASFASKAYLDHFSRALQYAYASKGIFVQSLIPFYVATS MTAPSNFLHRCISWLVSPKVIYAHAVSTLGISKRTTGYWSHSIQ FLFAQYMPPEWLWVGANILNRSRKEALSCTA
6321	1418	341	HRKAALGALMAGRLGKALAAVSLSLALASVTIRSSRCRGIQAF RNSFSSSWFHLNTNVMSSNGSKENSHNKARTSPYPGSKVERSQ VPNEKVGWLVWQDYKPEYTAVSVLGPRWADPQISENFSFK FNEKDGHVVERKSKNGLYEINGRPRNPAGRTGLVGRGLLGRWGP NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAKRKDCGEWA IPGGMVDPEKISATLKREFGEBALNSLQKSAEKREIEEKLHK LFSQDHLVIYKGYVDDPRNTDNAMMETEAVNYHDETEIMDNLM LEAGDDAGKVKWVDINDKLKYASHSQFIKLVAEKRAHWSSEDS EADCHAL
6322	2047	1083	NQELKNVSSRTVQPHFLEFLSLGWSVDVGRHPGWTGHVSTS WSINCCDDGEGSQQBEVISEDIGASIFNGQKKVLYYADALTEI AFVVPSPVESLTDLSLESNISDQSDSNMDLMPGILKQPSLTLEL FPNHTDNLSSQRLSPSSRMRLPQGRPVPLGPETRVSVVWVE RYDDIENFPLSELMTEISTGVETTANSSTSLRSTTLEKEVPVIF IHPLNTGLFRIKIQGATGKFNMIPLVDGMI VSRRALGFLVRQT VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT SLFQEVGLKNCSS
6323	1	656	PASTTDGAQEAEVPLDGAFWIPRPAGSPKGCFCACVSKPPALQA PAAPAPEPSASPPMAPTLFPMESKSSKTDVRAAGAPPACKHLA EKKMTNPTTVEVYVPTTEVNDYLLWSIFNFVYLNFCCLGFIA LAYSLLKVRDKLLNDLNGAVEDAKTDRLINITRSLAASCIMLW MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
6324	1	2061	EGAGMRRPCRCRSLNEAEAGALPAAARMGLEAPRGRRRQPGQQ RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPERAGLGPAGTES PQAEFWTDGQTEPAAAGLVETERPKQKTEPDRSSLRTHLEWSW SELGTTCLWTETGTDLWTDPHRSDLQFQPEBASPWTPQGVHGP WBLETHGSGTQPERVKSADNLWTHQNSSSLQTHPEGACPSKE PSADGSKWELYTDSRTQDDIEGPWTEPYTDGSKKQDTEAARK QPGTGGFQIQQDTSWTPSTDSQTAPGTDCLLGEPEDEGPLE EPEPEGLLTHLYSHLKCSPLCPVPRLIITPETPEPEAQFVGPSP RVEGSGGFSASSFDESEDDVAGGGGASDPEDRSGSKPWKKL KTVLKYSPFVVSFRKHYPWVQLSGHAGNFQAGEDGRILKRFQCQ EQRSLEQLMKDPLRPFPAYYGMVLQDGTFFNQMEDLLADFEFP SIMDCKMGSRTYLEEELVKARERPRPRKDMYEMVAVDPGAPT EEHAQGAVTKPRYMQWRRTMSSTSLGFRIEGIIKADGTCNTNF KKTQALEQVTKVLEDFVDGDHVLQKYVACLEELREALEISPPF KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP WAEGNREDGYLWGLDNMICLLQGLAQS
6325	165	944	GLRDPFRKRRLKPOVKMSNYVNDMWPGSPQEKDPSSTSRSGGS SRLSSRSRSRFSRSSRSRSHSVSSRFSRSSRSRSHSVSSRHHQ RKYRRYSRYSRSRSRSRSRRYRERYGFTTRYRSPSRYSR RSRSRSRGRSYCGRAYAIARGQRYYGFRTRYVPEHSRWRDRSR TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT VPSAKETSRGIGVSSNGAKPEVSIILGLSEQNFQKANCQI
6326	238	680	GEPSPATQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWITISFT VQTTLQPPGGLPAAPVSGRMFAFEPVGRDLARRMVPRAKRTQTL GARRVAAQGARPLPEDRRPKSGERLHVTAPCWEFVLPSVSLTA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6327	1	1337	QANGGVGQREASSGVP SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLSGSLCALFSDA DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQKKKKEEK GAEPTGS AVSAAQCQGPTRREL PESGIQLGTPREKVPAGRSKAE LRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKR LPEYPQVDDLLRLRLVKKPERQVPTRKDYGSKVSLFSLPQYS RQNSLTQFMSSIPSSVIHPAMVRLGLQYSQGLVRGNSNARCIALLR ALQQVIQDYTTTPNEELSRDLVNKLKPYMSFLTQCRPLSASMHN AIKFLNKEITSVGSSKREEEAKSELRAAIDRYVQEKIVLAAQAI SRFAYQKISNGDVILVYGCSLSVSRILQEAWTEGRRFRVUVVDS RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV GGEKV
6328	1030	276	HASAEVTTAAARGLOAMEEEMHTDAKTRAENGTSPPRGPGCSL RHFACEQNLLSRPDGSASFLOGDTSVLAVGYGPAEVKVSKEIFN KATLEVILRPKIGLPGVAEKSRERLIRNTCEAVVLGTLHPRTSI TVVLQVSDAGSLLACCLNAAACMALVDAGVPMRALFCGVACALD SDGTLVLDPTSKQKEARAVLTFALDSVERKLLMSSTKGLYS ELQOCLAAQAASQHVFRFYRESLQRRYSKS
6329	3	2016	SSEVAAGGGTRSAMAEAGSGEVTVSATGAANGLNNGAGGTSATT SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENS LRTRNL RGDIERKSLAINEBFVSIFKEVKEELESIEDVQAMSNCCQDMT SRLQAAKEQTQDLIVKTTKLOESQKLEIRAQVADAFLSKFQLT SDEMSLLRGTRREGPITEDFFKALGRVKQIHNDVKVLLRTNQQT GLEIMEQMALQETAYERLYRWAQSECRTLTQESCDVSPVLTQA MEALQDRPVLYKYTLDFGTARRSTVVRGFDALTRGGPPGGTFR PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALKHVTQGV ENIQEVVGHITEGVCRLKVRIEQVIVAEPGAVALLYKISNLLKF YHHTISGIVGNSATALLTTEEMHLLSKKIFFNLSLSHASKLMD KVELPPFDLGPSSALNQTMLLREVLASHDSSVVLDPARQADFV QVLSCLVDPLQMCCTVSASNLGTADMATFMVNSLYMMKTTLALF EPTDRRLMLQFQIRAHLDTLNEQASYVLTRVGLSYIYNTVQQ HKPEQGSANMPNLDVSLKAAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTELVCRAYGEVYAAMVNPINEYKDPENILHR SPQQVQTLLS
6330	1151	333	FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQOPL PVHQPHSLVSEGFTVKAMMKNSSVVRGPPAAGAFKERPTKPTAFR KFYERGDFFIALEHDSKGNKIAWKVEIEKLDYHHYLPFFDGLC EMTFPYEFFARQGIHDMLEHGNGKILPVLQQLIPIKNALNLRN RQVICVTLLKVLQHLVVSAMVGKALVPYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCILN
6331	3	495	QQQQRVTRGRACASATPLEGCVDSLSPRTHAALLKVAQMVT LIAFICVRSSLWNTYSAYSIFYEVVTTICDLIMILAFYLVHLFRFY RVLTICISWPLSELHLYLIGTLLLLIASIVAASKSYNQSGLVAGA IPGFMATFLCMASIWLSYKISCVTQSTDAV
6332	1	878	VTESNKFELVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLPQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTDDLIQLTAMCWMREFIQLAGRVMLEPY SSGILTAVLPCLAYDDRKSKIKEVANVCNQSLMKLVTPEDDELD ELRPGQRQAEPTPDALPKQEGTASGEWTPSLHLTSCRGPPEPD VIGVALGPHLSNQDYFMVYVTHIIVAAATQRSGSSGSPFFCRQDTG KLSTMATHSQLVKGTGTGLEPRQAVSSSH
6333	3	1467	TRTPSEAEAGGESQSCVSAASHSDWTAGKPVSLAPLIPPRGAG QPLTFSPSGRQPLRSLLVGMCSSGSGRRSSLSPTMRPGTGAERG GLMMGHPGMHYAPMGHMPMGQRANMPVPHGMMFPQMMFPMGPP MGQMPGMMSSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTAS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop Codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
6342	2	1191	PALRKVDQMPEPRYVVMGSCANGGGYYHYSYSVVRGCDRIVP VDIYIPGCPPTAEALLYGILQLQRKIKRERRLLQIWYRR DPRVRAMLATLARVAALRKTCFSGRGGGRGLWTGRPQSDMNNI KPLEGVKILDLTRVLGPFATMNLGDLGAEEVIKVERPGAGDDTR TWGPPFVGTESTYYLSVNRNKKSIIVNIKDPKGVKIIKELAAVC DVFFVENYVPGKLSAMGLGYEDIDEIAPHIIYCSITGYGQTGPIS QRAGYDAVASAVSGLMHITGPEVACLSHIAANYLIGQKEAKRWG TAHGSIVPYQAFKTKDGYIIVGAGNNQQPATVCKILDLPOLIDN SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG PINNMKNVFAEPQVLHNLGLVMEHEFTVVGKISVPGPAVRYSKFK MSEARPPFLGQHTTHILKEVLRYYDDRAIGELLSAGVVDQHEH GTAMVSDDELNLLVIVVDANFIWGWKQALKESQFTLSKCIDAV MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGDP GNPPEFNPSSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGQHT ETLLAGSLAKALCYIHRMNEKVKDNQEMKSRILVIAAEDSALQ YMNFMNVIFAAQQNILIDACVLDSDSLQQAACDITGGLYLKV PQMPSSLQYLLWVFLPDQDQRSQILIPPPVHVDRACFCRNL IBIGYVCSVCLSFICNFSPICTTCTAFKISLPPVLKAKKKKLK VSA
6343	2	936	TMPTATLGNLRGYGMASFGLAAPSLTPPQLATPNLQOFFPQATR QSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSSTPNRKDSSS QTMPVEDKSDPPPEGSEAAEPRMDTPEDQDLPPCPEDIAKEKRT PAPEPEPCASELPAKRLRSSSEEPTEKEPPGQLQVKAQPOARMT VPKQTQTPDLLPEALEAQLPRFPQPRVLQVQAQVQSQTQPRIPS TDTQVQPKLQKQAOQTQSPHLVLQKQVQVQPLQQAEPQKQVQ POVQPOAHSQGPQVQLQQAEPKQVQPOVQPOAHSQPPPRQVQ LQLQKQVQTQTPVQVHTQAQPSVQPEHPPAQSVSQPPEQTHEQ PHTQPVQVSLLAPEQTTPVVVHVCGLEMPDDAVEAGGMEKTLPEP VGTQVSMEEIQNESACGLDVGECENRAREMPGVWAGGSLKVTI LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALOFFCY ICKASCSSQQEFQDHMSEPQHQQRIDGEIQHMSQACLLSLLPVPR DVLETEDEEPPRRWCNTCLYYMGDLIQHRRTDHDKIAKQSLR PFCTVCNRYFKTPRKFEHVKSQGHKDKAKELKSLEKEIAGQDE DHFITVDVAGCFEGDEEBEBEDEDDEEBEIEVEEBLCKQVRSRDIS REEWKGSETYSNPTAYGVDFLVPVMGYICRICHKFYHSNSGAQL SHCKSLGHFENLQYKAAKNPSPTTRPVSRRCAINARNALTALF TSSGRPPSQPNTQDKTPSKVITARPSQPLPRRSTRLKT
6344	2508	147	PRVTRKILLVNDKKRYERVGGPKRLGRDVEMEEMIEQLQEKV HELEKNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK ANENAGLQECPRKGIKFQDADVAETPHPMFTTKYGNLSLLEARGE IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSE RIEELQDRINDLEKERELLKENYDKLYDSAFSAHEEQWKLKEQ QLKVQIAQLETAALKSDLTDKTEILDRLKTERDQNEKLVQENREL QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE QKNGDLSFLVKVDSEINKDLERSMRELOATHAETVQELEKTRNM LIMQHKINKDYQMEVEAVTRKMENLOQDYELKVEQYVHLLDIRA ARIHLEAQLKDIAYGTKQYKFKPEIMPDDSDVEFDETHILBERG ENLFEIHINKVTFSSSEVLQASGDKEPVTFCTYAFYDFELQTPPV VRGLHPEYNFTSYQLVHVNDLFLQYIQKNTITLEVHQAYSTEYE TIAACQLKFHEILEKSGRIFCTASLIGTKGIDPNFGTVVEYWFRL RVPMQDAIRLYRERAKALGYITSNFKGPEHMQSLSQAPKTAQL SSTDSTDGNLNLHITIRCCNHLQSRASHLQPHYPYVVKFFDFA DHDTAIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD DSDTQENIYIGKVNPLISLAHDCRISGIFELTDHQKHPAGTHI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VILKNKFAYLPPSGSITTEDLGNFIRSEEPVQRLPPASSVST LVLPAPRPKPRQLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN TEKMQQKDDVSLSEGQLAEQSLASSEDETEITLEDLEPEVEED MSASDSDDCIIPGPISKNIKQPSKIRIEIIALSLNDSQVTMDD TIQRLFVECRFYSLPABETPVSLPKPKSGQWVYNNYSNVIVDK ENNAKARDILKAILQKQEMPNSRLRFTVVDPPEDQDLECEDI GVAHVLDLDMFQEGRDLEQNIQNDVDFARADGEGIGKLRVTVEAL HALQSVYKQYRDDLEA
6346	2921	533	QDRRLRLRLQKTCQPTSTMSGSHTPACGPFSAITPSIWPQEIL AKYTQKEESAEPFYDFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLFTHNHDVGLTDWKIAVSLPRSEKRLSLVLA GIPHGMRLPQWMLSGALQKKRNSLSYREIVKNSNDETIAAK QIEKDLLRTMPSNACFASMGSGVPRRLRRLRALAWLYPEIGYC QGTGMVAACLLLFLEEDAFWMSAIIEDLLPASFYSTTLGLGVQ TDQVRLRLHIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRINWDLFFYEGSRVLFQTLGMLHLKEELIQSENSASI FNTLSDIPSQMEDAELLGVAMRLAGSLTDVAVETQRRKHLAYL IADQQLLGAGTLTNLSQVVRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVAIDLREAILRVARHFQCTDPKNCVSVSRQLPGLL PNTALTPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFFPAKFVEVLDERSKYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLEDGKVLTPPELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSLPTVEKWKYQWSPFLRSPGWVQIKC ELRVLCCFAFSLSDWELPAKREAQQPLKEGVDRMLVKHHLFSW DVDG
6347	2921	533	QDRRLRLRLQKTCQPTSTMSGSHTPACGPFSAITPSIWPQEIL AKYTQKEESAEPFYDFGFRVYKEEGDEPGSSLLANSPLME DAPQRLRWQAHLFTHNHDVGLTDWKIAVSLPRSEKRLSLVLA GIPHGMRLPQWMLSGALQKKRNSLSYREIVKNSNDETIAAK QIEKDLLRTMPSNACFASMGSGVPRRLRRLRALAWLYPEIGYC QGTGMVAACLLLFLEEDAFWMSAIIEDLLPASFYSTTLGLGVQ TDQVRLRLHIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV DIKLLLRINWDLFFYEGSRVLFQTLGMLHLKEELIQSENSASI FNTLSDIPSQMEDAELLGVAMRLAGSLTDVAVETQRRKHLAYL IADQQLLGAGTLTNLSQVVRRTQRRKSTITALLFGEDDLEAL KAKNIKQTELVAIDLREAILRVARHFQCTDPKNCVSVSRQLPGLL PNTALTPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL RGWFFPAKFVEVLDERSKYSIAGDDSVTEGVTDLVRGTLCPALK ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLEDGKVLTPPELLYRAVQSVNVTHDAVHAQMDVKLRSL ICVGLNEQVLHLWLEVLCSLPTVEKWKYQWSPFLRSPGWVQIKC ELRVLCCFAFSLSDWELPAKREAQQPLKEGVDRMLVKHHLFSW DVDG
6348	3	3679	AGAEKCFVTLACFLAQKQNKYKYECKDLIKSMLRNLQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLEKLEGRDASRSIN EHLQALLTPDEPKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEAEKVQKSSSPBEMQKAEKEVPEDSLBECAITCS NSHGPCDSNQPHKNIKITFEEDVNSTLVVDRESHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAANILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQNKYKYECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLEKLEGR DASRSLEHLQALLTPDEPKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEAEKVQKSSAPREMPKAEKEVPEDSLE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ECAITCSNSHGYPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEEKGPVSPRNLQSEEEVEVPQESWDEG YSTLSIPPEMLASYKSYSTFHSLEEQQVCMVDIGRHRWDQVK KEDHEATGPRLSRELLDEKGPVQLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEDQGPPCPRLSRELLEVVPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEKHVGFSLDVGEIE KKGKGGKRRGRRSKKERRRRGRKEGEEDQNPPCPRLSRELLDEK GPEVLQDSLDRCYSTPSGCLELTDSQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCY TSPSGCLELTDSQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEDQGPPCPRLSREL LEVVPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEKH VGFSLDVGEIEKKGKGGKRRGRRSKKERRRRGRKEGEEDQNPPC RLNSMLMEVEEPEVLQDSLDCYSTPSPMYFELPDSFQHYRSVY SFEEHHISFALYVDNRFFTLTTLVTSLSHLVFGMGVIFPQ
6349	3	3679	AGAEKCFVTLACFLAQKQNKYKYECKDLIKSMLRNELQFKKE KLAELQKQAEELRQYKVLVHSQERELTQREKLREGRDASRSLN EHLQALLTPDEPKSQGQDLQELAEQCRLAQHLVQKLSPENDN DDEEDVQVEAEKVQKSSSPREMKAEEKEVPEDSLECAITCS NSHGPCDSNQPHKNIKITFEEDVNSTLVVDRESSHDECQDALN ILPVPGBTSSATNVMVVSAGPLSGEKAANILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQNKYKYECKDLIKFMLRN ERQFKKEKLAELQKQAEELRQYKVLVHSQERELTQREKLREGR DASRSNLNEHLQALLTPDEPKSQGQDLQELAEQCRLAQHLVQK LSPENDNDDDEDVQVEAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGYPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEEKGPVSPRNLQSEEEVEVPQESWDEG YSTLSIPPEMLASYKSYSTFHSLEEQQVCMVDIGRHRWDQVK KEDHEATGPRLSRELLDEKGPVQLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEDQGPPCPRLSRELLEVVPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEKHVGFSLDVGEIE KKGKGGKRRGRRSKKERRRRGRKEGEEDQNPPCPRLSRELLDEK GPEVLQDSLDRCYSTPSGCLELTDSQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCY TSPSGCLELTDSQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEDQGPPCPRLSREL LEVVPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEKH VGFSLDVGEIEKKGKGGKRRGRRSKKERRRRGRKEGEEDQNPPC RLNSMLMEVEEPEVLQDSLDCYSTPSPMYFELPDSFQHYRSVY SFEEHHISFALYVDNRFFTLTTLVTSLSHLVFGMGVIFPQ
6350	3	3679	AGAEKCFVTLACFLAQKQNKYKYECKDLIKSMLRNELQFKKE KLAELQKQAEELRQYKVLVHSQERELTQREKLREGRDASRSLN EHLQALLTPDEPKSQGQDLQELAEQCRLAQHLVQKLSPENDN DDEEDVQVEAEKVQKSSSPREMKAEEKEVPEDSLECAITCS NSHGPCDSNQPHKNIKITFEEDVNSTLVVDRESSHDECQDALN ILPVPGBTSSATNVMVVSAGPLSGEKAANILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQNKYKYECKDLIKFMLRN ERQFKKEKLAELQKQAEELRQYKVLVHSQERELTQREKLREGR DASRSNLNEHLQALLTPDEPKSQGQDLQELAEQCRLAQHLVQK LSPENDNDDDEDVQVEAEKVQKSSAPREMPKAEEKEVPEDSLE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ECAITCSNSHGPYDSNQPHRKTITFEEDKVDSTLTIGSSSHVEW EDAVHII PENESDDEEEEEKGPVSPRNLQSEEEVVPQESWDEG YSTLSIPPEMLASYKSYSTFHSLEEQQVCMVDIGRHRWDQVK KEDHEATGPRLSRELLDEKGPVQLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLBPDLGQPYSSAVYSLEE QYLGLALDVDRIKKQEEEDQGPSPRSLRELLVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGGKRRGRRSKERRRGRKEGEEDQNPPCPRLSRELLDEK PEVLQDSLDRCYSTPSGCLELTDSQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCS TPSGCLELTDSQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKQEEEDQGPSPRSLRELL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGGKRRGRRSKERRRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDCYSTPSMYFELPDSFQHYRSVYF SFEEHISFALYVDNRFFTLTSLHLVFMGVIFPQ
6351	1291	319	REARRRTERSQGLRMLVVEVANGRSVWGAFAVQALRERLGVGG RTVGALPRGPRQNSRLGLPLLLMPEEARLLAEIGAVTLVSAPRP DSRHHSALTSFKRQEESEFQEQSALAAARETRRQELLEKITE GQAACKQKLEQASGASSQAEAGSSQAKEDETSQGQASGEQEEA GPSSSQAGPSNGVAPLPRSAALLVQLATARPVPVKARPLDWRVQS KDWPHAGRPAHELRYSIYRDLWERGFFLSAAGKFGGDFLVYPGD PLRFHAHYIAQCWAPEDTIPLQDLVAGRLGTSVRKTLTLLCSSPQ PDGKVVYTSQWASLQ
6352	235	923	WSEWLSPCAAKCKGLSMLRITMKTRAISSLAADATEFVQGRSAP AMARSLVHDITVYCLSVYQVKISPTPQLGAASSAEGHVGGGAPG LMGNMNPPEGVNHENGMMNRDGGMIPEGGGNQEPQQPFPPEE PAQAAMEGPPQENMQPRTRRTKFTLLQVEELESVFRHTQYPDVP TRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANELRADP DDCVYIVVD
6353	65	672	RFAGAGATPEARARPPDVQAAEEEEKEMDLPDSASRVFCGRILSM VNTDDVNAIILAQNMLDRFEKTNEMLLNPNLSSARLQQMSE FLHHTRTLVMKRDLSIFRIRTLKGLARQHPEAFSHIPEAS FLEEEDEDPIPPSTTTIATSEQSTGSCDTSPTVSPSLSPGFE DLSHVQPGSPAINGRSQTDDEEMTGE
6354	965	510	PSLRPMEPTRDCPLFGGAFSAILPMGAIDVSDLRVPVNDQEVFC HPVTDQSLIVELLEQAHVGEAAARYHFEDVGGVQGARAVHVE SVQPLSLENLALRGRCQEAWLSGKQQIAKENQQVAKDVTLHQA LLRLPQYQTDLLLTFFNQPP
6355	158	1662	RGSSAARFGSLRGAMIRRVLPHGMRGLLTRRPGTRRGGFSLD WDGKVEI KKKIKSILPGRSCDLLQDTSHPBHSDDVIVGGGV LGLSVAYWLKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQ QFSLPENIQLSLFSASFRLNINEYLAVVDAPPLDLRFNPSPGYLL LASEKDAAAMESNVKVRQREGAKVSLMSPDQLRNKFPWINTGV ALASYGMEDEGWDPWCLLQGLRRKQVSLGVLCQGEVTRFVSS SQRLMTTDDKAVVLKRIHEVHVKMDRSLEYQPVBCAIVINAAGA WSAQIAALAGVGEPPGTLGQTKLPVEPRKRYVYVWHCPQGPGL ETPLVADTSAGYFRREGLSNYLGGRSPTQEEEDPANLEVDHD FPQDKVPHLALRVPAFETLVKQSAWAGYDYNTFDQNGVVGPH PLVVNMYFATGFSCHGLQAPGIGRAVEMVLKGRFQTDLSPF LFTRFYLGEKIQENNI
6356	354	633	TGLTSSCLPLQVMMTKRTKDMGKFSSVTSTIDEDEEEIEAREV ADSYAQNAKVIKQLERKGMKRRRLQELAEAKKAKMKGTLID NQFK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6357	2	915	GLLRNMLLVRLRNQTSISQWVPVCSRLIPVSPQTQGGDRALS RTSQWPQMSQSQACGGSEQIPGIDIQLNRYHTTRKLTSTTKDSP QPVEEKVGAFTKIIBAMGFTGPKYKWKIKIAALRMYTSCVVK TDFEEFFLLRCQMPDTFNSWFLITLLHVWMLVRMKQEGRSQGYM CRIIVHFMWEDVQQRGRVMGVNPIYLKKNMILMTNHFYAILGY DEGILSDDHGLAALWRTFFNRKCEDPRHLELLVEYVRKQIQYL DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEGL
6358	2009	1040	ASDALHSLAPVLRLLSRSAARPATMTEQAISFAKDFLAGGIAA AISKTAVAPIERVKLLQVQHASKQIAADKQYKGIVDCIVRIPK EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHT QFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADVGSQGT REFRGLGDCLVKITKSDGIRGLYQGFSSVSQGI IYRAAYFGVY DTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRMM MQSGRKADIMYTGTVDCWRKIFRDEGGKAPFKGAWSNVLRGMG GAFVLVLYDELKKVI
6359	98	1086	VCRQEEKMKEDCLPSSHVPISDSKSIQKSELLGLLKTNYCYHE GKSFQLRHREEGTLIIIEGLLNIAWGLRRPIRLQMDDREQVHL PSTSWMPRRPSCPLKEPSPQNGNITAQGPSIQPVHKAESSTDS GPLEEAEEAPQLMRTKSDASCMQRPRPKCRAPGEAQRIRRHRS INGHFYNHKTSTVFTPAYGSVTNVRVNSTMTTLQVLTLLLNKFRV EDGPSEFALYIVHESGERTKLKDCYPLISRIILHGPCCKIARIF LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKLKEEEEREI I KLT MKFQALRLTMLQRLEQLVEAK
6360	1	345	GTRGAVPSTLEEVLPPRSRWFVHSGTMSKVSFKITLTSDP RLPYKVLSPVSTPFTAVLKFAAEEFKVPAATSIIITNDGIGIN PAQTAGNVFLKHGSELRIIPDRVGS
6361	615	158	RPGLGQLQHCALAPQAGNRRCRFHGRHLHALTRSTHRGKPMISQ FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC APGRWRRQITSQEFCHFIQGRCTFTPDGETLHIQAGDALMLPA NSTGIWDIQUETVRKTYLIL
6362	350	1576	TTMDGSHSAAKLKQLPPTSSSSAVSEASFYSKENLIGALLAIF GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWLGLFLMLLG ELGVFASAYAFAPLSLIVPLSAVSVIASAIIIGIIFIKEKWKPKDF LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW PFLYMLVEIILFCLLLYFYKEKNANNIIVILLVALLGSMTVV TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAFLSQ ASQMYDSSLIASVGYILSTTIAITAGAI FYLDFIGEDVLHICMF ALGCLIAFLGVFLITRNKKPIPFEPYISMDAMPGMQNMHDKGM TVQPBKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG VPYRVLEHTKKE
6363	21	1201	RRTRLGSSFFRRRDSSAMESYDVIANQPVVINDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDI FIGPKAEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVLVD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRLRLYLKREGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR RTLFSNIVLGGSTLFKGFGRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFFKMVWSKKEYBEDGARS IHRKTF
6364	21	1201	RRTRLGSSFFRRRDSSAMESYDVIANQPVVINDNGSGVIKAGFAG DQIPKYCFPNYVGRPKHVRVMAGALEGDI FIGPKAEHRGLLSI RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEHPVLLTEAPL NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVLVD SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRLRLYLKREGY DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYPDGS TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6365	234	1989	<p>RTLFSNIVLSGGSTLFRGFGDRLLSEVKKLAPKDVKIRISAPQE RLYSTWIGGSILASLDTFKMMVSKKEYEEDGARSIRHRTTF</p> <p>KHKSRASCAARAQAFGPSRERERVHSRFRSGLRRLGESNSGCCTM ASMGTLAFDEYGRPFLLIKDQDRKSRLMGLKSHIMAAKAVA NTMRTSLGPNGLDKMMVDKGDVTVTNDGATILSMDVDHQIAK LMVELSKSQDDEIGDGTGVVVLGALLLEAEQLLDRIHPIRI ADGYEQAAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGSKV VNSCHROMAEIAVNAVLTVADMERRDVPFELIKVEGKVGGRLED TKLIGKVIVDKDFSHPMQPKKVEDAKIALITCFEPKPKTKHK LDVTSVEDYKALQKYEKEKFEEMIQQIKETGANLAICQWGFDEE ANHLLQNNLPVWRVWGGPEIEILAIATGGRIVPRFSELTAEKL GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGNKMIIEE AKRSLHDALCVIRNLIRDNRVVYGGGAEEISCALAVSQEADKCP TLEQYAMRAFADALEVIMALSSENSGMNPIQTMTEVRARQVKEM NPALGIDCLHKGNTDMKQHVETLIGKKQISLATQMVRLMK IDDIRKPGESE</p>
6366	257	1898	<p>GNKEGAHSSTFWLLSIFLGAVAMLCKEQGITVLGLNAVFDILV IGKFNVLIVQKVLHKDKSLENLGLMRNGLLFRMTLLTSGGAG MLYVRWRIMGTGPPAFTEVDNPFASFADSMVRAVNYYYSINA WLLCPWWLCFDWSMGCIPLIKISDWRVIALAALWFLIGLIC QALCESDEGHKRRILTLGLGFLVIPFLPASNLFRVGVFAEVL YLPSVGYCVLLTFPGFALSHTKKKLIAAVVLGILFINTLRV LRSGEWRSEELFRSALSVCPLNAKVHYNIGKNLADKGNQTAI RYYREAVRLNPKYVHAMNNGNILKERNELQEAEBLLSLAVQIQ PDFAAAMWNLGIVQNSLKRFEAAEQSYRTAIKRRKYPDCYYNL GRLYADLNHRVDALNAWRNATVLPKEHSLAWNMIILLDNTGNL AQAEAVGREALELIPNDHSLMFLANVLGKSQKYKESEALFLKA IKANPNAASYHGNLAVLYHRWGLDLAKKHYEISLQDPTASGT KENYGLLRKLEBLMQKAV</p>
6367	287	1934	<p>SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS QKNLYRDVMQETFKNLTSGVKTWKVQNI EDEYKNPRNLSLMRE KLCESKESHHCGESFNQIADDMNRKTLPGITPCESSVCGEVGT GHSSLNTHIRADTGHSSEYQEYGENPYRNKECKKAFSYLDSFQ SHDKACTKEKPYDGKECTETFIHSCIQHRVMHSGDGPYKCKF CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER THTGVDNADECKEAGNAFSPSEIRRHRSHTGEKPYECKQCGKV FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG EKPYECQCGKAFRCSTDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSGEKECKGKVFYFSSLRHERTHTGEKPH ECKQCGKAFRYFSSLIHERTHTGDKPYECKVCGKAFTCSSSIR YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC GKAFIRASSCREHERTHINR</p>
6368	1	327	<p>RPVPAKLNPRSWPRTAGALPLRPPPLTMVPHDEVEIEDFQYDE DSETYFYPCPGDNFSITKBDLENGEDVATCPSCSLIKVIYDK DQFVCGETVPAPSANKELVKC</p>
6369	1	1745	<p>AGCCRDTRFPPTPRGPGSLCHNFCRSAACTVTRTIHSGPREDTGT PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET FKNLTSGVKTWKVQNI EDEYKNPRNLSLMREKLCESKESHHC ESFNQIADDMNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD TGHSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY DGKECTETFIHSCIQHRVMHSGDGPYKCKFCKGAFYFLNLCL IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVDNADECKE CGNAFSPSEIRRHRSHTGEKPYECKQCGKVFISFSSIQYHKM THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECQCGKA FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG EKPHHECKGKVFYFSSLRHERTHTGEKPHHECKQCGKAFRYF</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SSLHIHERHTHTGDKPYECKVCGKAFTCSSSIRYHERHTHTGEKPY ECKHCGKAFISNYIRYHERHTHTGEKPYQCKQCGKAFIRASSCRE HERTHTINR
6370	1711	329	FVLSEQRLRTERTWPRSPGLGRGAAAGARTAGAGLLRLLLGCG ALVGGRLRPVTMTTPANAQNASKTWELSLYELHRTPOEAIMDGT EIAVSPRSLHSELPCICLDMLKNTMTTKELHRFCSDCIVTALR SGNKECPTCRKKLVSKRSLRPPNFDALISKIYPSREYEAHQD RVLIRLSRLHNQQALSSSIEEGLRMQAMHRAQRVRRPIPGSDQT TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKRPGRGGAGG SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTGPPSPPGAPS PPEPGGEIELVFRPHPLLVKEGEYCQTRYVKTGNATVDHLISKY LALRIALERRQQEAGEPGGPGGASDTGGPDGCGGEGGGAGGG DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNE KFWKVSRLPLELCYAPT KDPK
6371	3	288	GVANMSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKC LHNNNFENALCRKESKEYLECRMERKMLQEPLEKLGFGDLTSG KSEAKK
6372	2141	625	RVSATASEGKAEERYKKLEDLLEKSFSLVKMPSLQPVVMCMKH LPKVPEKKLKLVMADKELYRACAVEVRRQIWDNQALFGDEVSP LLKQYILEKESALFSTELSVLHNFSPSPKTRRQGEVVRQLTRM VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRALLMSLHDLVGE EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKQGE QVLGLDSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL LLLRLLALGQGAWDMIDSQVFEKPKMEVELITRFLPMLMSFLVD DYT FNVDQKLPAEEKAPVSYPTLPESFTKFLQEQRMACEVGLY YVLHITKQRNKNALLRLLPGLVETPGDLAFGDI FLHLLTGNLAL LADEFALEDFCSSLDGFFLTASPRKENVHRHALRLLIHLHPRV APSKLEALQKALEPTGQSGEAVKELYSQGEKLEQLDHRKPSPA QAAETPALELPLPSVPAPAPL
6373	67	711	PSRAARASPARLPAMVSWIISRLVVLIFGLTYPAYYSYKAVKSK DIKEYVKWMMYWIIFALFTTAETFTDIFLCWPPFFYELKIAFVA WLLSPYTKGSSLLYRKVFVHTLSSSEKEIDDCLVQAKDRSYDAL VHFQKGRGLNVAATAAVMAASKGQALSERLRSFSMQDLTTIRGD GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSSGTA
6374	535	2105	HKLFCSYISTSEFPSSTRHSCPTHTFCNYTSSTIFLSSTRDHS CPTHTFCNYTSSTIFLSSTRDHSCTHTSCNYTSSTIFLSSTRD HSCPTHTSCNYTSSTIFLSSTRDHSCTHTFCNYPRPIIRLSSC CPAELQTEGSNGKKEVLSGFQVLEDTVLFPEGGGQPDRTGTIN DISVLRTVTRRGEQADHFTQTPLDGSGVLRVVDWERRFDHMQQH SQQHLITAVADHLFLKLTTSNELGRFRSAIELDTPSMTAEQVAA IEQSVNEKIRDRLPVNVRELSDDDPEVEQVSGRGLPDDHAGPIR VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGGKNRNTNIFL SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL QKNNTLLRLDLAVHIAHSLRNSPDWGGVVILHRKEGDESEFMNII ANEIGSEETLLPLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE
6375	1	1535	AIMAAATRPVRLPEAGCEGRERCWNPSSRSRSHSGEGGLAAWSRT CPGRFRPPGQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK PPGRACSNPSFLRFQLDYQVYFLALAADWLQAFYLYKLYQHYY FLEGQIATILYVCGLASTVLFGLVASSLVDWLGKNSCVLFSLTY SLCCLTKLSDQDYFVLLVGRALGGLSTALLFSFAFEAWYIHEHVER HDFFPAEWIPATFARAFAFNHVLAVVAGVAAEAVASWIGLGPVAP FVAAPILLALAGALALRNWGENYDRQAFSRTCAGGLRCLLSDR RVLLLTGIIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFTSTP GQESPVESPIAFLLIELACGLYFPPMSFLRRKVIPTETQAGVLN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			WFRVPLHSLACLGLLVLDSDRKTGTRNMFSCSAVMVMALLAV VGLFTVVRHDAELRVPSPTTEPYAPEL
6376	380	1437	ISSTDIDHYRFSFLVNSKMPSKESWSGRKTNRRAVHKSKQEQGRQ QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQSLTVLRRATLKE NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAQGVKCADC GLNVHKQCSKMVPNDCKPDLKHVKVYSCDLTTLVKAHTTKRPM VVMCIRESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGEKAD ISVNMVEDINIITGALKLYFRDLPIPLITYDAYPKFIESAKIMD PDEQLETLHEALKLPPAHCETLRYLMAHLKRVTLHEKENLMNA ENLGIVFGPTLMRSPELDAMAALNDIRYQRLVVELLIKNEIDL
6377	2311	1845	SRIRRRSSRRPREPPGPSRRRRRRRPPDPTMPSEKTFKQRRTFE QRVEDVRLIREQHPKIPVIERYKGBKQLPVLDTKTKFLVDPHV NMSELIKIRRRQLNANQAFLLVNGHSMVSVSTPISEVEYSE KDEGFLVMVYASQETFGMKLSV
6378	686	191	GAGPWEAFPDGIGRRSRRLPQYKRPGRVGGGDSGRNMMAVA DLALIPDVVIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYK WAEYHADIYDKVSGDMQKQGCDCCLGGGRISHQSQDKKIHVYG YSMAYGPAQHAISTEKIKAKYPDYEVTTWANDGY
6379	35	378	BRAGSPSPSRAALRRCAPQRSQAPRWPDRACRRSFQGSQGRAY LFNSVNVNCGGPABERVLTLGLHAVADIYCENCKTTLGWKYEHA FESSQKYKEGKYIIELAHMIKONGWD
6380	1414	462	PAVQQRGAGPPTGRGSGNMAFALTIVRHGETRFNKEKIIQQGQ GVDEPLSBTGFQAAAAGIFLNNVKFTHAFSSDLMRKTQTMHGI LERSKFKCDMTVKYDSRLRERKYGVVEGKALSELAMAKAAREE CPVFTPPGGETLDQVVMRGIDPFEPCLQLILKEADQKEQFSQGS PSNCLETSLAEIFPLGRNHSSKVNDSGIPGLAASVLVSHGAY MRSLFDFYFLTDLKCSLPATLSRSELMSTPTNGMSLFIINFEEG REVKPTVQICIMNLQDHLNGLTENSGLNLPSKSNHFEPLKGV LALFTSLLC
6381	1668	218	AVVRAQGSRGFSGAGWRPRQAAAMNFSEVFKLSLLCKFSPDGK YLASCQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFILC AMYKRGVLQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT TEPHLRITVWSLCTKSVSYIKYPKACLGITFTRDGRYMALEA RDCKDYVSI FVCSWDQLLRHFDITDQDLTGIEWAPNGCVLAVWD TCLBYKILYSLDGRLLSTYSAYEWSLGIKSVAVSPSSQFLAVG SYDGKVRILNHVTWKMITFEGHPAAINDPKIVVYKEAKSPQLG LGCLSFPFPRAGAGPLPSSSESKYEIASVPVSLQTLKPVTDRA NPKIGIGMLAFSPDSYFLATRNINPNAVWWDIQKLRLFAVLEQL SPVRAFQWDPQPRLAICTGGSRLYLWSPAGCMSVQVPGBGDFA VLSLCHWLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT
6382	2	1062	FEEDERNLCLLAIYPLKGDHGIIVDNDCEPKSKLLRWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEFEWLKKSEVLYY TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFI LENLTSRYEVPVLDLKMGTQHGDDASEEKAANQIRKCOQSTS AVIGVRVCGMQVYQAGSGQLMFNMKYHGRKLSVQGFKEALFQFF HNGRYLRRELLGPVLKKTTELKAVLERQESYRFYSSLLVIYDG KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG E
6383	3159	1061	SPAPGRPSPHGSQPAARAAAAPAMPSAKORGSKGHGAASPSEK GAHPSAARPLAAPTAAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKORGSKGHGAASPSEKGAHPSGGADDVAKK PPAPAPQPPPPAPHPQHPQHPQHPQHPQHPQHPQHPQHPQHPQ SSSSASASAAAAAASSASCSRLGRALNLFYALVAALVAAAFS GWCVHHVLEEVQVRRSHQDFSRQREELGQGLQGVQKQVQSLOA TFGTGESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LKDLSDGIHVVKDARERDFTSLENTVEERLTETLTKSINDNIAIF TEVQKRSQKEINDMKAKVASLERSEGNKQDLKALKEAVKEIQTS AKSREWDMEALRSTLQTMESDIYTEVRELVSLLKQEQQAFKEAAD TERLALQALTEKLLRSEESVSRLEPPIRLEELRQLKSDSHGP KEDGGFRHSEAFALQKQSQGLDSRLQHVDEGLVSMQVASARQT ESLESLLSKSQEHEQRLAALQGRLEGLSGSEADQDGLASTVRSI GETQLVLYGDVEELKRSVGEPLPSTVESLQKQVEQVHTLLSQDQA QAARLPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAI SVKIETNENNLESAGLLDLDRLDRLFVKVEKIEKV
6384	738	1904	IWEVFPVCLTHLLHQQANQPLPPFPSSSINEEDADEANRAIGKEK AAPDSGKKPKTPKTKQQKDPNEPQKPVSAIALFFRDTQAAIKQG NPNATFGEVSQIVASMWDSLGEQKQVYKRKTEAAKKEYLKAIA AYRASLVSKAAESAQAQTIRSVQQTLASTNLTSSLLNTPLSQ HGTVSASPQTQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP SNIGAPLISSMGTMTVGSAPSTQVSPSVQTQQHMQQLQQQQQQQ QQQMQQMQQQLQQHMQHQQIQQQMQQQHQQHMQHQQHQQHQQH LQQQINQQQLQQQLQQRLQLQQHMQHQSQSPRQHSVPASQI TSPIPAIGSPQFASQQHQSQIQSQQTQTQVLSQVSI
6385	2	1584	PRVRAADVAAGAAQVVSAGMAKSNENGPRAPAAGESLSGTRES LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG ALEEVPLEVLRRQRESKWLDMNNWDKWMKXKHKIRLRQCKGIP PSLRGRAWQYLSGGKVKLQONPGKFDELDMSPGDPKWLVDIERD LHRQFPFHEMFVSRGGHQQDLFRVLKAYTLRPEEGYQQAQAP IAAVLLMHMPAEQAFWCLVQICEKYLPGYVSEKLEAIQLDGEIL FSLQKVPVPAHKHLSRQKIDPLLYMTEWFMCAFRTLPWSSVL RVWDMFFCEGVKIIIFRVGLVLLKHALGSPEKVKACQGGYETIER LRLSPKIMQEAFLVQEVVELPVTERQIEREHLIQLRRWQETRG ELQCRSPFRLHGAAILDAEPGPRPALQPSFIRLPLDAPLPGS KAKPKPKQAQKEQRKQMKGRGQLEKPPAPNQAMVVAAGDACP PQHVPKDSAPKDSAPQDLAPQVSAHHSQESLTSQESSEDITL
6386	819	195	TVCGSFYLGIMQASRLKRELHMLATEPPPGITCWQDKDQMDL RAQILGGANTPYEKGVPKLEVIIPERYPFEPPQIRFLTPYIYHN IDSAGRICLDVLKLPKGAWRPSLNIAITVLTISQLLMSEPNDD PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEEMLDNL PEAGDSRVHNSQKRAKASQLVGIEKKFHPDV
6387	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAEVLKR KQELAETLANLERQIYAFEGSYLEDQMYGNIIRGWDRYLTNQK NSNSKNDRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK REPGSGTESDTSDFHNQNEPSQEDPEDLDGVSQGVKPKKAAS STSSGSHSHSHKKRKNKNRHSPPSGMFDYDFEIDLKLNKKPRADY
6388	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAEVLKR KQELAETLANLERQIYAFEGSYLEDQMYGNIIRGWDRYLTNQK NSNSKNDRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK REPGSGTESDTSDFHNQNEPSQEDPEDLDGVSQGVKPKKAAS STSSGSHSHSHKKRKNKNRHSPPSGMFDYDFEIDLKLNKKPRADY
6389	1074	497	AEPGDRMAGHRLVLVLGDLHTPHRCNSLPKAFKLLVPGKIQHI LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNPQKVVTVG QFKIGLIHGHQVPIWGDMAALQRFQVDVILISGHTKFEAF EHENKFYINPGSATGAYNALETNIIPSVFLMDIQASTVVTVVYQ LIGDDVKVERIEYKKP
6390	158	535	GEERKEGRAPGKAFAPERNPAKMEKEETTRELLEPNWQSGSHG LTIAGRDDGVFVQEVTONSPAARTGVVKEGDQIVGATIFYDNLQ SGEVTQLLNTMGHHTVGLKLRKGRDRFPFSLGQTWDP
6391	5386	2897	VRWNSKTECYLSIQTQENFPANLNLVNCIVISSLVTTORLKA MSLLGSRNQLARAVLNPNMDFCTKDLLTTTSERIIAYLRDFNE DQKKAIETAYAMVKHSPSAKICLIHGPPGTGSKTIVGLLYRL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LTENQRKGHSDENSNAKIKQNRVLVCAPSNAAVDELMKKIILEF KEKCKDKKNPLGNCGDINLVRGPEKSINSEVLKFSLDSQVNRH MKKELPSHVQAMHKRKEFLDYQLDELRSQRALCRGGREIQREL DENISKVSKERQELASKIKEVQGRPQKTQSIIILESHIICCTLS TSGLLLESFAFRGQGGVFPFSCVIVDEAGQSCIEITLPLIHRCN KLILVGDPKQLPPTVISMKAQYGYDQSMARFCRLLEENVEHN MISRLPILQLTVQYRMHPDICLFPSNYVYNNRNLKTRQTEAIR SSDWPFPQYLVFDVGDGSERRDNDYINVQEIKLVMETIKLIKID KRKDVSRNIGIITHYKAQKTMQKDLDEKDFDRKGAPEVDTVDA FQGRQKDCVIVTCVRANSIQSGSIGFLASLQRLNVTITRAKYSLF ILGHLRTLMEHQHWNQLIQDAQKRAIIKTCCKNYRHDAVKILK LKPVLQSRSLTHPPTIAPEGSRPQGGPSSKLDGSPAKTSVAASL YHTPSDSKEITLTVTSKDPERPFPVHDQLQDPRLLKRMGIEVKG IFLWDPQPPSPQHPGATPPTGEPFPVVDLQSHVQPPAAVVAA LSSHKPPVRGEPFAASPEASTCQSKCDDPEEELCHRRARAFSE GEQEKCGSETHHTRNSRWKRTLEQEDSSSKKRKLL
6392	972	186	GRTGVDLASSMAHRLQIRLLTWDVKTLLRLRHLGEAYATKAR AHGLEVEPSALEQGFQRAYRAQSHSFPNYGLSHGLTSRQWLDV VLQTFHLAGVQDAQAVAPIAEQLYKDFSHPTQWQVLDGAEDTLR ECRTGRLRLAVISNFDRLLEGILGGLGRLREHDFVLTSEAAGWP KPDPRIFQELRLAHMPEVVAHVGDNYLQDYQGPRAVGMHSFL VVGPOALDPVVRDSVPKEHILPSLAHLPLALDCLEGSTPGL
6393	2017	730	TGGSMAAVATCGSVAASTGSAVATASKSNVTSFQRRGPRASVT NDSGPRLVSIAGTRPSVRNGQLLVSTGLPALDQLLGGGLAVGT LLIEEDKYNISPLLFKYFLAEGIVNGHTLLVASAKEDPANILQ ELPAPILLDDKCKKEFDEVDVNHKTPESNIMKIAWRYQLLPKME IGPVSSSRFGHYDASKRMPQELIEASNWHGFFLPEKISSTLKV EPCSLTPGYTKLLQFIQNIIEEGFDGSPQKKQRNLRIGIQN LGSPLWDDICCAENGCSHSLTKFLYVLRGLLRTSLSACIITM PTHLIQNKAIARVTTLSDDVVGLSEFIGSERETNPLYKDYHGL IHIRQIPRLNLLICDESDVKDLAFKLKRLFTIERLHLPDDLSD TVSRSSKMDLAESAKRLGPGCGMMAGGKKHLDF
6394	1418	511	GAAAGGEGARRRPAAMATVMAATAAERAVLEEFWRLLHDEVHA VLKQLQDILKEASLRLPLPGSGTEGPAKQENFILGSCGTDQVK VLTQGDALSQADVNLKMPRNQLLHFAFREDKQWKLQIQDAR NHVSQAIYLLTSRDQSYQKTGAELVLMADAVMLQLTRARNRLT TPATLTLPEIAASGLTRMFAPALPSDLLVNVYINLNKCLTVYQ LHALQPNSTKNFRPAGGAVLHSPGAMFEGSQRLVSHVHKVEEC VIPWLNDAVYFTVSLQLCQQLKDKISVFSSYNSYRPF
6395	13	658	PSGRPTRPLCCAARRGAARHGGSVSCWPAGRTPTETSNPGSSVM ESVTFEDVAVEFIQEWALLDSARRSLCKYRMLDQCRTLASRGTP PCKPSCVSQLGQRAEPKATERGILRATGVAWESQLKPEELPSMQ DLLEEASSRDMQMGPGFLPLRMQLVPSIEERETPLTREDRPAEQE PPWSLGCTGLKAAMQIQRVVIVPPTLGHNRNPWVARDSGE
6396	1	1221	ANILSSPSKRGQKGTGLIGYSPEGTPLYNFMGDAFQHSQSIPRF IKESLQKILEESDSRQIFYFLCLNLLFTFVELFYGVLNTSLGLI SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF INGFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL IGICAFSHAHSHAHGASQGSCHSSDHS SHHMHGSHDHGHGSH GSAGGMNANMRGVFLHVLADTLGSGIGVIVSTVLIEQFGWFIAD PLCSLFIAILIFLSVVPLIKDACQVLLRLPPEYEKELHIALEK IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSVDVLEQRIVQQV TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTIYM
6397	391	122	GAGGVGRFEAIRAPARMIEVVCNDRLGKRVKVCNTDDTIGDLK KLIAAQGTGRWNKIVLKKWYTFKDHVSLGDYEHGDMNLELYY

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			Q
6398	353	1306	HKQMGLINRCKKILLPTTVPPATMRIWLGLLPLFLLLSGLQ RPTGESEVAIKIDFDAPAGSFDDQYQGCSKQVMEKLTQGDYFTK DIEAQKNYFRMWQKAHLAWLNQGVLPQNMTHAVAILFYTLN SNVHSDFTRAMASVARTPQQYERSPHFKYLHYLTSAIQLLRKD SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQFLSTSLLKEEA QEPGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYELFKVINMSYH PRGDWLQLRSTGNLSTYNQCLLKASSKKCIFDPIAIASLSFLTS VIIFSKSRV
6399	75	1245	PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSXRGVAVSGPTK RRGMADSLSTPLPSPEDRLAKLHPSKELEYQKMAECEAEN EDLLKKLELYKEACEGQHKLECDLQOREEELAEQLKALSDMQVC LFQEREHVLRLYSENDRLRIRELEDDKKIQNLALVGTDAEVT YFCKEPPHKVTILQKTIQAVGECEQSESSAFKADPKISKRRPFR ERKSSEHYQORDIQTLLIQVEALQALGEQTKLSREQIEGLIED RRIHLEEIQVOHQRONQNKIKELTKNLHHTQELLYESTKDFLQLR SENGNKEKSWMLEKDNLSMKIKQYRVQCKKEDKIGKVLPMHE SHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM
6400	2520	1053	KTMKCEVVEVQSAILRHNCGYAMKTGKFFHNLMERKDFETWL DNISVTFSLSLDLQKNETLDHLISLSGAVQLRHLNNLETLLKR DFLKLPLLELSFYLLKWLDPTLLTCLVSKQWKNVISACTEVW QTACKNLGWQIDDSVQDALHKKVYLKAILRMKQLEDHEAFETS SLIGH SARVYALYYKDGLLCTGSDDL SAKLWDVSTGQC VYGIQT HTCAAVKFDEQKLVTSFDNTVACWEWSSGARTQHFRGHTGAVF SVDYNDEL DILVSGSADFTVKVWALSAGTCLNTLTGHTEWVTKV VLQKCKVKSLLHSPGDYILLSADKYEIKIWPIGREINCKCLKTL SVSEDRSICLQPRLHFDGKYIVCSSALGLYQWDFASYDILRVIK TPEIANLALLGPGDIFALLFDNRVLYIMDLRTESLISRWPLPEY RKSKRGSSFLAGEASWNLGLDGHNDTGLVFATSMPDHSIHLVLW KEHG
6401	109	766	PGAAWSRPDLRGCTGPQPALRMLVLPSPCPQPLAFSSVETMEG PPRRTCRSPPEGPSSSIGSPQASSPPRPNHYLLIDTQGVPTVL VDEESQREPGASGAPGQKKCYSCPVC SRVFYMSYLQRHSITHS EVKPFECDCGKAPKRAHSLARHHSIHLAGGGRPHGCPLCPRRF RDAGELAQHSRVHSGERPQCPCPRRFMEQNTLQKHTRWKHP
6402	1196	279	TTSCQGGIRQSSAIPVAMEFAATCLRNALLLPPEEQDPKQEN GAKNSNLGGNTESSESSETCSSKSHDGDKFIAPPSSPLRKKQE LENLKCSILACSAYVALALGDNLMALNHADKLLQPKLSGSLKF LGHLYAAEALISLDRISDAITHLNPENVTDVSLGISSNEQDQGS DKGENEAMESSGKRAPQCYPPSSVNSARTVMLFNLSAYCLRSEY DKARKCLHQAASMIHPKEVPPEAILLAVYLELQNGNTQLALQII KRNQLLEPAVKTHSEVRKKPVFPVHP IQPIQMPAFTTVQRK
6403	2	1690	RGIHTSVLQGNLQNMYSHNVVIMNLLNLTQVQQRNLTNLQ RSVDDTSQAIQRIKNDQNLQVFLQAKKDDWLKQVSLQTL AANNSALAKANNDTLEDMSQLNSFTGQMENITTISQANEQNLK DLQDLHKDAENRTAIFKNQLEERFQLFETDIVNIIISNISTAHH LRTLTSNLNEVRTTCTDTLTKHTDDLTSNLNTLANIRLDSVSLR MQQDLMSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP PGPRGPRGRGSGQPPGPTGNKGQKGEKGEPPGPPAGERGP PAGPPGERGGKSGSGQPKSGRSGPGKPGPGQSGDPGPPGPP GKEGLPGPGPPGFGQLQGTVEPGVPGPRGLPGLPGVPGMPG KGPPGPPGPGSGAVVPLALQNEPTAPEDNSCPPHWKNFTDKCYY FSVEKEIFEDAKLFCEDKSSHLVFINTRREEQWIKKQMVGREH WIGLTDSEERENWKWDGTS PDYKNWKAGQPDNNGHGHGPGEDC AGLIYAGQWDFQCEDVNNFICEKDR ETVLSSAL
6404	1012	222	AAALAMAAAPAGLISVFSSSQELGAALQALVAQRAACCLAGARA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			RFALGLSGGSLVSMLELPAAPVAPAGPASLARWTLGFCDBRLV PFDHAESTYGLYRTHLLSRLPIESQVITINPELPVEEAADYA KKLRQAFQGDSIPVFDLLILGVGPDGHTCSLFPDHPQLQEREKI VAPISDSKPPPPQVRVTLPLVLAARTVIFVATGEGKAAVLKRI LEDQEENPLPAALVQPTGKLCWFLEDAARLLTVPFEKHSPL
6405	1	1456	AALPRPTPRAPLGGREGTGSDEMAASMFYGRVAVATLRNHRER TAQRAAAQVLGSSGLFNNHGLQVQQQQQRNLSLHEYSMELLQE AGVSVPKGYVAKSPDEAYAIKLLGSKDVVIAQVLAGGRGKGT FESGLKGGVKIVFSPPEAKAVSSQMGKLLFTKQTGEKGRICNQ VLVCERKYPREYFYFAITMERSFQGPVLIGSSHGGVNIEDVAE TPEAIKEPIDIEEGIKKEQALQLAQKMGFPNIVESAAENMVK LYSLFLKYDATMIBINPMVEDSDGAVLCMDAKINFDSNSAYRQK KIFLDQDWTQEDERDKDAKANLNYIGLDGNIICLVNAGLAMA TMDIILKHGGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL VNIGGIMRCDVIAQGIVMVAKDLEIKIPVVRLQGRVDDAKA LIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKQLP I
6406	1036	167	HPRQMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD DDDDHDDHEDNDKMNDSGMDPERLKAFFMVFRLFDENLDRM VPIKQPKKEKIQAIIESCSRQFPFQERARKRIRTYLKSRRMK KNGMEMTRTPPHLTSAMAENILAAACESETRKAAKMRLEIYQ SSQDEPIALDKQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN YSYRGYALSSNLQPPASLQTNHNSGESGEARALASRPAPSWV CRAALGSGMGRGKQRPVMERGCLTA
6407	492	150	VGLCLAVSQTVLAQLDALLVFPQQVAQLSCTLSPOHVTIRDYGV SWYQQRAGSAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNAC VLTISPVPQPEDDADYICSVGYGFSF
6408	1458	903	RGCTSSQAWRLFGGVTGRGNMREIKCYFCSGPIYPGHMMFVR NDCKVFRFCCKXCHKNFKKRNPRKVRWTKAFRKAAGKELTVDN SFEFEKRRNEPIKYQRELWNKTIDAMKRVEEIKQKQAKFIMNR LKKNKELQKVQDIKEVKQNIHLIRAPLAGKQKLEEKMVQQLQE DVDMEDAP
6409	150	446	NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDFGP GPACLPKTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFQGS HGRAYLFNSV
6410	85	607	RGGTAGCVACLGCGQSSSPKAAPFAGSACLADSCPCLLFQAC AISGLFNCITIHPLNIAAGVWMIMNAFILLCEAPFCQFIEFA NTVAEKVDRLRSWQKAVFYCGMAVVPVIVISLTTLTLLGNAIAPA TGVLVGLSALGKKGDAISYARIQQORQQADEEKLAELEGEL
6411	302	772	RLSIMASSLNEDPEGSRTYVKGDLFACPKTDSLACISEDCRM GAGIAVLFKKKFGGVQELLNQKKSGEVAVLKRDGRYIYYLITK KRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDRLQ WENVSAMIEEVFEATDIKITVYTL
6412	61	1709	RPVTSFSPPLPGSCGGRLGTRTMLGRSLREVSAALKQGITPTL CQKCLSLIKKTKFLNAYITVSEVALKQAESEKRYKNGQSIGD LDGIPIAVKDNFSTSGIBTTCASNMLKGYIPPNATVVQKLLDQ GALLMGKTNLDEFAMGSGSTDGVEGVPVKNPWSYSKYREKRQK PHSENEEDSWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGIILTRCVDDAAIV IGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV PELSSEVQSLWSKAADLFESEGAKEVIEVSLPHTSYISVCVHVL TSEVASNMARPDGLQYGHRCIDIVSTEAMYAATRREGFNDVVRG RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLL TPPTLSEAVPYLEFIKEDNRTRSQQDDIFTQAVNMAGLPAVSIP VALSNQGLPIGLQFIGRAFCDQQLLTAKWFEKQVQFPVQLQE LMDDCSAVLENEKLASVSLKQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6413	2	885	HEPRCAGMAASLWMDLEPYMDENFISRAFATMGETVMSVKIIR NRLTGIPAGYCFVEFADLATAEKCLHKINGKPLPGATPAKRFKL NYATYGKQPDNSPEYSLFVGDLTPDVEDGMLYEFFVKVYPSCRG GKVVLDQTGVSKGYGFVKPTDELEQKRALTECQGAVALGSKSPVR LSVAIPKASRVKPEYSQMYSSYNQYQQYQNYAQQWGYDQNT GSYSYSPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTANKEF MEQSEELYDALMDCHWQPLDTSVEIPAMM
6414	1	538	RGGRAALLPWRRFPCCRPRPQPARPSSSRATPGDRSPGMATSIGV SFSVGDGVPAAEKNAEPENTYILRPVFPQQRFRPSVVKDCIHAV LKEELANAESPEEMPQLTKHLSENIKDKLKEMGFDYKVVQV VIGEQRGEGVFMAARCFWDADTDNYTHDVFMDNSLFCVVAAPGC FYY
6415	2	1168	FVRQWQSSHRRACGLGCEARAGGGEPRGRASSVAGWVGAFRAP FIEAAVAGLGAGSGKRRRGWMPVHSRGDKKETNHHDEMEVDYA ENEGSSSEDEDESSSVSEDDGDSSEMDDEDCERRRMECLDEMSN LEKQFTDLKDQLYKERLSQVDAKLQEVIAKAPYLEPLATLQE NMQIRTKVAGIYRELCELVKNKYECEIQASRQHCESEKLLLYD TVQSELEBKIRRLBEDRHSIDITSELWNDELQSRKKRKPFPWD KKKPGVVGSPYIVYMLQDLDDLEDWTTIRKAMATLGPVRKTEP PVKLEKHLHSARSEEGRLYYDGEWYIRGQTCIDKKDECPTS AV ITTNHDEVWFKRPDGSKSKLYISQLQKGYKSIKHS
6416	410	1519	EIAPADLEIPACAPVLLSRATSSMTSGGKMAPSLTQEIILSHL GLASKTAAGWTLGLTLRTFLNFSVDKDAQRLLRAITGQGVDRSAI VDVLTNRSREQRQLISRNFQERTQQDLMKSLQAALSGNLERIVM ALLQPTAQFDAQELRTALKASDVAIDVAIRLATRTPPQLQEC AVYKHNFQVEAVDGITSETSGILQDLALLALAKGGRDSYSGIIDY NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS TQGELEEAVQNRFGDAQVALLGLASVIKNTPLYFADKLHQAALQ ETEPNYQVLIRILISRCETDILLSIRAEFRKKFGKSLYSSLDQAV KGDCQSALLALCRAEDM
6417	1	845	RGESRVLWSELEGEAGGAGGWASSLNARMONRFATAPVIACVLS LISTIYMAASIGTDFWYEYRSVPQENSSDLNKS I WDEPISDEAD EKTYNDALEFRYNGTVGLWRRCTIPKNMHWSPPERTESFDVVT KCVSFTLTBQFMKEFVDPGNHNSGIDLLRTRYLWRCQFLPFVSL GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCV AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA AHTNRKEYTLMKAYRVA
6418	2	662	TRTRPRRPPGLGAAVGKAGARSTSTPAGASFAAAYQADPPPPAH TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIPTTQQAELVQ YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMPQAAPGRRRRGRQ TYSRFQTLLEKEFLFNPLYLTKRRRIEVSHALALTERQVKIWFQ NRRMKWKKENNKDKFPVSRQEVKDGETKKEAQELEEDRAEGLTN
6419	1	973	PGRPRVRNFDLNSKILQEFFECTRSIQIPANRSKTAMSKCPIFP MARSISTSGPLDKEDTGRQKLITSGSLPATLQCATDSLGLWHL PSPDPVTVPYLSPLVWKELESLLBNEGDAITVADFVDHHPV FWNLVWYFRRLDPLSNLPLGLILSSEHCNKYSKI PRHCSSEDSKY VLIQMLWDMKHLQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF NQELLKSMVKS I KMNDVYGPMQIETLNKCPHFQRQSLYREI LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP STGVMECRKTFGEPLYL
6420	207	1187	RKMDKNQTCGVGQDSVPYMICLIHILEWFGVEQLEDYLNAN YLLWVFTPLILLILPYFTIFLLYLTII FLHIYKRKNVLKEAYSH NLWDGARKTVATLWDGHAHVHGYEVHGMKIPEDGPALIF YH GAIFIDFYFMAKIF IHKGRTRCVVADHFVKIPGFSLLLVDVFC ALHGPREKCVIELRSGHLLAISPGGVREALISDETYNIWVGHR GFAQVAIDAKVPIIPMFTQNI REGFRSLGGTRLFRWLVEKFRYP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FAPMYGGFPVKLRITYLGDFIPYDPQITAEELAEKTKNAVQALID KHQRI PGNIMSALLERFH
6421	1844	362	WALSLRRQPERMSNKLSPHPHSVVLRFSEFKMASSPAVLRSRL YQWSLKSSAQFLGSPQLRQVGQIIRVPARMAATLILEPAGRCW DEPVR IAVRGLAPEQPVTLRASLRDEKGFQAHARYRADTLGE LDLERAPALGGSFAGLEPMGLLWALEPEKPLVRLVKRDVRTPLA VEVELDGDHDPDGRLLCQTRHERYFLPPGVRRPVRVGRVGRGT LFLPPEPGPFPGIIVDMFGTGGGLLEYRASLLAGKGFVMAALAY NYEDLPKTMETLHLEYFEEAMNYLLSHPEVKGPVGVLGISKGG ELCLSMASFLKGITAAVINGSVANVGGLTRYKGETLPPVGVNR NRIKVTKDGYADIVDLNSPLEGPDQKSFIPVERAESTFLFLVG QDDHNWKSEFYANBACKRLQAHGRRKPQIICYPETGHYIEPPYF PLCRASLHALVGSPIIWGGEPRAHAMAQVDANKQLQTFHKKHLG GREGTIPSKV
6422	181	2133	EGENLSWQEFWGDIAKEFYWKTPCPGPFRLRYNFDVTGKIFIE WMKGATTNICYNVLDRNVHEKLGDKVAFYWEKNPEGETTQITY HQLLVQVCQFSNVLRKQGIHKGRVATYMPMIPELVVAMLACAR IGALHSIVFAGFSSESCLERILDSSCSLLITDAFYRGEKLVNL KELADEALQCKQEKGFVPRCCIVVKHLGRAELGMDSTSQSPPI KRSCPDVQISWNQIDLWHELMQEAGDECEPEWCDAEDPLFIL YTSGSTGKPKGVVHTVGGYMLYVATTFKYVDFHAEDVFWCTAD IGWITGHSYVTYGFLANGATSVLFEIGIPTYPDVNRLSIVDKYK VTKFYTAPTATIRLLMKFGDEPVTKHSRASLQVLGTGVEPINPEA WLWYHRVVGARQCFIVDTFWQTETGGHMLTPLPGATPMKPGSAT PFFFGVAPAILNESGEELEGEAEGYLVFKQPWPGIMRTVYGNHE RFETTYFKKPGYYVTGDGQORDQDGYWITGRIDDLNLSVSHL LSTA EVESALVEHEA VAAVVGHPHPVKGECLYCFVTLCDGHT FSPKLTEELKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV LRKIAQNHDHLDGDMSTVADPSVISHLPFSHRCLTIQ
6423	614	1237	ANLKEIPRDLPPETVLLYLDNQTITSIPNEIFKDLHQLRVNLNS KNGIEFIDRHAFKGVAEITLQTLDSLNRISQSVHKQAFNNLKARA RIANNPWCHDCDTLQQLRSMASNHETAHNVICKTSVLDEHAGRP FLNAANDADLCNLPKKTDYAMLVTMPGWFMTMVISYVVVYVRQN QEDARRHLEYLKSLSRQKKADEPDDISTVV
6424	1	1188	KKVSWPVAAMVHCSCVLFKRYGNFIDKRLFLTRGGSGMGYPRL GGEGGKGGDVVVVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA LKSGKGDWEIPVPVGISVTDENGKIIGELNKENDRILVAQGG LGGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGPFPNAGKSSLLSC VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKFLKHIERTRQLLFVVDISGFLSSHTQYRTAFETII LLTKELELYKEELQTKFALLAVNKMDLPDAQDKFHELMSQLQNP KDFLHLFEKNMIPERTVEFQHIIPISAVTGEIEELKNCIRKSL DEQANQENDALHKKQLNLNLSIDTMSSTEPSKHAVTTSKMDII
6425	1850	1144	LAMEGGGGIPLTLKEESQSRHVLPAFVNSLQKSNWGFLLTG LVGGTLVAVYAVATPFVTPALRKVCLPFVPMKQIENVVKMLR CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLWVYSRYRA WREGVHGS AKFYISDLWKVTFQSQSNVVI FGVPQMMQLQLEKKLE RELEDDARVIA CRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE KRPC TSMHFQLPIQA
6426	30	565	SRGA AVGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR LHAEEFAERDWEQFHQPRNLLLALVGEVGE LAELFQWKTDGEPG PQGWSPRERAALQEELSDVLIYVALAARCRVDLPLAVLSKMDI NRRYP AHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT ST
6427	145	959	AASWGPFPVPRAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK NIREYVRMMYWIWVAFALFMAAEIVTDIFISWFFPYEIKMAFVL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			WLLSPYTKGASLLYRKFFVHPSLSRHEKEIDAYIVQAKERSYETVLSFGKRGRLNIAASAAVQAATKSQGALAGRLRSFSMQDLRSISDAPAPAYHDPLYLEDQVSHRRPPIGYRAGGLQSDTEDECWSDTEAVPRAPARPREKPLIRSQSLRVVVKRPPVRBGTSSRLKVRTRKKTVPDSDVS
6428	1982	444	SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIREKINAAIQDMPSEEEIAQLLSGSYIHYFHCRLRLDLLKGTEASTKNIFGRYSSQRMKDQWEIIALYEKDNLYLVELSSLVRNVNVEIPSLKKQIAKQQQLQQEYSRKEEECQAGAAEMREQFYHSCQKQYGITGENVRGELLALVKDLPQLAEIGAAAQQSLGEAIDVYQASVGFVCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEELPEQVAEDAIDWGDGVEAVSEGTDSGISAEAAAGIDWGIFFPSDSKDPGGDGIDWGDAAVALQITVLEAGTQAPGVARGPDALTLEYTETRNQFLDELMELEIFLAQRAVELSEADVLSVSQFQLAPAILQQQTKKEMVTMVSVLEDLIGKLTSLQLQHLFMILASPRYVDRVTEFLQQLKQSQLLALKKELMVQKQQAEEQAALPEKLDLLEKTKELQKLIADISKRYSGRPVNLMTSL
6429	3413	3442	EPSSWTAAPRGPLAAHPLEAAVQEDDRRLSFDSSRIKVPFANGTLVVKSVTDKADGDLVCARNKVGDDYVVLKVDVVMKPAKIEHKEENDHKVFFYGGDLKVDCAVATGLPNPEISWSLPGSLVNSFMQSDDSGGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENQVQKDEMVRVKVVTAPATIRNKTCLAVQVPYGDVVTVACEAKGPEMPKVTWLSPTNKVIPTSSSEKYIYQDGTLLIQKAQRSDSGNYTCLVRNSAGEDRKTVWIHVNVPKPKINGNPNPITTVREIAAGGSRKLDCKAEGIPTPRVLWAPPEGVVLPAPYNGNRI TVHNGSLDIRSLRKSQSVQLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGHTISLNCSAAGTPTPSLVVLPNGTDLQSGGQLQRFYHKADGMLHISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNLLVSIINGETLKLPTPPGAGQGRFSWTL PNGMHLEGPQTIGRVSLDNGTLTVREASVFDRTGYVCRMETEYGPSVTSIPVIVIAYPPRITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWBLPKSHLKGQVQARLYGNRFLHPQGSLLTIQHATQRDAGFYKCMKNILGSDSKTYIHVF
6430	1946	602	RTRVSTGLRRTLLWSEAVGASSTRGDTGIPSGEGGAGPGGGEGAMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIBDFNKFCSFVLAYAGYIPPSKEESDWPASGSSSPLRGESAADSDGWSAPSDDLRTIQTFVKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKMKLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLSHPPRKDRKNRKLGPAGAGFVLRPRPTPGDGEKRSRIKKSCKRKLKKAERGDRLLPPGPPQAPPSTDSEEEEEEEEEEEBEMATVVGGEAPVPVLPPTPEAPRPPATVHPEGVPPADSESKEVGSTETSQDGDASSSEGENRVMDEDIMVESGDDSDWDLITCYCRKPFAGRPMIECSLCGTWIIHLSCAKIKKTNVPDFFYCQKCKELRPEARLGGPCKSGEP
6431	3	605	WNNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGRLEEEALRRKRLKALREKTRKDKEDGEPKTKHLREEEEGEKHRELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKSQLEAAKPEPVIIEVDLANLAPRKPDWDLKRDVAKKLEKLKRTQRAIAELIRERLKGQEDSLASAVDAATEQKTCDS
6432	56	1692	GGLGTMGSRIKQNPETTFEVYEVAYPRTGGTLDPEVQRQFPEDYSDQEVQLTLTKFCFPFYVDSLTVSQVGQNTFVLTIDSKQRFGFCRLSSGAKSCPCILSYLPWFVEFYKLLNILADYTTKRQENQWNELLETLHLKLPIDPGVSVHLSVHSYFTVPDTRLEPSIPENRNLTEYFVAVDVNNMLHLYASMLYERRILIIICSKLSTLTACIHGSAAMLYPMYQHVYIPVLP PHLLDYCCAPMPYLIGIHLSLMEKVRNMALEDVVILNVDNTLTETPFDDLQSLPNDVISSLNRLKKVSTT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TGDGVARAFLLKAQAAPFGSYRNALKIEPEEPITFCBEAFVSHYR SGAMRQFLQNATQLQFKQFIDGRLLDLSGEGFSDVFEEIINM GEYAGSDKLYHQWLSTVRKSGAILNTVKTKANPAMKTVYKFDI AENGCAPTPEEQLPKTAPSPLEAKDPKLREDRRPTTVHFGQVR PPRPHVVKRPKSNIAVEGRRTSVPSPEQNTIATPATLHILQKSI THFAAKFPTRGTWSSSH
6433	1524	484	APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA PTTPPQPGWCLCGKDFKSSCQTPGREKERRLATMHGSCSFLMLL LPLLLLVAATTGPVGALTDEEKRLMVELHNLRYAQVSPITASDML HMRWDEELAAFAKAYARQCWVGHNKERGRGENLFAITDEGMDV PLAMEEWHHEREHYNLSAATCSPGQMGCHYTQVVNAKTERIGCG SHFCEKLQGVETNIELLVNYPEPGNVKGRFPYQEGTPCSQCP SGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDRKMG AEGPDKPSVSVGLNSGPGHVWGPLLGLLLLLPPLVLGIF
6434	40	2002	MPQLNFGMADPTQMGLSMLLLAGEHALGTPEVFSGTCTRPDVSE SPELRQKSPFLQFAEISSSTSHSDASTKQCQTSAFLQFAEISSN TSQLGGAEPVKRCGKSALFQLAEMCLASEGMKMEESKLKAKES DGGRIKELEKGEKEEIKMEKTDETRLQKEAEFEKSARENLRDS KELRNFEALQIDDIAMAKMEDPKEIRKEELEEDHKCSHFPDFSY SASSKIIISDVPSRKDHMCHPHGIMIIEDPAALNKPELKKKKK KSKMDRHGNDKSTPKKTKCKRQSSSESDIESVIYTI EAVAKGDWG IEKLGDTPRKKVRTSSSGKGSILDAKPPKKVKRSREKMSKEKS SDTTKESRPDPFISISASKNISGETPEGIKAEPLTPMEDALPPS LSGQAKPEDSDCHRKIETCGSRKRSERCKGALYKTLVSEGMLTS LRANVDRGKRSSGKGNSSDHEGCWNEESWTFSSQSGTSGSKKPKK TKPKEDCLLGSAKLDEEFKFNLSLPQYSPVTFDRKCVVPVRKK KKTGNVSSEPTKTSKSGDKWSNKQLFLDAIHPTAIFSEDRNT MEPVHKVNKIPSI FNTPEPTTARTFGGQPKESKENPDYSFCQ DTQRAGYHHEEVLWMTNLMNCGGVYKQLRHTAMTNA
6435	2227	657	ALQRDAAAAYAHPEYEEFLQBEETVSQQINSIELLQTRPLALPE VVKSQRPQVHLRGRPASQPTVIRGITYYKAKVSEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA VTDLNARTAPWSSALPQSTSDPSIANHASVGPTLQTTVSVPD PTRESVLQSPQVPATTVAHTATQQAAPAPPAVSPREALMEAM HTVPVPPTTVRTSLGKDAPAGRGTTPASPTLSFEEEDDIRNVI GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVINY GNTLVEFRNLNENFKQGRWSNSYKLPYSWIGTGHVYNGAFYNNR AFTRNIIKYDLKQRYVAAWAMLDVAEEATPWRWQGHSDVDFA VDENGLWLIYPALDDEGFSQEBIVLSKLNADLSTQKETTWRG LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHNTQIVPR LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY
6436	1295	341	GACRPPVRQDPDSGPDYEALPAGATVTHMVAGAVAGILEHCV YPIDCVKTRMQSLQPDPAARYRNVLALWRIIRTEGLWRPMRGL NVTATGAGPAHALYFACYEKLKKTLSDVHPGGNSHIANGAAGC VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDVRAVWQNEGAG AFYRSYTTQLTMNVPFOAIHFMTYEFLEHFNQRRYNPSSHVL SGACAGAVAAAAATPLDVCKTLLNTQESLALNSHITGHITGMAS AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIANSVVEFFKYLIT KRQEEWRAGK
6437	1828	360	PPAPAPPASPARHVTRTARGHLEGGSRAPFLQAVFLQIKNMVK LIHTLADHGDDVNCCAFSFLLATCSLDKTIIRLYSLRDFTELPH SPLKFHTYAVHCCCFSPSGHILASCSTDGTTLVWNTENGQMLAV MEQPSGSPVRVCQFSPDSTCLASGAADGTVLWNAQSYKLYRCG SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLHSEKHA DLGITCCDFSSQPVSDGEQGLQFPRLASCGQDCQVKIWIVSFTH ILGFELKYKSTLSGHCAVLACAFSHDGQMLVSGSVDKSVIVYD

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TNTENILHTLTQHTRYVTTCAFAFNTLLLATGSMKDTVNIWQFD LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAQDLKDLVGIFKM NNIDGKELLNLTKESSLADDLKIESLGLRSKVLRIEELRTKVKS LSSGIPDEFICPITRELMKDPVIASDGYSYEKAMENWDPAKRN RTSP
6438	109	901	EVQILRAKMFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNV NPALPLSPTGLAGSLTNALSNGLLGGGLGILENPLLDILKPG GGTSGGLLGGLLGKVTSPVPLNNIIDIKVTDPLLELGLVQSP DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD KQERIHVLGDCTHSPGSLQISLDDGLGPLPIQGLLDSLTGILN KVLPELVQGNVCPVNEVLRGLDITLVHDIWNMLIHGLQFVIK SIQTASAITTEMASQSQGIQQLLQAEKRAEKVADARKRKARRL KQAKESAEQMEVEQYRREREHEFQSKQQAAMGSQGNLSAEVEQAT RRQVQGMQSSQQRNRERVLAAQLGMVCDVRPQVHPNYRISA
6439	23	412	RARWNSDMGDLPLVRLSLALRIQPNDDGPFYKVDGQRFQGNRT IKLLTGSSYKVEVKIKPSTLQVENISIGGLVLPLELKSKEPDGD RVVYTGTYDTEGVTPTKSGERQPIQITMPFTDIGTFETVWQVKF YNYHKRDHCQWGSPPFSVIEYECKPNETRSLMWVNKESFL
6441	234	1373	KSGGLRRRQRPGRSAAGVEEELPPGMEKFKAAMLGSGVDALGY RNVCKENSTVGMKIQEELQSRGGLDHLVLSPEWPFVSDNTIMHI ATABALTTDYWCLDDLYREMVRCEIVEKLPERRPDPATIEGC AQLKPNYLLAWHTPFNEKSGSGFAATKAMCIGLRYWKPERLET LIEVSVECGRMTHNHTGFLGSLCTALFVSFAAQGKPLVQWGRD MLRAVPLAEFYCRKTIRHTAEYQEHWFYFEAKWQFYLEERKISK DSENKAI FPDNYDAEERBKYRKWSSEGRGRRGHADPMIAYDA LLAAGNSWTELCHRAMFHGGESAATGTIAGCLFGLLYGLDLVPK GLYQDLEDKEKLEDLGAALYRLSTEEK
6442	34	796	AEDFAGGLAGQDTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS LQQRSLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQEEMTQ DGTWRTVAPQAAERAPLDRLVSTELCRAAWGQEGANPASGLGD GHTQGPVSDLCPVTSQAAPRHLQSSAWEMDGPRENRSFHKSLD QIFETLETKNPSCMEELFSDVDSPYYDLDTVLGTGMGGARPGPC EGLEGLAPATPGPSSSCKSDLGELDHVVEILVET
6443	2	555	MASPAASSVRPPRPKKEPQTLVIPKNAEEQKLERLMKNPDK AVPIPEKMSWAPRPPPEFVRDVMGSSAGAGSGEFHYRHLRRR EYQRQDYMAMAQKQLDAEFQKRLEKNKIAAEEQTAKRRKKRQ KLKEKKLLAKMKLEQKKQEGPGQPKQEGSSSSAEASGTEEBEE VPSFTMGR
6444	390	899	GSTPRGKMRAPIEPKPGDLIEIFRPFYRHWATYVGDGYVWHIA PPSEVAGAGAASVMSALTDKAIKKELLYDVAGSDKYQVNNKHD DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA RSDQVRDVI I AASVAGMGLAAMSLIGVMFSRNKRQKQ
6445	2	753	AGAAGAAGAARSPPQAHTKGVRLPSRRRSPDCGRMELAGSF SEEQFWEACAEELQPPALAGADWQLLVETSGISYRLLDKKTGLY EYKVFVLEDCSPTLLADIYMSDYRKQWDQVVKELYEQECNGE TVVYWEVKYPPFMSNRDYYLRQRRDLMEGRKIHVILARSTSM PQLGERSGVIRVKYKQSLAIESDGKKGSKVFMYYFDNPGGQIP SWLINWAAKNGVFNFLKDMARACQNYLKK
6446	1	1651	RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEDLPELS DSGDEAAWEDDEDADLPHGKQQTCLFCNRLFTSAERTFSHCKS EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV PWEKEEYLPVLEDDLLQFVDELDYEPVSVFSPYNGLSENTS VVEKLKHEARALSAAALARAREDLQMKQFAQDFVMHTDVRT CSSSTSVIADLQEDDGVYSSYGHYGIHEEMLKDKIRTESYRD FIYQNPFIKDKVVLVDVCGGTGILSMFAAKAGAKKVLGDVQSEI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LYQAMDIIRLNKLEDITITLIKGTIEEVHLPVEKVDVIIEWMGY FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKHA DRIAFWDDVYGFKMSCMKAVIPEAVVEVLDPKTLISEPCGIKH IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHN RVVFTSGPQSTKTHWKQTVFLEKPPSVKAGEALGKQVTVHKNK KDPRSLTVTLTNNSTQTYGLQ
6447	1554	1068	RLGPAEWHLSGPGCHATLGAANRGRALGVRAAWRGAPLQCRVMMMP SRTNLATGIPSSKVYSRLSSTDGDIYDLQPKKTPPKIPYKAIA LATVFLIGAFLLIIIGSLLSGYISKGGADRAVPVLIIGILVFL PGFYHLRIAYVASKGYRGYSYDDIPDFDD
6448	74	559	GQVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEBTTEFGLOK FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAIVLSTYLEMG AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER QFIVRVKHYDPEKDVHIYEAKRKNQKEDL
6449	597	1876	EYGVNENLRKLEITGVSCRDVYAKLLHRYRHILGLWQPDIGPYG GILNVVVDGLFIIGWMLPPHDPHVDDPMRFKPLFRIHLMERKA ATVECMYGHKGPHHGHIIQVKKDEFSTKCNQTDHHRMSGGRQEE FRTNLREBWGRTLEDIFHEHMQELILMKFIYTSQYDNCCLTYRRI YLPSPSRPDDLKPGLFKGTGYSGHLEIVMLSFHGRRARGTKITG DPNIPAGQQTVEIDLHRHIQLPDLENQRNFNELSRIVLEVREVR RQEQQEGGHEAGEGRGQGPRESQPSPAQPAEAPSKGPDGTPG EDGGEPEGDAVAAAEQPAQCGGQPFVLPVGVSSRNEDYPRTCRM CFYGTGLIAGHGFTSPERTPGVFILFDEDRFGFVWLELKSFSLY SRVQATFRNADAPSPQAFDEMLKNIQSLTS
6450	848	269	FVPAPRTVSGKRSPLGEWEERGEQRTGREFSNGNGRAVEAAR MRLLCGLWLWLSLLKVLQAQTPTPLPLPPMQSFGQNGQFQGEWF VLGLAGNSFRPEHRALLNAFTATFELSDDGRFEVWNAMTRGQHC DTWSYVLIPAAQPGQFTVDHRVWTHEQAGRPQDQPAQQLVAAS RDAGPVHLPGQSSGPLG
6451	232	939	HSPPTPTSPRASTMEDVKLEFPSPLPQCKEDAEWYTPMRREMGE ILPGLFLGPYSSAMKSLPVLOKHGITHIICIRQNIENFIKEN FQQLFRYLVDIADNPVENIIRFPMTKEFIDGSLQMGKVLVH GNAGISRSAAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGF VHQLQYEYAIYLAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHE EEDDFGTMQVATAQNG
6452	1	652	RTRGESSNMEPLAAYPLKCSGPRAKVFVLLSIVLCTVTLFLLQ LKFLPKINSFYAFEVDAKGRVTSLEKYKGKVSLLVNVASDCQ LTDNRNVLGLKELHKEFGPSHFSVLAPPNCNQFGBSEPRPSKEVES FARKNYGVTFPIPHKIKILGSEGEPAFRPLVDSSKKKEPRWNFWK YLVNPEGQVVKFWRPEEPIEVIRPDIAALVRQVIIKKKEDL
6453	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC RDKNCKVVFSSQQLRKRLTPLQYHVTQEKGTESAFEGEYTHHK DPGIYKCVVCGTPLFKSETKFDGSGGWPSFHDVINSEAITFTDD FSYGMHVRVETSCSQCAHLGHI FDDGPRPTGKRYCINSAALSFT PADSSGTAEGGSGVASPAQADKAEL
6454	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC RDKNCKVVFSSQQLRKRLTPLQYHVTQEKGTESAFEGEYTHHK DPGIYKCVVCGTPLFKSETKFDGSGGWPSFHDVINSEAITFTDD FSYGMHVRVETSCSQCAHLGHI FDDGPRPTGKRYCINSAALSFT PADSSGTAEGGSGVASPAQADKAEL
6455	1042	173	RVHLATVSASAAWDALGLPVRSHMQGSTRMGVMTDVHRRFLQL LMTHGVLEEDVKRLQTHCYKVHNRNATVDKLEDFINNINSVLE SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLF RKALELIIDSETGFASSTNINLVDQLKGKMRKKEAEQVLQKF VQNKWLEKEGEFTLHGRAILEMEQYIRETYPDAVKICINCHSL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LIQGGQSCETCGIRMHLPVAKYFQSNAPRCPCNDYWPHEIPK VPDPEKERESGVLKSNKKSLRSRQH
6456	2	555	RPQSRISIMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCCKGA TVEAEALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR RPAPFEVVFVSADGSSQEMLDPMRELHGAWLALPFHDPYRHELK KRYNVTAIPLKLVIVKQNGEVITNKGRKQIRERGLACFDQWVEAA DIFQNFVS
6457	23	892	PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLTLLLET IILGKQYSLNIIILSVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCLGFLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTLLSSQLKPKPVGEENICLDLKS
6458	23	892	PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLTLLLET IILGKQYSLNIIILSVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCLGFLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTLLSSQLKPKPVGEENICLDLKS
6459	23	892	PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLTLLLET IILGKQYSLNIIILSVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCLGFLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTLLSSQLKPKPVGEENICLDLKS
6460	23	892	PTTGFPVTFNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV KLFPLPLLYVGNHISGLSSTSLSLPMFTVLRKFTIPLTLTLLLET IILGKQYSLNIIILSVFAIILGAFIAAGSDLAFLNLEGYIFVFLND IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG DLQQATEFNQWKNVVFILQFLLSCLGFLLMYSTVLCSYNSAL TTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRY SFLTLLSSQLKPKPVGEENICLDLKS
6461	1653	360	LQQRTRLRITAVGQTHPIAWMAWEPISLGAFFGPASFITFVNCMYF LSIFIQLKRHPERKYELKEPTEEQORLAANENGEINHQDSMSLS LISTSALENEHTFHSQLLGASLTLLLYVALWMFGALAVSLYPL DLVFSFVFGATSLSFSAFFVHVHCNREDVRLAWIMTCCPGRSS YSVQVNVQPPNSNGTNGEAPKCPNSSAESSCTNKSASSFKNSSQ GCKLTNLQAAAAQCHANSPLNSTPQLDNLSTEHSMDNDIKMHV APLEVQFRITNVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE GSVQNGLPKSRILGNNEGHSRSRRAYLAYRERQVNPQQDSSDAC STLKSSRNFEKPVSTTSKKDALRKPAVVELENQKSYGLNLAI QNGPIKSNQEGPPLLGTSTGNVRTGLWKHETTV
6462	3	773	SEELDREKCLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH PDSQSMEESEKLNDDRTPVNWKDSRGTRVAVSSPMSQHQSYIQ YLHAYPYPMYDPSHPAYRAVSPVLMHSPGAYLSPGFHYVPYG KMSGRETEKVNTPSPVNTKTTTESKALDLLQHANQYRSKSPA PVEKATAEREREAERERDRHSFPQQRHLTHHHTHVGMGYPLIP GQYDFPQGLTSAALVASQVAAQASAGMFPQQRRE
6463	2	350	VILCILGGWIFKNADRSMBKKKGEPRTAEARFVWDELDKSSD LHQAEEDAWEQSEENVEHIPFSHNHYPEKEMVKRSQEFYELL NKRRSVRFISNEQVPMVEIDNVIRTAGL
6464	12	1154	GILRQKEREERNRIHKKEILFLEHLLVVPSEMSSSLGKQVQTVLG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>LVPSKLGRTLTTHELAMTFDCCYCPFPFQCEAISKEPTVMKNL</p> <p>YWIQKNAYSHKENLQNLQETEAKEELLYFKANGGGALVENTTT</p> <p>GISRDTQTLKRLABETGVHIISGAGFYVDATHSSETRAMSVEQL</p> <p>TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH</p> <p>AQAQLGCPVIIHPGRSSRAPFQIRILQEAGADISKTVMSHLDR</p> <p>TILDKKELLEFAQLGCYLEYDLFGTELLHYQLGPDIDMPDDNKR</p> <p>IRRVLLVEEGCEDRILVAHDHTKTRLMKYGGHGYSHILTNVV</p> <p>PKMLLRGITENVLDKILNIENPKQWLTFK</p>
6465	126	1396	<p>KMTVFFKTLRNHWKKTAGLCLLTWGGHWLYGKHCDMLLRRAC</p> <p>QAAQVFGNQLIPPAQVVKATVFLNPAACKGKARTLFEKNAAPI</p> <p>LHLSGMDVTIVKTDYEGQAKLLELMENDTVIIVAGGDGLQEV</p> <p>VTGVLRRDTDEATFSKIPGFIPLGETSSLSHTLFAESGNKVQHI</p> <p>TDATLAIKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGV</p> <p>KVSKYWLEPLKIKAAHFFSTLKEWPQTHQASISYTGTPERPEN</p> <p>EPEETPVQRPSPLYRRLRLRLASYWAQPDALSQEVSPVWMDVQ</p> <p>LSTIELSITTRNNQDPTSKEDFLNICIEPDTISKGDFITIGSR</p> <p>KVRNPKLHVGEQTECLQASQCTLLIPEGAGGSFSDSEYEAMPV</p> <p>EVKLLPRKLQFFCDPRKREQMLTSPQ</p>
6466	1134	828	<p>VARGTELSQLEKAHPPADMGRKSKRKPFPKKMTGTLETQFTC</p> <p>PFCNHEKSCDVKMDRARNRGVISCTVCLEEFQTPITYLSEPV</p> <p>YSDWIDACEAANQ</p>
6467	301	2571	<p>GRLRVLALAHGELACHAVLTASLLSLRSLRMSDMDYERPNVET</p> <p>IKCVVVDNAVGKTRILICARACNATLTQYQLLATHVPTVWAIQ</p> <p>YRVCQEVLEERSRDVDDVSLSRLWDTFGDHHKDRRFAYGRSDV</p> <p>VVLCFSIANPNSLHHVKTWMPYPIKHFCPRAPVILVGCQLDLRY</p> <p>ADLEAVNRARRPLARPIKPNELPPEKGREVAKELGIPYETSV</p> <p>VAQFGIKDVFDAIRAAALISRRHLQFWKSHLRNVQRPLLQAPFL</p> <p>PPKPPPIIVVPDPSSSEECPAHLLDPLCADVILVLQERVRI</p> <p>FAHKIYLSSTSSKFYDLFLMDLSEGLGSPSEPGGTHPEDHQGH</p> <p>SDQHSHHHHHHGRDFFLLRAASFVDCESVDEAGSGPAGLRAST</p> <p>SDGILRGNGTGYLPGRGRVLSWSRAVFSIQEEMAEDPLTYKSR</p> <p>LMVVVKMDSSIQPGPFRAVLKYLTYTGELDENERDLMHIAHIAEL</p> <p>LEVFDLRMMVANILNNEAFMNQEITKAFHVRRTNRVKECLAKGT</p> <p>FSDVTFILDDGTISAHKPELLISSCDWMAAMFGGPFVESSTREVV</p> <p>FPYTSKSCMRVLELYLTGMFTSSPDLDMMKILILANRLCLPHL</p> <p>VALTEQYTVTGLMEATQMMVDIDGDVLVFLLELAQFHCAQLADW</p> <p>CLHHICTNYYNNVCRKFPFRDMKAMSPENQYEFKRWPPVWYLKE</p> <p>EDHYQRARKEREKEDYLHLKRPKRRLFWNSPSSPSSSAASSS</p> <p>SPSSSSAVV</p>
6468	3	1374	<p>DAWAGTNMAALAPVGPASRGPRLAAGLRLPLMLGLLQLLAEPG</p> <p>LGRVHHLALKDDVRHKVHLNTFGFFKGYMNVNSSLNLNEPED</p> <p>KDVTIGFSLDRTKNDGFSSYLDDEDVNYCILKKQSVSVTLILD</p> <p>SRSEVRVKSPEAGTQLPKIIFSRDEKVLGQSQBPNVNPASAGN</p> <p>QTQKTQDGGKSKRSTVDSKAMGEKSFVHNNGGAVSFQFFFNIS</p> <p>TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA</p> <p>GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL</p> <p>PFTKLSLVLFAIDYHYISSQGFPIEGWAVVYVITHLLKGALLF</p> <p>ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES</p> <p>TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD</p> <p>GKGKPSRAHFVLLSLL</p>
6469	3	1374	<p>DAWAGTNMAALAPVGPASRGPRLAAGLRLPLMLGLLQLLAEPG</p> <p>LGRVHHLALKDDVRHKVHLNTFGFFKGYMNVNSSLNLNEPED</p> <p>KDVTIGFSLDRTKNDGFSSYLDDEDVNYCILKKQSVSVTLILD</p> <p>SRSEVRVKSPEAGTQLPKIIFSRDEKVLGQSQBPNVNPASAGN</p> <p>QTQKTQDGGKSKRSTVDSKAMGEKSFVHNNGGAVSFQFFFNIS</p> <p>TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GEIPLPKLYISMAFFFLSGTIWIHILRKRNDVFKIHWLMAAL PPTKSLSLVFHAIDYHYISSQGFPIEGWAVVYIYTHLLKGALLF ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLNVAYIIIES TEEGTTEYGLWKDSLFLVDLLCCGAILFPVWVSIRHLQEASATD GKGKFSRAHFVLLSLL
6470	2726	1437	AAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPSAPRS GPLPREDGCRTPGPQLPLPGALLRPRTLLSSAAETGRSRHPDT QHPSSGGRCRGGTESPSAAGRPAEMAEEDCHSDTVRADDDDE ENESPAETDLQAQLQMFRAQWMFELAPGVSSSNLENRPCRAARG SLQKTSADTKGKQEQAKEEKARELFLKAVEEQNGALYEAIFY RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDSKMADLLS YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFRWVVS SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVGWGRSCIKLV PYTSWREMFLEPRPRVFDGVYISKTTYIRQGEQSLDGFYRAWHQ VEYYRYIRFFPDGHVMMMLTTPPEPQSIVPRLRTR
6471	1750	299	FFFDKMAAGSGVGKRSKSDADSGFLGLRPTSVDPALRRRRR GPRNKKRGWRRLAQEPLGLEVDQFLEDVRLQERTSGGLLEAPN EKLFFVDTSKEKGLTKKRTKVQKKSLLKKPLRVDLILENTSK VPAPKDVLAHQVPNAKLLRKEQLWEKLAKQGELEPREVRAQAR LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDEFFLE QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQTLIS AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCEGLLE ESDGEPEGQEGEGPEAGDAEVCPTPARLATTEKKTEQQRREKA VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR ROARREAEADKPRRLGRKYQAPDIDVQLSSELTDSLRLTKPEG NILRDRFKSFQRRNMIEPRERAKFKRYKVKLVKRAFREIQL
6472	3	897	SCGSDRAQWAMEFFFDVDALEPFRITVLDQHLRPFARRPGTTTP ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY ILKDSARPAKGAIIGFIKVGYKKLFVLDREAHNEVEPLCLL DFYIHESVQRHGHGRELFQYMLQKERVPHQLAIDRPSQKLLKF LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATHRSRAA AVDPTPAAPARKLPKRAEGDIKPYSSSDREFLKVAVEPPWPLN RAPRRATPPAHPPRRSSSLGNSPERGPLRPFVP
6473	22	912	SSAVEFVWEGEKMAAEFNKTEIQTLFKRLRAVPTNKACFDGAK NPSWASITYGVFLCIDCSGVHRSGLVHLSFIRSTELDSNNWFQ LRQMVGGNANATAFFRQHGTANDANTKYNSRAAQMYREKIRQ LGSAAALRHGTDLWIDNMSSAVPNHSPEKKDSDFTEHTQPPAW DAPATEPSGTQQPAPSTESSGLAQPEHGPNLDLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFEIERQAQVAE KLREQQAADAKKQAEESVMASMLAYQELQIDR
6474	3	462	LQRQRQHPAAAPAVPVRCTFCFTDIVIMPKRKSPENTEGKDG KVTKEPTRRSARLSAKPAPPKPEPKRKTSAKKEPGAKISRGA KGKKEEKQEGKEGTAPSENGETKAEIHSRSTVNVSTSRGTP PSTLSVKQIETVRVKGTEN
6475	3	462	LQRQRQHPAAAPAVPVRCTFCFTDIVIMPKRKSPENTEGKDG KVTKEPTRRSARLSAKPAPPKPEPKRKTSAKKEPGAKISRGA KGKKEEKQEGKEGTAPSENGETKAEIHSRSTVNVSTSRGTP PSTLSVKQIETVRVKGTEN
6476	106	1090	ARAMAQYKGTMRAGRAMHLKKRERQREQMEVLKQRIAEETIL KSQVDRKRFSAHYDAVEAEKLSSTVGLVTLNDMKARQEALVRE RQLAKRQHLEEQRLQQRERQREQRRERKRKISCLSFALDDLLD QADAAEARRAGNLGKNPDVDTSLPDRDREEEENRLREELRQW EAQREKVKDEEMEVTFSYWDGSGHRRTRVRVKGNVTQQFLKKAL QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIARARGK SGPLFSFDVHDDVRLSDATMEKDESHAGKVVLRSWYKXKHIF PASRWEAYDPEKKWDKYTIR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6477	227	915	LQGHLMGIMAASRPLSRFWENGKNIVCVGRNYADHVREMRSAVL SEPVLFLKPSTAYAPEGSPILMPAYTRNLHHELELVVMGKRCR AVPEAAAMDYVGGYALCLDMTARDVQDECKKKGLPWTAKSFTA SCPVSFAFVPKEKIPDPHKLKLWLKVNGLRQEGETSSMIFSIPIY IISYVSKIITLEEGDIILTGTPKGVGPVKENDEIEAGIHGLVSM TFKVEKPEY
6478	2	1495	FVSSRIIPESLASSEASTLEAMGRKEEDDCSSNKKQTTNIRKTF IFMEVLGSGAFSEVFLVKQRLTGKLFALKCKIKKSPAFRDSSLEN EIAVLKKIKHENIVTLEDIYESTTHYYLVMLVSGGELFDRILE RGVYTEKDASLVIOQVLSAVKYLHENGIVHRDLKPENLLYLTP ENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKA VDCWSIGVITYILLCGYPPFYEETESKLFKEKIEGYEFESFPW DDISESAKDFICHLEKDPNERYTCEKALSHPWIDGNTALHRDI YPSVSLQIQKNFAKSKWRQAFNAAAVVHMRKLHMLHSPGVRP EVENRPPETQASETSRSPSPETITTEAPVLDHVSALPALTQLPC QHGRRTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCC SSCLNIGSKGSSYCSBPTLLKKANKKQNFSEVMVPVKASGSS HCRAGQTGVCLIM
6479	3	949	SCRGPQWHFAGGQAGAMELLSALSGLGELALSFSRVPLFPVFDLS YFIVSILYLKYEPAVELSRRHPIASWLCAMLHCFGSYILADLL LGEPLIDYFSNNSSILLASAVYLIFFCPLDLFYKCVCFPLPKL IFVAMKEVVRVKIAVGIHHAHHHHYHGWFMATGWVKGSGLVA LMSNFEQLLRGVNKPETNEILHMSFPPTKASLYGAILFTLQQT LPVSKASLIFITFLFMVSCKVFLTATHSHSSPFDALGYICFVL FGSACGGDHHHDNHGSGHSGGGPGAQHSAMPAKSKEELSEGRK KKAKKAD
6480	192	514	DFMSIYFPIHCPDYLRSKMTVEVMNTQPMEEIGLSPRKDGLSY QIFPDPSDFDRCKLKDRLPSIVVEPTGEVESGELRWPPEEFL VQEDQDNCEETAKENKEQ
6481	110	1131	KSRMDLDVVMFVIAGGTLAIPILAFVASFLLWPSALIRIYYWY WRRTLGMQVRYVHEDYQFCYSFRGRPGHKPSILMLHGFSAHKD MWLSVVKFLPKNLHLVCDMPGHEGTTRSSLDLSDIQQVKRIH QFVECLKLNKKPFHLVGTSMGGQVAGVYAAYPSDVSLWLVC AGLQYSTDNQFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQ SYVRFKVPQIILQGLVDVRI PHNNFYRKLFLEIVSEKSRYS LHQ NMDKIKVPTQIINGKQDQVLDVSGADMLAKSIANCQVELLE NCG HSVMERPRKTAKLIIDFLASVHNTDNNKKLD
6482	2517	568	EPVSKVSQSRKAGVPTANIEESQAVEAAMANVPWAEVCEKFOA ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPED EDE RPEAEDGPGAGDHALGLPAEVVEPEGPVAQRAVRLAVIE FHLGV NHIDTEELSAGEEHLVKCLRLRLRYRLSHDCISLCIQA QNNLGI LWSEREEIETAQAYLESSEALYNQYMKVGSPPLDPT ERFLPEE EKLTEQERSKRFEKVYTHNLYLAQVYQHLEMF EKAHYCHSTL KRQLEHNAYHPIEWAINAATLSQFYINKLCF MEARHCLSAANVI FGQTGKISATEDTPEAEGEVPELYHQR KGEIARCWIKYCLTLMQ NAQLSMQDNIGELDLDKQSEL RALRKKELDEESIRKKAVQFGT GELCDAISAVEEKVS YLRPLDFEARELFLGQHYVFEAKEFFQ IDGYVDHIEV VQDHSALFKGLAFFETDMERRCKMKHRRIAMLE PLTV DLNPQYYLLVNRQIQFEIAHAYYDMMDLKVAIADRL RDPD SHIVKINNLNKSAKYQLFLDSLRLDPNKV FPEHIGEDVLRPA MIAKFRVARLYGKIITADPK ELENLATSLEHYKFIVDYCEKHP EAAQIEVELELS KEMVSLPTKMERFRTKMALT
6483	3	623	NSHLLCGLRARAPLSANGREARAMEQLABFRAARKRAGLAAQP PAASQGAQTPGEKAEAAATLKAAAGWLKRLVWVKPRPASARAQP GLVQEAQPGSTSETPWNTAIPSPCWDQSFLTNITFLKVLW LVLLGLFVELEFGLAYFVLSLFYWMYVGTGROPEEKKEGEKSAYS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6484	201	965	VFNPGCRAIQGTLTAEQLERELQLRPLAGR QLAVKTKMSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCQRLF MILWLKGVKFNVTVDVMDTRKPEELKDLPAGTNPFFLVYNKELKT DFIKIEEFLEQTLAPPRYPHLSPKYKESFDVGCNLFAPKPSAYIK NTQKEANKNFEKSLLEKPKRLDDVLTPLDDEIDPDSEAEPPVS RRLFLDGDQLTLADCSLLPKLNIIKVAACKYRDFDIPAEEFSGVW RYLHNAYAREEFTHTCPEDKEIENTYANVAKQKS
6485	6	1091	FVDLVRAVEFLPCPDQSKLEKECQSSSEBSMGSNSMRISILEDEE DEEPPRVLLYHEPRSEFVGMVLVWHKHKYFPWPAPVVKSVRQDK KASVLYIEGHMNPMMKGFVTVSLKSLKHFDCKEKQTLNQAQEDF NQDIGWCVSLITDYRVLGCGSFAGSFLEYAADISYPVRKSIQ QDVLGTLKPLSKGSPPEEPVVGCPGQRPCKRMLPDRSRAARD RANQKLVEYIGKAKGAESHLRAILKSRKPSRWLQTLFSSSQYVT CVETYLEDEGQLDLVVKYLGQVYQEVGAKVLQRTNGDRIRFILD VLLPEAIIICASAGDEVYKTABEKYIKGPSLSYREKEIFDNQL LEERNRRRR
6486	10	581	LVLQAGGAHLSPSRVTOGIYMLAFSEMPPDYSELSDSLTLA GGTGRFSGLPHRAWMMNFRQRMGWIGVGLYLASAAAFYYVFE ISETYNRLALEHIQQHPEEPLEGTWTHSLKAQLLSLFPWVWTV IFLVPYLMFLFLYSCTRADPKTVGYCIIPICLAVICNRHQAFV KASNQISRLQLIDT
6487	352	863	SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN YYNGCIFHRNIIKGFVMTQDPTGTGRGGNSIWGKKFEDEYSEYL KHNVRGVSMANNGPNTNGSQFFITYGKQPHLDMKYTVFGKVID GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPPAQ
6488	878	241	TALQEFGTSGPPLSLRFALPSGTGRFKPLPGARGPSWPPSPRPV MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH KDEFFFGSGGSISSCPGGTLLGPPDSVVDVGSTEVTEEIFLEYL SSLGESLFRGEAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLP SEVLSTPPGQALRPLDLSIQIPPGSSVGRPNGQS
6489	1457	375	KVAKMATALSEEELDNEDYVSLNVRREASSEELKAAYRRLCML YHPDKHRDPELKSQAERLFLNVHQAYEVLSDPQTRAIYDIYGKR GLEMEGWVVERRRTPAEIREEFERLQREBERRLQRTNPKGT ISVGVDATDLFDYDEEYEDVSGSSFPQIEINKMHISQSIAPL TATDTAILSGSLSTQNGNGGGSINFALRRVTSAGKGGELEFGAG DLQGPLFGLKLFRLNLTFRCFVTNICALQFSSRGIRPGLTTVLAR NLDKNTVGYLQWHCSSLQVORPHRNTACAPEPSFRPFLHVP TWDACSGARTPSTAWTSAAVKLREACLSPGSGSGHQLLLTTPR SKRRTGGG
6490	3	1183	HEAGCEVWLGYGPRAAAAAAATVLEGGAGPTETMFVARSTIADH KDLIHDSVDFPHGRMATCSSDQSVKVDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCDFRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVNMNLSQWSLQHEISCKLSCSISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDVPVHDIAFAPNL GRSFHILAIATKDVRIFTLPVKRKELTSSGGPTKFEIHIWAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL KNGSPVNGSSSQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
6491	3	1183	HEAGCEVWLGYGPRAAAAAAATVLEGGAGPTETMFVARSTIADH KDLIHDSVDFPHGRMATCSSDQSVKVDKSESGDWHCTASWKT HSGSVWRVTWAHPEFGQVLASCDFRTAAVWEEIVGESNDKLRG QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE APDVNMNLSQWSLQHEISCKLSCSISWNPSSSRAHSPMIAVGSD DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDVPVHDIAFAPNL GRSFHILAIATKDVRIFTLPVKRKELTSSGGPTKFEIHIWAQFD NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6492	34	2573	<p>KGNGSPVNGSSOQGTSNPSLGSNIPSLQNSLNGSSAGRKHS</p> <p>IPFLKSCCCCLFDFPPPPPLDQVQEECEVERVTEHGTTPKPFRRK PDSVAFGESQSEDEQFENDLETDPPNWQQLVSRVLLGLKPCEI KRQEVINELFYTERAHVRTLKVLQDVFFYQVRVSREGILSPSELRK IFSNLEDILQLHIGLNEQMKAVRKRNETSVIQIGEDLLTNFSG PGEEKLKHAATFCSNQPFALMIKSRQKKDSRFQTFVQDAESN PLCRRLLQKLDIPTQMQLTKYPLLDNIATYTEWPTEREKVKK AADHCROILNYVNOAVKEAENKQRLQEDYQRRLDTSCLKSEYPN VEELRNLDLTKRKMIHEGPLVWVNRDKTIDLYTLLEDILVLL QKQDDRLVLRCHSKILASTADSKHTFSPVILKSTVLVRQVATDN KALFVISMDSNGAQIYELVAQTVSEKTVQDLICRMAASVKEQS TKPIPLPQSTPGEGDNDEEDPSKLKEEQHGISVTGLQSPDRDLG LESTLISKPKQSHSLSTSGKSEVRDLFVAERQFAKEQHTDGTLK EVGEDYQIAIPDSHLPVSEERWALDALRNLGLLQKLLVQQLGLT EKSVDQEDWQHFPYRTASQGPQTDVSIQNSENIKAYHSGEGHMP FRITGTGDIATCYSPTSTESFAPRDSVGLAPQDSQASNILVMDH MIMTPPEMPTMEPEGGLDSDGEHFFDAREAHSDENPSEGDAVNG EEKDVNLRISGNYLILDGYDPVQESSTDEEVASSLTLPMTGIP AVESTHQQHSQPNTHSDGAI SPFTPEFLVQQRWGAMEYSCFEI QSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYTLICQLRAGS ALTDKHSKDS</p>
6493	557	1147	<p>TPARMAYQGSSTSDCMSKTLDSASAHFAASAVVSAVPVSRSEVA KEONTGHNINGVVPQSGTSKTLYSTNMALSSSPGISAVQLVRT VGHTTTNHLIPALCTSSPQTLPMNNSCLTNVHLNNVSVVSPVN VHINTRTSAPSPTALKLATVAASMDRVPKVTSSAISSIARENH EPERLGLNGIABTTVAMEVT</p>
6494	2425	1052	<p>AVAGGARPCSTPSSPHRRRHRPRPLPRPPAAIMSASAVVLD LKGVLCRNRYRGDVMSEVEHFMPILEKEEEMLSPILAHGG VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEIYITQEGHKL ETGAPRPPATVTVNAWSRSEGIKYRKNEVFLDVIESVNLLVSAN GNVLRSEIVGSIKMRVFLSGMPELRRLGLNDKVLFDNTGRGKSKS VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK PLIWIESVIEKSHSRIEYMIKAKSQFKRRSTANNVEIHIPVFN DADSPKFKTTVGSKVWPENSEIVWSIKSFPGGKEYLMRAHFGL PSVEAEDKEGKFPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL PWVRYITQNGDYQLRTQ</p>
6495	2425	1052	<p>AVAGGARPCSTPSSPHRRRHRPRPLPRPPAAIMSASAVVLD LKGVLCRNRYRGDVMSEVEHFMPILEKEEEMLSPILAHGG VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEIYITQEGHKL ETGAPRPPATVTVNAWSRSEGIKYRKNEVFLDVIESVNLLVSAN GNVLRSEIVGSIKMRVFLSGMPELRRLGLNDKVLFDNTGRGKSKS VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK PLIWIESVIEKSHSRIEYMIKAKSQFKRRSTANNVEIHIPVFN DADSPKFKTTVGSKVWPENSEIVWSIKSFPGGKEYLMRAHFGL PSVEAEDKEGKFPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL PWVRYITQNGDYQLRTQ</p>
6496	247	559	<p>LRAVSLPLQLVLPEYSIHSFLFCIMFLCAQEWLTGLNVPLLFY HFWRIFYHCPADSSSELAYDPPVVMNADTLSCYQKEAWCKLAFYLL SFFYYLYCMIYTLVSS</p>
6497	1053	352	<p>ANTQICRLCPRRHLPCCGAKMNGTEEDYNFVFKVVLIGESGV GKTNLLSRFRNEFSDHSRTTIGVEFSTRVMTLGAATAVKAQIWD TAGLERYRAITSAYYRGAVGALLVFDLTKHOTYAVVERWLKELY DHAEATIVVMLVGNKSDLSQAREVPTTEARMFAENNGLLFLETS ALDSTNVELAFETVLKEIFAKVSKQRQNSIRTNAITLGAQAQO</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6498	2636	272	<p>EPGPGEKRACCISL</p> <p>SLRLCPWGTHTLAGPTTMRLLSSLLALLRPALPLILGLSLGCSLSL LRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLDQSDDEDFKPRI VPYRDNPKNPKYKVLRLTRYIQTELGSRRLLVAVLTSRATLSTL AVAVNRTVAHHFPRLLYFTGQGARAPAGMQVVSNGDERPAWIM SETLRHLHTHFGADYDFFFIMQDDTYVQAPRLAALAGHLSINQD LYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG DILSARPDWLGRLCLIDSLGVGCVSQHQGGQYRSFELAKNRDP KEGSSAFLSAFVHPVSEGTLMYRLHKRFSALELERAYSEIEQL QAQIRNLTVLTPEGEAGLSWVGLPAPFTPHSRFEVLGWDYFTE QHTFSCADGAPKCPQGASRADVGDALETALEQLNRRYQPRLRF QKQRLNLNGYRRFDPARGMEYTLDLLLCEVTQRGHRRLARRVSL LRPLSRVEILPMPYVTEATRVQLVPLPLVAEAAAAPAFLEAFAA NVLEPREHALLTLLLVYGPREGGRGAPDFLGVKAAAELEERRY PGTRLAWLAVRAEAPSQVRLMDVVSXKHPVDLFFLTTVWTRPG PEVLNRCRMNAISGWQAFFPVHFQEFNPALSPORSPPGPPGAGP DPPSPGADPSRGAPIGGRFDRQASAEAGCFYNADYLAARARLAG ELAGQEEEEALEGLEVMDFLRFSGHLHFRVPEGLVQKFSRLRD CSRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQA NST</p>
6499	3	2040	<p>SCSADTRPSGQAWPTVGLRAAAGAFRTGSPLALGPETPQVACL GHPVVRPQVSGGPGAMPDPAHLFFFYGSISRAEAEHKLKLAGM ADGLFLLRQCLRSLLGGYVLSLVHDVRFHHPPIERQLNGTYAIA GKAHCGPAELCEFYSRDPDGLPCNLRKPCNRPSEGLEPQPGVDFC LRDAMVRDYVRQTKLEGEALEQAIISQAPQVEKLIATTAHERM PWYHSSLTREEAERKLYSGAQTGKFLLRPRKEGQTYALSLIYG KTVYHYLISQDKAGKYCIPGTFKFDTLWQVLEYLKLKADGLIYC LKEACPNSSASNASGAAAPTLPAHPSTLTHPQRRIDTLNSDGYT PEPARITSPDKPRPMPMDTSVYESPYSDPEELKDKKFLKRDNL LIADIELGCGNFGSVRQGVYMRKKQIDVAIKVLKQGTETKADTE EMMREAQIMHQLDNPIYVRLIGVQAEALMLVMEMAGGGPLHKF LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAARNVLL VNRHYAKISDFGLSKALGADDSYRTASAGKPLKMYAPBCINF RKFSRSRDVWSYGVMTWEALS YGQKPYKMKGPEVMMAFIBQGR MECPPECPPPELYALMSDCWIYKWE DRPDLTVEQRMRCYYSLSA SKVEGPPGSTQKAEACA</p>
6500	1773	726	<p>TGPTHASADAWGLVRSVTEWCANVRGNPCAAALSCPAVLDAAGK MLESSESSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHL QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWA AVKE TWTKHCDKAEFFSSENVKVFESINMDTNDMMLMRKAYKYAFDK YRDQYNWFFLARPTTFAIENLKYFLLKKDPSQPFYLGHTIKSG DLEYVMEGGIVLSVESMKRLNSLLNIPEKCPPEQGGMIWKISED KQLAVCLKYAGVFAENAEDADGKDVFNKSVGLSKEAMTYHPN QVVEGCCSDMAVTFNGLTPNQMHVMYGVYRLRAFGPYFQ</p>
6501	1	570	<p>LVGMSGGGTETFPVGC EAAPGGGSKKRDLSLGTAGSAHLIIKDLGE IHSRLDHRPVIQGETRYFVKEFEKRLREMRVLENLKNMIEHE TNEHTLPKCRDTRMDSLSQVLQRLQAANDSVCRLLQOREQERKKI HSDHLVASEKHMLQWDNFMKEQPNKRAEVDDEHRKAMERLKEQ YAEKEDLAKSTF</p>
6502	213	1650	<p>AGNKEDDPWAGNRRTAVLPDVSVFHREDVGWNRSLQSSYQAVKE KSSEALEFMKRDLEFTQVQVQHD TACTIAATASVVEKELATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTAKARLYSLQSDPATYCNEPDGPPPELFDWLSQFCLBEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRFYFVHQLQEQ EQARRDALKQRAEQSISEEPGWEEEEEELMGI SPISPKAEKVPV AKISTFPEGEPGPSPCEENLVTSVEPPAEVTPSESSSESISLVT QIANPATAPEARVLPKDLQKLLASLEEQGLAVDVGETGSPSP</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFEINSDSG KSTPSNNGKKGSSTDISSEDWEKDFDLDMTEEEVQMALESKVDASG EVSGPGGSEGSEPNPGPCESSPQPAQLSPQEGPCSCLR
6503	213	1650	AGNKPDPAWGRNRTAVLPDVSVFHRREDVGGWRSWLQQSYQAVKE KSSEALEFMKRDLEFTQVVOHDTACTIAATASVVKEKLATBGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTAKRLYSLOSDPATYCNEPDGPPPELFDWLSSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLQEQ ARRDALKQRAEQSISEEPGWEEEEEEELMGISPISPKEAKVPV AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESESISLVT QIANPATAPEARVLPKDLSQLLEASLEEGLAVDVGETGSPSP IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFEINSDSG KSTPSNNGKKGSSTDISSEDWEKDFDLDMTEEEVQMALESKVDASG EVSGPGGSEGSEPNPGPCESSPQPAQLSPQEGPCSCLR
6504	2131	1294	GKVCILVAHWVCLSLSPPPAGMKT PNAQEAEGQQTAAAGRATG SANMTKKKVSQKKQGRPSQPFCRNIVGCRISHGWKEGDEPITQ WKGTVLDQVPINPSLYLVKYDGDICVYGLELHRDERVLSLKILS DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA PIMKAWFYITYEKDPVLYMYQLDDYKEGDLRIMPESSESPTTE REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF DDDFHIYVYDLVKKS
6505	2131	1294	GKVCILVAHWVCLSLSPPPAGMKT PNAQEAEGQQTAAAGRATG SANMTKKKVSQKKQGRPSQPFCRNIVGCRISHGWKEGDEPITQ WKGTVLDQVPINPSLYLVKYDGDICVYGLELHRDERVLSLKILS DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA PIMKAWFYITYEKDPVLYMYQLDDYKEGDLRIMPESSESPTTE REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF DDDFHIYVYDLVKKS
6506	1	1350	EVSPPTSCCLTVAVADPGVSEGFGRFGAGCEMPGRGRCPDCGST ELVEDSHYSQSQLVCSDCGCVVTEGVLTTFSDENLREVITYSR STGENEQVSRSQQRGLRRVRDLCRVLQLPPTFEDTAVAYYQAY RHSGIRARLQKKEVLVGCCVLITCRQHNWPLTMGAICTLLYAD LDVFSSTYMQIVKLLGLDVPSLCLAEVLKTYCSSFKLFQASPSV PAKYVEDKEKMLSRMTQMLVELANETWLVTRHPLPVITAATFLA WQSLQPADRLSCSLARFCKLANVDLPYPASSRLQELLAVLLRMA EQLAWLRVLRDLKRSVVKHIGDLLQHRQSLVRSFAFRDGTAEVET REKEPPGWGGQGEVGNNSLGLPQGRKPASPALLPPCMLKS PKRICPVPVSTVTGDNISDSEIEQYLRTQBEVRDFQRAQAAR QAATSVPNPP
6507	1878	929	RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWQNKPHGA ARSVVRRIGTNLPLKPCARASFETLPNISDLCLRDVPPVPTLAD IAWIAADEEETVARVRSOTRPLRHTWKPSPLIVMQRNASVFNLR GSEERLLALKKPPALPALSRTTELQDELSHLSQIAKIVAADAAS ASLTPDFLSPGSSNVSSPLPCFGSSFHSTTSFVISDITEETEVE VPPELPSVPLLCASPECCCKPEHKAACSSSEEDDCVSLSKASSFA DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRKFPALKE EDISRKGN
6508	862	342	WEARKRPQRPWPSERREVRVPPPHLQGRSGLEPGTFRKMAAARP SLGRVLPGSSSVFLCDMQEKFHRNIAFFQIVSVAARMKNTTL DLLDRGLQVHVVDACSSRSQVDRVLVALARMRQSGAFLSTSEGL ILQLVGDVHPQFKEIKLKEPAPDSGLLGLFQGNSSLH
6509	2	1053	FVWNPGRGKRKRRAAVTQAATRASGTPSPRDGMTQGLSVAN KAPTEGQQQVHGEKKEAPVPSAPPSYEEATSGEGMKAGAFPP APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHDLFTTFSWDDQKV RRVFVRKYVTILLIQLLVTLAVVALFTFCDPVKDYVQANPGWY ASYAVFFATYTLTACCSGPRRHFPWNLLLTFTLSMAYLTGML

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
			SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL LMTLFFSGILAILLPQYVPWLHAYVYALGAGVFTLFLALDTQ LLMGNRRHSLSPPEYIFGALNIYLDIIYIPTFFLQLFGTNRE
6510	37	1156	PCALDGCPCQGAHVHPLSSAMGLLAFLLKQFVLHLLVGFVFWVS GLVINFVQLCTLALWPVSKQLYRRRLNCRLAYSLWSQLVLMLEWW SCTECTLFDTQATVERFGKSHAVIILNHNFEIDFLCGWTMCERF GVLGSSKVLAKKELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVV EGLRRLSDYPEVMWFLLYCEGTRFTETKHRVSMEEVAAKGLPVL KYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGIL YGKKYEADMVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY NQKGMFPGEQFKPARRPWTLNFLSWATILLSPLFSFVLGVFAS GSPLLILTLGFGVAGNGHCR
6511	2541	1425	GEEQLAAAPTECLEQVIGGAGDPGTWASFPSPFGPAPLKGKK TMAFNFSDIVKQGYVKMKSRKLGIRRCWLVRKSSSKGPQRLE KYPDEKSVCLRGCPKVTETISNVKCVTRLPKETKRQAVAIIFDD SARTFTCDSELEAEWEYKTLSEVCLGSRLNDISLGEPLDLAGV QCEQTDTRFNVFLPCPNLDVYGECKLQITHENIYLDIHNPRVK LVSWPLCSLRRYGRDATRFTFEAGRMCDAGEGLYTFQTQGEQEI YQRVHSATLAIABQHKRVLLEMEKNVRLNKGTEHYSTPPTT MLPRSAWWHITGSQNTAEASSYAGEGYGAAQASSETDLLNRFI LLKPKPSQGDSSSEAKTPSQ
6512	159	807	FGKKSFWFLSRSLRVASGRSCKLGHGGYTGSGPGFGEPRDSGA EVPSSGSRATGCGERGVRGARQGRAPGSSIWRKEPRMVCTRKT TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGQEPAPDKKL EDKGDTLKIIRLDHLENIKQHIQEPAPKEAEAEPTDSS LFAHWGQELSPEGRRVALKQFYGYGYNALSDRLPLDRP
6513	2	756	FVSPFPGFSLAQLNLIWQLTDTKQLVHSFAEGDQGSAYANRTA LFPDLAQQNASLRLQVRVADEGSFTCFVSIIRDFGSAAVSLQV AAPYSKPSMTLEPNKDLRPGDVTITCSSYQGYPEAEVFWQDQ GVPLTGNVTTSMANEQGLFDVHSILRVVLGANGTYSCLVRNPV LQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDLTRCSF SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGDQGSAYANRTALF PDLLAQQNASLRLQVRVADEGSFTCFVSIIRDFGSAAVSLQVAA PYSKPSMTLEPNKDLRPGDVTITCSSYQGYPEAEVFWQDQGV PLTGNVTTSMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDLTRCSFSP EPGFSLAQLNLIWQLTDTKQLVHSFTEGR
6514	985	302	VGIPGPTISSAAEMEDLLDLDEELRYSLATSRKMGRRQQESA QAENHLNGKNSSLTLTGETSSAKLPRCROGGWAGDSVKASKFRR KASEEIEDFRLRPQSLNGSDYGGDIPIDPLEVQEEDFVLQVA APPSIQIKRVMTYRDLNDLMKYSATQTLDEIDLKLLTKVLAP EHEVRERNPSWQDDVGWDHDLFTEVSSSVLTWDPLQTEKEDP AGQARHT
6515	1345	305	GRVGSRRRGAAPVPGCGAGSTQLEVSASASCGALGSADMNPVIV VHGGGAGPISKDRKERVHGMVRAATVGYGILREGGSAVDAVEG AVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKDLGAVSA VQCIANPIKLARLVMEKTPHCFLLTDQGAQFAAAMGVPEIPGEK LVTERNKKRLEKEKHEKGAQKTDCCQKNLGTGVAVALDCKGNVAY ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL KVNLARLTLFHIEBQKTVEEAADLSLGYMKSRVKGLGGLIVVSK TGDWVAKWTSTSMWAAAKDGKLFHFGIDPDDTTITDLP
6516	1	1402	FRRLRYLGQDATAAARLDLRLTRGLQGYCPSATARQQVLVSALQQL KGRRSEHRNENQEMPYSTNKEILIGIMVGTAGISLLLLWYHKVR KPGIAMKLPEFLSLGNTFNSITLQDEIHDDQGTTFVPOERQLQI LEKLNELLTNMEELKEEIRFLKEAIPKLEEYIQDELGGKITVHK ISPQHRARKRLPTIQSSATSNSSSEAESEGGYITANTDTEEQS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=-possible nucleotide deletion, \=possible nucleotide insertion)
			FPVPKAFNTRVEELNLDVLLQKVDHLRMSSESGKSESFELLRDHK EKFRDEIEFMWRFARAYGDMYELSTNTQEKKHYANIGKTLSERA INRAPMNGHCHLWYAVLCGYVSEFEGLQNKINYGHLEHLDIA IKLLPEEPFLYYLKGRYCYTVSKLSWIEKKMAATLFGKIPSSTV QEALHNFLKAEELCPGYSNPNYMLAKCYTDLEENQNALKFCNL ALLLLPTVTTKEDKEAQKEMQKIMTSLKR
6517	3	1414	GRVWGSSSSILNAMVYVRGHAEDYERWQRQARGWDYAHCLPYFR KAQGHHELGAARYRGADGPLRVSRGKTNHPLHCAFLEATQOAGYP LTEDMNGFQQEGFGWMDMTIHEGKRWSAACAYLHPALSRTNLKA EAETLVSRVLFEGTRAVGVEYVKNQSHRAYASKEVILSGGAIN SPOLLMLSGIGNADDLKKLGI PVVCHLPGVGNLQDHLIYIQQ ACTRPTLHSAQKPLRKVCIGLEWLWKFTGEGATAHLETGGFIR SQPGVPHFDIQFHLPSQVIDHGRVPTQGEAYQVHVGPMTGTSV GWLKLRSANPDHPVIQPNYLSTETDIEDFRLCVKLTREIFAQE ALAPFRGKELQPGSHIQSDKEIDAFVRKADSAYHPSTCKMGQ PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGNLNAPTIMIA EKAADIKQGPAWLDKDVVYKPRTLATQR
6518	242	1098	PAWNPGESEPTTRVRPRARSFPLPPRAPRRRRHLLRAVPGPSR RHRCCRRAPPPPSTMGDAGSERSKAPSLPPRCPCGFWGSSKTMN LCSKCFADFKQKQPDSDSAPSTNSQSDLFSEETSDNNNTSIT TPTLSPSQQLPTELNVTSPSKEEGCPTDTAHVSLITPTKRSC GTDQSSENEASPVKRPRLLENTSEETSRSKQSRRCFCQCQT KLELVQQLGSCRCGYVFCMLHRLPEQHDCTFDHMGGRGEEAIM KMKVLDKRVGRSCQRIGEGCS
6519	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSL AKKVRTEKKAPRRVNGEGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLPAAAAAASANAKSRPKKREKERRRHGL GGAREAGGASREENGVEVKPLPRDKIKDKIKERDKEKEREKKKH VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKVKKKKKKKKH ENKRRKPKMYSKSIQITCSGLLTDVEDQAAGIILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLRLDLEFKQLI HIEHQPNGGASVIHCLQ
6520	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSL AKKVRTEKKAPRRVNGEGSGGNSRQLQPPAAPSPQSYGSPAS WSFAPLSAAPSPSSSRSSFSFAGTAVPSSASASLSQPGPRKLL VPPTLLHAQPHHLLPAAAAAASANAKSRPKKREKERRRHGL GGAREAGGASREENGVEVKPLPRDKIKDKIKERDKEKEREKKKH VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKVKKKKKKKKH ENKRRKPKMYSKSIQITCSGLLTDVEDQAAGIILNDNIKDYVG KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLRLDLEFKQLI HIEHQPNGGASVIHCLQ
6521	184	1798	KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP IRRTVNSTRETTPPKSLAEGEEKPEPDISSEESVSTVEEQNE TPPATSSAEQPKGEPENBEKEENKSEETKDEKQSKKEKK VKKTIPSWATLSASQLARAQKOTPMASSPRPKMDAILTEAIKAC FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA LQRAVERGQLEQITGKGASGTFLKKSGEKPLLGGSLMEYAIL AIAAMNBPKTCSTTALKKYVLENHPTNSNYQMHLKKTLOKCE KNGWMEQISGKGFSGTFQLCFYPPSPGVLFPPKEPDDSRDEDE DEDESSEEDSEDEPPKRRRLQKKTAKSPGKAASVKQSGSKPA PKVSAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKPSGGSS KKPATSAKKE
6522	1042	391	NKWLRPSPRSHRTPESGRVLSLFRLLPFPGMALSGSTPAPCWEED

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ECLDYVGMLSLHRMFVVGQLTECELELLAFLLEAPGAAGGLSRARSGLKLLLELERRGQCDESNRLRLGQLRLVLAHDLPLHLARKRRRPFVSPERYSYGTSSSSSKRTEGSCRRRRQSSSSANSQQGSPPTKRQRRSRGRPSGGARRRRRGPPHPSSSQSPDPLPLKAK
6523	2	1097	ASCQTRRRRTAALDSGERIAGRRSPIALAMASNFNNDIVKQGYVKIRSRKLGIFRRCWLVFKKASSKGPRRLKFPDEKAAYFRNFHKVT ELHNIKINITRLPRETKKHAVAIIFHDETSKTFACESELEAEWC KHLCECLGTRLNDISLGEPLDLAGVQREQNERFNVYLMPTFN LDIYGECTMQITHENIYLWDIHNKVKLVMPPLSSLRRYGRDST WTFESGRMCDTGEGLFTFQTRREGMIYQKVHSATLAEQHER LMLEMEQKARLQTSLTEPMTLSKISLPRSAWWHITRQNSVGE IYSLQGNHENRHSDLTGKSKCTSENRFLEENAPLVMYGITHHLF MDTSTCKVVHDL
6524	2	1097	ASCQTRRRRTAALDSGERIAGRRSPIALAMASNFNNDIVKQGYVKIRSRKLGIFRRCWLVFKKASSKGPRRLKFPDEKAAYFRNFHKVT ELHNIKINITRLPRETKKHAVAIIFHDETSKTFACESELEAEWC KHLCECLGTRLNDISLGEPLDLAGVQREQNERFNVYLMPTFN LDIYGECTMQITHENIYLWDIHNKVKLVMPPLSSLRRYGRDST WTFESGRMCDTGEGLFTFQTRREGMIYQKVHSATLAEQHER LMLEMEQKARLQTSLTEPMTLSKISLPRSAWWHITRQNSVGE IYSLQGNHENRHSDLTGKSKCTSENRFLEENAPLVMYGITHHLF MDTSTCKVVHDL
6525	1	1859	GESPFSEBESIEFNPSSSGRSARTVSSNFCSDDTGWSSSQSVSPVKTPSDAGNSPIGFCPGSDEGFTRKCKTIGMVGEISQSSRYK KESKSLVKGSEADFSSSSTGSSISAPEVHMSTAGSKRSSSR NRGPHGRSNGASSHKPGSSPSPREKDLLSMLCRNQLSPVNIHP SYAPSSPSSSNSGYSKGSDCSPIMRRSGRYMSCGENHGVPPNP EQYLTPLQKKEVTVRHLKTKLESERLHERESEIVELKSQLAR MREDWIEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADK KGIQKYFVDINIQNKLESLLQSMEMAHSGSLRDELCLDFPCDS PEKSLTLNPLDTPMADGLSLEEQVTGEGADRELLVGDSTANSTD LEDEIVTATTESGDLELVHSTPGANVLELLPIVMQEEGSSVVV ERAVQTDVVYPSPAISELISVLQKLQDPCPSLASPDESEPS MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR LMRELDFAACVEERLDGVIPLARGGVVRQYWSSFLVDLLAVAA PVVPTVLWAFSTQRGGTPVYNIGALLRGCCVVALHSLRRTAFRIKT
6526	2	2034	SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQOLEEAYSSGKGCN GRVVPDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESNNREIILHNP KLMVHYQPVAGSDDWGSTMEOGRPRTVKRGVENISVDIHCGEP LQIDHLVFFVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK KAQENQIGRVEFLPVNWHSPHISTGVVDLQRIITLPSINRLRH FTNDTILDVFFYNSPTYCQITVDTVASEMNRIYTLFLQRNPDK GGVSIAGHSLGLILFDILTQKDSLGLIDSEKGS LNIVMDQGD TPTLEEDLKKLQLSEFFDI FEKEKVDKEALALCTDRDLQEI LGP RKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPCTCKGFFNIYHPDPVAYRIEPMVVPGEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPIV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTOGIFLDQPLQ
6527	1	922	GWVFLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKQCRGDL FIFNGDAAPSESFVLDNEQKVYQRIHHEESEMTEEEVDILMS SDIYSATLSTKSI SFTRAQTGWLFRDKTERVGNFLADFYLVNG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LVLESRRKRREHLSEEDILRNKAIMESLSKGGNIMEONFEPIRRQSLTPPPQNTITWEEYISAENGKAPHLGRELVCESKKTFFKATIAMSQEFPLGIELLLNVLEVVPFKHFNKLREFVQMKLPPGFPVKLDIPVFPPTITATVTFQEFRYDEFDGSIFTIPDDYKEDPSRFPDL
6528	1	1073	LTGPAAAEPRCAADAGMKRALGRRKGWLRRLRKILFCVLGLYIAIPPLIKLCPGIAQAKLIPLNFVRVPYFIDLKKPQDQGLNHTCNYYLQPEEDVTIGVWHTVPAVWKNAGQKQDMWYEDALASSHIPILYLHGNAGTRGGDHRVELYKVLSSLGYHVVTFDYRGWGDVSGTPSERGMTYDALHVFWDWIKARSGDNVPYIWHGSLGTGVATNLVRLCERETTPDALILESPTNIREEAKSHPFVVIYRYPGFDWFFLDPI TSSGIKFANDENVKHISCPILLHAEDDPVVPFQLGRKLYSIAAPARSFRDFKVQFVPFHSDLGYRHKYIYKSPELPRILREFLGKSEPEHQH
6529	363	2215	THIRYNKIGVVKTMSCGNEFVETLKKIGYPKADNLNGEDFDWLFEGVEDESEFLKWFPCGNVNBQNVLSERELEAFSILQXSGKPILEGAALDEALKTKTSDLKTPRLDDKELEKLEDEVQTLKLKLNKIQRRNKCQLMASVTSHKSLRLNAKEEATKKLKQSQGIILNAMITKISNELQALTDEVQQLMMFFRHSNLGQGTNPLVFLSQFSLEKYLSEEQSTAALTLYTKKQFFQGIHEVVESSESQFFNFKIQTPSICDNQEILEERRLEMARQLAYICAOHQLIHLKASNSMKSSIKWAEESLSLSLTSKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPAVRENAQLLNMPVVKGDFDLQIAKQDYTTARQELVLNQLIKQKASFELLQLSYEIELRKHRDIYRQLENLVQELSQSNMMLYKQLEMLTDPVSQSQINPRNTIDTKDYSTRHLYQVLEGENKKELFLTHGNTDEEVAEKLKQNISLVQDQLAVSAQEHSFFLSKRNDVDMCLDTLYQGGNQLLLSDQELTEQPHKVESQLNKLNLHLLTDILADVKTTRKTLANNKLHQMEREFVYVFLKDEDYLDKDIVENLETQSKIKAVSLED
6530	128	2966	GAAHGGAIVQVHPLLPSSSTIMHDLCLVFPAPAKAVVYVSDIQELYIRVVDKVEIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRAASPIITLVALDEALDNYTITFLIRGVAIGQTSLTASVTNKAGQRINSAPQQIEVFPPFLMPRKVTLIGATMQVTSEGGPQPQSNILFISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVIISQDLVQVEVLLRAVRIRAPIMRMRTGTQMPIYVTGITNHQNPFSFGNAVPLTFHWSVTKRDVLDLGRGRHHEASIRLPSQYNFAMNVLGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVFEKLQLLNPEIEAEQILMSPNSYIKLQTNRDGAASLSYRVLDGPEKVPVYHVEKGFSLASGSMIGTSTIEVIAQEPFGANQTIIVAVKVPVSYLRVMSFPVLHTQNKALVAVPLGMTVTFTHFDNSGDVPHAHSSVLNFATNRDDFVQIGKGTNTNTCVVRTVSVGLTLRLRVWDAPHGLSDFMPLPVLQAI SPELSGAMVVGDVLCATVLTSLGLESGTWSSANSILHIDPKTGVAVARAVGSVTYVEVAGHLRTYKEVVSVPRIMARHLHPITQTSFQBATASKVIVAGDRSSNLRGECTPTQREVIQALHPETLISCQSQFKPAVDFPSPQDVFTVEPQFDTALGQYFCSITMHRITDKQRKHLMSKKALVVSASLSSSHFSTEQVGA EVFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGSPAVLAFAKEKSFGWPSFITVTGVLDPAAGSQGPLSTTLTFSSPVTNQAIAIPVTVAFFVDRRGPGPYGASLFQHFLLDSYQVMFFTLFALLAGTAVMIIAYHTVCTPRDLAVPAALTTPRASPGHSPHYFAASSPTSPNALPPARKASPPSGLWSPAYASH
6531	845	1425	PSASIPPSASPDVPDIRTCHFCLEDPVSGCISGSEKCTISSSLCMVITIIYDVKVRFIIVRGCGQYISYRCQEKNTYFAEYWQAQCCQYDYCNSSPQLQSSLPBPHDRPLALPLSDSQIQWFYQALNLSLPLPNFHAGTEPDGLDPMVTLNLSNLGLSFAELRRMYLFLNSGLLVLPQAGLLTPHPS
6532	2	954	AAGPPSEVVNQDSLFEPEPEGPAPQVLLGPQGGPLIKGVAPPTL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ITDSTGTHLVLTVTNKNHSPGLSRGSPQQPSSQPGSPAPAPSA QMDLEHPLQLPFGTPTSLKKKEPPGYEAMSQQPKQENGSSSQ QMDDLFDILIQSGEISADFKPEPSPGKPKSPKTVCSPLAAQ PSPSAELPQAAPPPPGSPSLPGRLEDPLESSTGLPLTSGHDGP EPLSLIDDLHSQMLSSTAILDHPSPMDTSELHFVPEPSSMTGL DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLPSTDFLDGHD LQLHWDSC
6533	1798	373	STISWLRARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGIEG GAKLCSKLKAEKFLQKVEAGKVAIKESHLQSTNLTHLRAIVES AENLEEVSVLHVFGYDTLGEKQTLVVDVANGGHTWVKAIGR KAEALHNIWLGKQYGDKSIIEQAEDFLQASHQPPVQYSNPHII FAFVNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELQPSSES ESDDGPELLQVTRVDRENILASVAFPTKIVDVCKRVNLDITT LITVVSALSYGGCHFIKFKVLTQAEQERKEQVLPOLEAFMKD KELFACESAVKDFQSILDTLGGPGERERATVLIKRVNVPDQPS ERALRLVASSKINSRSLTIFGTGDTLKAITMTANSGFVRAANNQ GVKFSVFIHQPRALTESKEALATPLPKDYTTDSEH
6534	47	596	KATRFISAAPVVLNKGQVSPAKLPHTSWWSLQTLSPFLSGDLA EKSQCFPCSAMLELIPLLGIHFVLRARAQSVTPQDIHITVS EGASLELRCNYSYGATPYLFWMERTVEEAFILVCLKPWRVASS LEKKEKEDESQQLLGSRYNVLKAHCLLPILRWLTSGDLSLSAQ PHCPQGL
6535	250	964	LIKTFFRDVAIQRDLLPKEKNLETLTLTAPLEIDKAFSSHARLS ADATLLTSGTTATVALLRDLGVVASVGDRAILCRKGKPMKL TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD LDLKTSGVIAEPETKRIKLHADDSPVLVTTDGINFMVNSQEIW DFNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN SEINFSSFRSFASSGRWA
6536	242	1174	SLVKEMTNQYGILFKQEQAHDDAIWSVAVGTNKKENSETVVTGS LDDLVKVKWRDERLDLQWSLEGHQLGVVSDISHTLPAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV GKVNIFGVESGKKEYSLDTRGKFILSIAYS PDGKYLASGAIDGI INIFDIATGKLLHTLEGHAMP IRSLTFS PDSQLLVTA SDDGYIK IYDVQHANLAGTSLGHASWVLNVAFCPDDTHFVSSSSDKSVKVV DVGTRTCVHTFFDHQDQVWGVKYNNGSKIVSVGDDQEIHIYDC PI
6537	1638	921	NRFNPPPTQGPDPVSVYRFPDVPDEAVKDKASFRNYTSGPLLDV FTTYKLMHTHTQTVDFVRSKHAQFGGFSYKMTVMEAVDLLDGLV DESDDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV LALPGEPQWAVVGDTPFVGC RPQASVVFCDSTFQDNPDLDQPRY STELGMYQPHCGLDRLVMSWGHGDEARGGQWGGGGRWGTVG GGG AEAVPAGDTLSPQSTCTR
6538	3345	2412	PYLYDFLDALITCOTAPEEAFIKLDGLAGMLTEQLRRLTKQVQB ARHNRDDEAIKAVNEYDETMEXYIPVLMQAQKIYWNLENYPMV EKIFRKSVEFCNDHDVWKLNVAVLFLM QENKYKEAIGFYEPYIVK KHYDNI LNVSAILANLCVSYIMTSQNEKAEELMRKIEKEEBQL SYDDPNRMYHLICIVNLVIGTLYCAKGNVEFGISRVIKSLPEYN KKLGTDTWYAKRCFLSLENMSKHMIVIHDSVIEQCVQFLGHC ELYGTNIPAVIEQPLEEERMHVGNKNTVTDESRLKALIYEIIGW NK
6539	218	339	FLGAASPHPHFSSSLAPHPDQPEFTPVQDELEAMELWGPV
6540	3	391	LERLWLLLRRRPEDAMAECPTEGAVTDHDLRLWAWK FVYLDE KQHAWLPLTIEIKDRLQLRVLLRRREDVVLGRPMPTPTQIGPSLLP IMWQLYPDGRYRSSDSFWRLVYHIKIDGVEDMLLELPPDD

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6541	1165	536	RTLVRRLMLLRKPARGRDLRGRGRGTPRGRKGLLPTPDEFF RFEGGRKPDSDGNREPFGPGHEHFRDTPRPHPPHGHSPASRE RSSSLQGMDSLPPRKRPHWDGPGTSEHREMEAPGGPSSEDRGG KGRGGPGPAQRVPKSGRSSLDGEHHDGYHREDFPGGPPGSGTP SRGGRSGSNWGRGSGNMNSGPPRRGASRGGGRGR
6542	3	3775	SWPRGRGETGGHFGALRTRTMQKSVRYNEGHALYLAFLARKEGT KRGFLSKKTAESRWHEKWFALYQNVLFYFEGEQSCRPAAGMYLL EGSCERTPAPPRAGAGQGGVRDALDKQYYFTVLFGEHGGKPLE LRCEEEQDGKEWMEAIHQASYADILIEREVLQKQYIHLVQIVET EKIAANQLRHQLEDQDTEIERLKSEI IALNKTERRMPYQSNQE DEDPDIKKIKKQVSMRGWLCRRKWKTIQDYICSPHAESMRKR NQIVFTMVEASEYVHQLYLTVNGFLRPLRMAASSKKPPISHDD VSSIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM LNIYQEFVRNHQYSQVLNCKQNRDFDKLLKQYEANPACEGRM LETFTLYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDSQTFTIRQG SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLETKHFLICTRS SGGKLHLLKTGGVLSLIDCTLIEEPDASDDSKSGSQVFGHLDF KIVVEPPDRAAFTVLLAPSRQEKAAWMSDISQVDNIRCNGLM TIVFEENSKVTVPHEIKSDARLHKDDTDICFSLTNSCKVPQIR YASVERLLERLTLRFLSIDFLNTFLHTYRIFTTAAVVLGKLSLSD TYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCRKFSSP PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTSSSPPTTTTQS PAASPPPHGTQIPLDLSRGLSSPEQSPGTVEENVNDNPRVDLCKN LKRSIQKAVLESAPADRAGVLESSPAADTTLSPCRSPSTPRHLR YRQPGGQTADNAHCSVSPASAFAIATAAGHGSPPGFNNTERTC DKEFIIRRTATNRVLNVLRHVSKHAQDFELNNELKMNVLNLE EVLRLDPLLQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGQGWMLDK NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIEKWWAV ADICRCLHNYNGVLEITSALNRSATYRLKKTWAKVSKQTKALMD KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMVLTDLAFIEBGT PNFTEEGLVNFPSKMRMISHIIREIRQFQQTSYRIDHQPQVAYL LDKDLI IDEDTLYELSLKIEPLPA
6543	1857	950	FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCTHPLDL LKVHLQTOQEVKLRMTGMALRVVRTDGILALYSGLSASLCRQMT YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLGSGVSLAGGFVG TPADLVNVRMNDVKLPQGGRRNYAHALDGLYRVAREGLRRLF SGATMASSRGALVTGQLSCYDQAKQLVLTGYLSDNIFTHFVA SFIAGGCATFLCQPLDVLKTRLMNSKGEVQGVFHCIVETAKLGP LAFYKGLVPAGIRLIPHTVLTFFVLEQLRKNFGIKVPS
6544	630	79	PSPCFIRSLDGGQPMWAGLEAWLSQNFSLHQPSRVVRRASIS EPSDTPPEPRTLNPSPAGWVQVQHPHELELMSSFRERFGRNWLQY RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPPSPQBEAR GPQES PQKMSEEVRAEPQEEEE3KEGKEEKEGEMAPLPEAHIG EGKQKECP
6545	176	560	PPHSHAALLPAAMTPLLTLILVVLMLPLAQLDCHVCAYNGDN CFNPMRCPAMVAYCMTTRTYTPTRMKVS KSCVPRCFETVYDGY SKHASTTSCCQYDLNCTGLATPATLALAPIILLATLWGLL
6546	1657	364	HLNLGLDEVAFFVADLGAIVRKHCFCLKCLPRVRPFYAVKCN SPGVLKVLQQLGLGFSKANKAEMELVQHIGIPASKIICANPCQ IAQKYAAKHGIQLLSFDNEMELAKVVKSHPSAKMVLCIATDDS HSLSCLSLKFGVSLKSCRHLENKHHVEVGVSPHIGSGCPD PQAYAQSIADARLVFEMGTGLGHKMHVLDLGGGFPGTGAKVRF EEIASVINSALDLYFPFGCGVDIFAELEGYYVTSAPTVAVSIIA KKEVLDDQPGREEENGSTSKTIVYHLDEGVYGFNSVLFNDNICP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TPILQKKPSTEQPLYSSSLWGPVAVDGCDCVAEGLWLPQLHVGDW LVFDNMGAYTVGMGSPFWGTQACHITYAMSRVAWEALRRQLMAA EQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM
6547	1	541	LHASKYLAPALCSQPGMMRCCRRRCCCRQPPHALRPLLLPLVLL PPLAAAAAGPNRCDTIYQGFACELIRLGDSMGRGGELETICRSW NDFHACASQVLSGCPEEAAVWESLQQEAPQAPRENNLHTLCGA PVHVRERGTGSETNQETLRATAPALPMAPPLPAAALALAYLL RPLA
6548	2	219	FVSRLSVRDVRFPFTFLGGHGADAMHTDDPYSAAYVPIETDAEDG IKGCGITFTLGKGTVEVGELKILSRFQNA
6549	73	1490	ETGRVCEADARPACGSRSSRRRKEAAPGIPTPSPSSSSPTSSRPA ARAFSKAPARLSRPRAREPPDPGRRIYQEEIIQARKHKLIKMC SSVAAKLWFLTDRIREDYPQKEILRALKAKCCEELDPRAVVM DEVVLTIEQGNLGLRINGELITAYPQVVVVVRVPTPWVQSDSIT VLRHLEKMGCRMLNRPQAILNCVNKFWTQFELAGHGVPDPDTS YGGHENFAKMIDEAEVLEFFPMVVKNTGRHGRKAVFLARDKHHLA DLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMLRCST DGRMQSNCSLGGVGMCSLSEQKQLAIQVSNILGMDVCGIDLL MKDDGSFCVCEANANVGFIADFACNLVDVAGIADYAASLLPSG RLTRRMSLLSVVSTASETSEPELGPASTAVDNMSASSSSVSDSD PESTERELLTKLPGGLFMNQLLANEIKLLVD
6550	2293	922	FRVSRDGAPODCGIEQOMGLAMEHGGSVARAGGSSRGWCWYLRVFF LFVSLIQFLIILGLVLFMVYGNVHVSTESNLQATERRAEGLYSQ LLGLTASQSNLTKEINFTTRAKDAIMQMWLNARRDLDRINASF QCQGDRIYITNNQRYMAAIILSEKQCRDQPKDMNKSCDALLFML NQKVKTLVEIAKEKTICTKDKESVLLNKRVAEQVLECVKTR LQHQRQLAKEQLQKVQALCLPLDKDKFEMDLRLNLRDSDIIPRS LDNLGYNLYHPLGSELASIRACDHMPMSLSSKVEELARSLRAD IERVARENSDLQOKLEAQOGLRASQEAQKQVEKEAQAREAKLQ AECRSQTQLALEEKAVLRKERDNLAKELEKKREAEQIRMELAI RNSALDTCIKTKSQPMMPVSRPMGPVNPQPIDPASLEEFKRKI LESQRPPAGIPVAPSSG
6551	157	748	IQPPDPNRNMTLAAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPFEN ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIENNFIKMAKEKLAQKMSNKENREAHLAAMLERLQ EKDKHAAEEVRKNKELKEEASR
6552	157	748	IQPPDPNRNMTLAAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPFEN ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER EVIQKAIENNFIKMAKEKLAQKMSNKENREAHLAAMLERLQ EKDKHAAEEVRKNKELKEEASR
6553	2	1807	FVWSKMAAHLISYGRVNLNVLREAVRRELREFLDKAGSKAIVWD EYLTGPFGLIAQYSLLKEHEVEKMFLLKGNRLPAADVKNIIFFV RPRLELMDIIAENVLSEDRRGPTTRDFHILFVPRRSLCEQRLKD LGVLSGFIHREYSLDLIPFDGDLMSSEGAFFKCYLEGDQTS LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG SQNSIFPVFDNLLLLDRNVLLTPLATQLTYEGLIDEIYGIONS YVKLPPEKFAPKKQGGDKLPTEAKKLQNSAEBLYAETRDKN FNAVGSVLSSKKAKIIISAAFEERHNAKTVEIKQFVSQLPHMQAA RGSANHTSIAELIKDVTTSDDFKLTVEQEFMSGIDTDKVN YIEDCIAQKHSIKVLRVLVCLQSVCSGLKQKVLDDYKREILQT YGYEHILT LHNLEKAGLLKPTGGNNNYPTIRKTLRLWMDVNE QNPTDISVYSGYAPLSVRLAQLLSRPGWRSIEEVLRIPLGPHF EERQPLPTGLQKKRQPGENRVTLIFFLGVTFAEIAALRFLSQL EDGTEYVIATTKLNGTSWIEALMEKPF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6554	119	1244	FEMGSQVSVESGALHVIVVGGGFGGIAAASQLQALNVPFMLVDM KDSFHHNVAALRASVETGFAKKTFFISYSVTFKDNFRQGLVVGID LKNQMVLQGGGEALPFSHLILATGSTGPPPGKFNEVSSQQAIIQ AYEDMVRQVQSRFIVVVGGSAGVEMAAIBIKTEYPEKEVTLIH SQVALADKELLPSVRQEVKEILLRKGVLQLLSERVSNLEELPLN EYREYIKVQTDKGTEVATNLVILCTGIIKINSSAYRKAFESRLAS SGALRVNEHLQVEGHSNVYAIGDCADVTPKMAYLALGHANIAV ANIVSVKQRPLOAYKPGALTFLLSMGRNDGVGQISGFYVGRIM VRLTKSRDLFVSTSWKTMROSPP
6555	1552	498	IHMALLRKINQVLLFLIVTLCVILYKKVHKGTVPKNDADDESE TPEELEEEIPVVICAAAGRMGATMAAINSISNTDANILFYVVG LRNTLTRIRKWIHESKLEINFKIVEFNPMGLKGIKIRPDSSRPE LLQPLNFVRFYLPPLIHQHEKVIYLDVDDVIVQGDIIQELYDTTLA LGHAAAFSDDCDLPSAQDINRLVGLQNTYMGYLDYRKKAIDKLG ISPSTCSFNPVGIVANMTWKHORITKQLEKWMQKNVEENLYSS SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL QEAKLLHWNHGRHKPWPDPSPVHNDLWESWFPDPAGIFKLNHHS
6556	241	1449	ASLCKGCFVTHVLVILPISLQSPFTFGFLDDIGVLVRGHRVI PAALKAFRRLVNSQGGQLRVVVFVTNAGNIIQHSKAQELSALLG CEVDADQVILSHSPMKLFSEYHEKRMLVSGQGPMENAAQGLGFR NVVTVDLRLMAFPLDMVDLERRLKTTPLRNDFPRIEGVLLLG EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPLPVLASNMDLL WMAEAKMPRFGHGTFLCLETIYQKVTGKELRYEGLMGKPSILT YQYAEGLIRROAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY LQKATHDGAPELGAGGTROQQPSASQSCISILVCTGVYNPRNPQ STEPVLGGGEPPFHGHRDLCPSPGLMEASHVVDVNEAVQLVFR KEGWALE
6557	2598	1534	RMCGRTSCHLPRDVLTRACAYQDRRGQQLPEWRDPDKYCFPSYN KSPQSNPVLRLHFEKDADSSERIAPMRWGLVPSWFKESDP SKLQFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWQRC QGTNRQOPYFIYFPQIKTEKSGSIGAADSPENWEKVWNNWRLIT MAGIFDCWEPEPBGDDVLYSYTIITVDSCKGLSDIHRMPAILDG BEAVSKWLDGFEVSTQEALKLIHPTENITFAVSSVNNSRNNT PECLAPVDLVVKELRASGSSQRMQLQWLATKSPKKEDSKTPQKE ESDVPQWSSQFLQKSPLPTRKGTAGLLEQWLKREKEEPPVAKRP YSQ
6558	21	1138	FHGRRRGGKRMELGSCLEGGREAAEEGEPEVKKRRLLCVEFAS VASCDAAVAQCFLAENDWEMERALNSYFEPPEESALERPETI SEPPTYVDLTNEETDSTTSKISPSSEDTOQENGSMFSLITWNID GLDLNNLSEARAGVCSYLALYSPDVIPLQEVIPPYYSYLKKRSS NYEIIITGHEEGYFTAIMLKKSrvKLKSQEIIPFPSTKMMRNLLC VHVNVSGNELCLMTSHLESTRGHAARMNQLKMLVKKMQEAFES ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTW DQMNNSNLGITAAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKL DCGRFPSDHWGLLCNLDIIL
6559	3	364	GPESGLPTRPKKLANQTPIAMDCCASRSCSVPTGPATTICSS DKSCRCGVCLPSTCPHTVWLEPTCCDNCPPCHIPQPCVPTCF LLNSCQPTPGLETNLNLTFTQPCCEPCLPRGC
6560	3	1435	TATSGGIWLRKRWCHWRPLPQSCVGTGGGLQVRDTSRIAGK GVDHTKMSLHGASGGHERSDRRSSDRSDSSHERTESQLTPC IRNVTSPTRQHHVEREKDHSSSRPSSPRQKASPNGISISSAGNS SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSEVTLIVD NTRFVVDPSIFTAQPNMLGRMFGSGREHNFTRPNEKGEYEVAB GIGSTVFRAILDYKGTGIRCPDGISIPELREACDYLCISFEYS TIKCRDLSALMHLSNDGARRQFEFYLEEMILPLMVASAQSGER ECHIVVLTDDDDVDWDDEYPPQMGEYSQIIYSTKLYRFFKYIE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKRPGGRPEVTYN YVQRPFIRMSWEKEEGKSRHVDFOCVKSKSITNAAAAADIPQD QLVVMHPTPQVDELDILPIHPPSGNSDLDPAQNPML
6561	3	1086	PGRRFRKKESSSRWFADCLLGLRGPASSLLSPFSPSPWFSHS PCPMAALTDLFSFMYRWFKNLGNLSEKVFITGCDSGFGNLL AKQLVDRGMQVLAACFTEEGSQKLQRDTSYRLQTTLLDVTKSES IKAAAQWVRDKVGEQGLWALVNNAGVGLPSGPNEWLTQDDFVKV INVNLVGLIEVTLHMLPMVKRARGRVNMSSSGGRVAVIGGGYC VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES RMRKLERLQETRDSYGEDYFRIYTDKLNIMQVAEPVRVDVI NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKLPTPVTDFILSRY LRPADSV
6562	1	1562	MSTLYDIRAHKAQLRRFFASSDSNKALEQRRTLHTPKLEHLDRV LYEWFGLGRSEGVPSVSGPMLIEKAKDFYEQMLTEPCVFSGGWL WRFKARHGIKKLDASSEKQADHQAEEQFCAPFRSLAEHGLSA EQVYNADETGLFWRCPLNPTPEGGAFFGPKQGDRLTVLMCANA TGSRLKPLAIGKCSGPRAFKGIOHLEVAYKAQGNAWVDKEIFS DWFHIFVPSVREHFRITGLPEDSKAVLLDSSRAHPQEAELVS SNVFTIFLPASVASLVQPMEQGIRDFMRNFINPPVPLQGPBAR YNMNDALFSVACAWNAVPSHVFRARWRKLWPSVAFAGSSSEEE LEAECEFFVKPHNKSFAHILELVKEGSSCPGQLRQQAASWGVAG REAEGGRPPAATSPAENVVSSBKTPKADQDGRGDPGEGEVVAWE QAAVAFDAVLRFAERQPCFSAQEVGQLRALRAVFRSQQVRRRR GALGAVVKVEALQEGPGGCGATAQSPLPCSSTAGDN
6563	1319	2694	LARPAQPVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHDPLEA HEHPLPCDQMFWRMGHLMVBEANSRGVVMGIGYDHTAWVYTG GYGGGCFQGLASSTSNITYQSDVKCVHIYENQRWNPVTGYTSRG LPTDRYMWDASGLQECTKAGTKPPSLQWAWVSDWPFDFSVPEG TDQEGWQYASDFPASVYHGSKTKMDFVRRRCWARCKLVTSGPWL EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS ELNPAGSSWLHVGTQDPFASISIGACYQWAVARDGSAFYRGSV YPSQPADGCWYHIPSPPRQLKQVSAGQTSVYALDENGNLWYRQ GTTPSYPGSSWEHVSNNVCRVSVGLDQVWVIANKVQSSHLS RGTVCHRTGVQPEPKGHGWDYIGGGWDHISVRANATRAPRSS SQEQEPSAPPEAHGPVCC
6564	1	975	APGSCALWSYCGRGWSRAMRGCOLLGLRSSWPGDLLSARLLSQE KRAAETHFGPETVSEEEKGKVYQVFESVAKKYDVMNDMMSLGI HRVWKDLLLWKMHPLPGTQLLDVAGGTGDIARFLNYVQSQHQR KQKRLRAQQNLSWEEIAKEYQNEEDSLGGSRVVVCIDINKMLK VGGKALAAQGYRAGLAWVLGDAEELPFDDDKFDIYTLAFGIRNV THIDQALQEAHRVLKPGGRFLCLFESQVNNPLISRLYDLYSFQV IPVLGEVIAGDWKSYQYLVESIRRFPSQEEFKMDIEDAGFHKVT YESLTSGIVAIHSGFKL
6565	1464	999	RSAVANGLTKRRMGLKNGRYISLILAVQIAYLVQAVRAAGKCD AVFKGFSDCLLKLGDSMANYPQGLDDKTNIKTCTYWFHFSCT VTALTDCEGAKDMWDKLRKESKNLNIQGSFLFELCGSGNGAAGS LLPAPFVLLVLSLAALATWLSF
6566	3	1385	KYESAQPGGTQPEPGLGARMATHKALVMCLGLPLFLPFGAWAQG HVPFGCSQGLNPLYNNLCDSGAWGIVLEAVAGAGIVTTFVLT IILVASLPFVQDTKKRSLGTQVFFLLGLTGLFCLVFACVEKPDF STCASRRFLFGLVFAICFSLAAHVFAFNFLARKNHGPRGWVIF TVALLTLVEVINTENLITLVRGSGEGGPQGNSSAGWAVASP CAIANMDFVMALIYVMLLLGAFGLAWPALCGRYKRWKHHGVFV LLTTATSVAIWVWIVMYTYGNKQHNSPTWDDPTLALALANAW AFVLFYVIVEVSQVTKSSPEQSYQGDMPYTRGVGYETILKEQKG QSMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTMAL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MHKVPSEGAYDILPRATANSQVMGSANSTLRAEDMYSAQSHQA ATPPKDGKNSQVFRNPYVWD
6567	125	863	TKRSNLKAYACSIHHIRTSYVFNVDSSQTNVPLLQACIDGDFN YSKRLLSESGFDPNIRDSRGRTGLHLAAARGNVDICQLLHKFGAD LLATDYQGNLTALHLGCHVDTIQPLVSNGLKIDICNHQGATPLVL AKRRGVNKDVIRLLESLEEVEKGFNRGTHSKLETMQTAESESA MESHSLLNPNLQQGEGVLSFRFTWQEFVEDLGFWRVLLIFVI ALLSLGIAYVSVGLPFVENQPELVH
6568	3	1183	HASDRLLVLPDNYSHFSQASANLQGPSRTTELPHPTLASISSPM LEGAELFYNVHDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL KIHLLQTTDYGNFANHTNPLTVSKIDTEMKRRLCGEFYFRNHS LEPLSTFLTYMTCSYVIDNVILLMNGALQKKSVEKILGKCHPLG RFTMEAVNIAETPSDLFNAILIETPLAPFPQDCMSENALDELN IELLRNKLYKSYLEAFYKFCNKHGVDVAEVMCPILFEADRRAF IITLNSFGTELSKEDRETLPTFGKLYPEGLRLLAQAEFDQMK NVADHYGVYKPLFEAVGSGGKTELDVFYEREVQMNVLAFNRQF HYGVFYAYVKLEKEQIRNIVWIAECISQRHRTKINSYIPIL
6569	205	1532	RRRGFQRLGHRPTPLLCRWRTAGPSHWEKQARAQGLRPVDP RMSWLFPLTKSASSAAGSPGGLTSLQOQKQRLIESLRNHS AEIQKDVEYRLPFTINNLININILLPPQFPQEKPVISVYPPIR HHLMDKQGVYVTSPLVNNFTMHSGLGKIQLSLDEFWKNPPVLA PTSTAPPYLYSNPSGMSPYASQGFPLPPYPPQEAANSITSLV ADTVSSSTTSHTAKPAAPSGVLSNLPLIPTVDASIPTSQNG FGYKMPDVPDAFPELSELSVSQSLTDMNEQEEVLLQFLTLPLQK QIITDKDDLKVSIEELARKNLLLEPSLEAKRQTVLDKYELLTQM KSTFEKKMQRQHELESSESASALQARLKVAHEAEESDNIAED FLEGKMEIDDFLSSFMKRTICHCRRAKEEKLQQAAMHSQFHA PL
6570	330	1304	ARLFRLTFLREGFLYVLLSHWVFGAPRPPASDWSKGLVPSAP PASRKMGSKALPAPIPLHPSLQLTNYSLQAVNTFPATVDHLQ LYGLSAVQTMHMHNTLGYPNVHEITRSTITEMAAQGLVDARF PPPALPFTTHLFHPKQGAIAHVLPALHKDRPRDFANLAVAATQ EDPFKMGDLSKLSPLGLSPISGLSKLTPDRKPSRGRPLPSKTKK FICKFCGRHFTKSYNLLIHERHTDERPYTCDICHKAFFRRQDHL RDHRYIHSKEKPFKCQECGKFCQSRTLAVHKTLLHMQTSSTPTAA SSAAKCSGETVICGGT
6571	169	656	APDMNRKKLQKLTDTLTNCKHLFRGFDKNDGCVNVLEWIGHL SLFLRGSLEEKMKYCFEVDLNGDGFISKEEMFHLKNSLLKQP SEBDPDEGIDKLVETLKKMDHDHDKLSFADYRLAVREETLLL EAFGPCLPDPKSKMEFEAQVFKDPNEFNDM
6572	49	1646	TPERAQPGALLGAAGCCVCGGRWPRSHERGYPSSAKMGSKRRN LSCSERHQKLVDENYCKKLHVQALKNVNSQIRNQMVQENENDNV QRKQFLRLQLNEQFELDMEEAIQAEENKRLKELQLKQEEKLAM ELAKLKHESLKDEKMRQVRENSIELRELEKLLKAAVMKERRAA QIAEKDAIKYEQMKRDAEIAKTMEEHKRIIKEENAAEDKRNKA KAQYLLDLEKQLEBQEKKKQBAEQLLKEKLMIDEIVRKIYBED QLEKQKLEKMNAMRRYIEEFQKEQALWRKKREEMEEENRKII EFANMQQREEDRMKVQENBEKRLQLQNALTQKLEMLRQRED LEQVRQELYQEEQAEIYKSKLEEAEEKLRKQKEMKQDFEEQMA LKLVLQAAKEEENFRKTMKFAEDDRIELMNAQKQRMKQLE HRAVEKLIERRQOFLADKQRELEEWQLQORRQGFINAIIEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK
6573	767	275	GGGGGESQSFRAQDGTPTATDCLMYLQGPRLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELQORNILKPRNEQEEQEEKREIKRRL TRKLSQRPTVEELRERKILIRFSDYVEVADAQDYDRRADKPWTR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LTAADKVSRGECWRVGGRTVCWVSLGSPGVS
6574	204	1159	LESSVPVSVGVFWACGVSWTGAAGLQDGLSDTMARNAEKAMTA LARFRQAQLEEGKVKERRPFLASECTELPKAEKWRRIIGEISK KVAQIQNAGLGEFRIRDLNDEINKLLREKGHWEVRIKELGGPDY KVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELFEKEPLPP PRKTRAEMLKAIDFEYGYLDEDDGVIVPLEQYEEKLRAELVE KWKAEERARLARGEKEEEEEEEINIYAVTEESDEEGSQEKG GDDSQKFIHVFPVPSQGEIEALVRRKKMELLQKYASETLQAQ SEEARLLGY
6575	117	820	SPALASQSGGITEEKMLEPQENGVIDLPDYEHVEDETFFPPFPF ASPERQDGEGETEPDEESGNGAPVPPPKRTVVRNIPKLDARLI SERGLPALRHVFDKAKFKGKGHEADLKMLIRHMEHWAHRLFPK LQFEDFIDRVEYLGSKKEVQTCIKRIRLDLPILHEDFVSNNDDEV AENNEHDVTSTELDPFLTNLSESEMFASELSISLTEEQQQRTER NKQLALERRQAKLP
6576	1	1060	PEPQALVGGKRGALRLVLRVLTVSAPAEVRRRVLRLPVLSWMD RETRALADSHFRGLGVDVPGVQAPGRVAFVSEPGAFSYADFVR GFLLPNLPVCFSSAFTQGWGSRRRWVTPAGRPFDFHLLRTYGDV VVPVANCQVQYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGL YLKDWHLCDRDFPVEDVFTLPVYFSSDWLNEFDALDLDVDDYRFVY AGPAGSWSPFHADIFRSFSWSVNVCGRKKWLLFPFGQBEALRDR HGNLPYDVTSPALCDTHLHPRNQLAGPPLBITQEAGEMVFPVPSG WHQVHNLVMCCFSCPLSGAFIQEDGSTTSPLSQPELGWNGVAH G
6577	2271	987	SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKDYPSNTTSS TSNSGNETSGSSTIGETSNRSRDRDRYRRNSRSRSPGRQCHRR RSRWDRRHGESRSRDHRRDRVHYRSPPLATGYRYGHSKSPHF REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFSAV KGVDRVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLG VPIIVQASQAEKNRLAAMANNLQKNGGPMRLYVGSLLHFNITD MLRGIPEPFGKIDNIVLMKDSDTGRSKGYGFIITFSDSECARRAL EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG RFQLMAKLAEGAGIQLPSTAAAAAQAALQNGAVPLGA LNPAALTALSPALNLASQCLQLSSSLTPQTM
6578	377	1489	PSSSATMNRAPLKRATILHMAITGASDPSAAEANGKEPFLRLA LQIALVVSLEYWVTSISMVFLNKYLLDPSLRLDTPIFVTIFYQCL VTLLCKGLSALAACCPGAVDFPSLRDLRVARSVPLSVVFIG MITFNNLCLKYGVAFYVNGRSLTTFVFNVLSSYLLKQTTSFYA LLTCGIIIGGFVLGVDQEGAEGTSLWLGTVFGVLASLCVSLNAI YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLGELQALRDF AQLGSAHFWGMMTLGGLPFGAIGYVTGLQIKFTSPLTHNVSGTA KACAQTVLAVLYEETKSFLWNTSNMMVLGGSSAYTNVRGWEMK KTPEEPSPKDSEKAMGV
6579	2	711	RPRVWYPPELRELSAAAPRWSHRTAPGIMVIFYTSSSVNSSAYT IYMGDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRHLKGENI EDIKPEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM DVGGIGFHRQKQDKIVTVBKKVNEILNRLEKTKVERFPDLAAEK ECRDREERNEKKAQIQEMKKREKEMKKREMDLRSYSSLMKV ENMSSNQDGNDSDEFM
6580	62	1571	LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP RPPQEQVGPLMVKVEEKEEGKYLPSLEMFRRQFRQFGYHDTGP PREALSQRLVLCCEWLRLPEIHTKEQILELLVLEQFLTLPLQELQ AWVQEHCPESAERAATLLEDLERELDEPGHQVSTPPNEQKPVWE KISSSGTAKESPSSMQPQPLETSHKYESWGPLYIQESGEEQEFA QDPRKVRDCRLSTQHEESADEQKGSAAEGLKGDIIISVIANKPE ASLERQCVNLNEKGTKPPLQEQAGSKKGRESVPTKPTPGERRYI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CAECGKAFSNSSNLTKHRRHTTGEKPYVCTKCGKAFSHSSNLTTHYRTHLVDPRPYDCKCGKAFGQSSDLLKHQRMHTEEPYQCKDCGKAFSGKGSIRHYRIHTGEKPYQCNECGKSFSQHAGLSSHQRLHTGEKPYKCKCEGKAFNHSSNFNKHRIHTGEKPYWCHHCCKTFC SKSNLSKKHQRVHTGEGEAP
6581	228	476	RVFLKDLSTPMASNNNTASIAQARKLVEQLKMEANIDRIKVSKAADLMAYCEAHAKEDPLLTPVASENPFREKKFFCAIL
6582	1428	718	CFTTKTHCSFVSPYLSPLVLRKELESLENEGQVHTSSFINQHPIIFWTLVWYFRRLDLPNLPGILITSEHCNEGQLPLSSLSQDSKLVYIQLLDNINLHQEPREPLYVSWRNFNSEKSSLLSEEQQETSTLVETIRQSIQHNNVLKPINLLSQMKPGMKRQRSLYREILFLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLQKIDAPPSASVEWCRKCKGAPLI
6583	487	41	RIFMSTSGRLRWCTWRPATALWSASLRGLTSSMHPSPRSISLPLSMLSLPLSPNTRGLSPALFRSPDSEHATSCPRHLWRCRAPLRSFSLGRLQVLRPSPLHVHTHNSGKEVLGLQVQRSRSRGTPAC SQAGSGAVQGGNWCIF
6584	189	1750	PLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVN FATWNQARLERDLSNKKIYQEEEMPESGAGSEFNRLREBARRKKYGYVLKEFRPEDQWLLRVNGKSGRKFKGIKKGVTEINTSYIIFTC PDGAFEAFFVHNWYNFTPLARHRTLTAEEAEWERRNKVLNHFSIMQRRRLKDQDQDEDEEEKEKRRRKASELRIDHLEDDLEMS SDASDASGEEGGRVPAKAKKAPLAKGGRKKKKKGSDDAEFEDS DDGDFEGQEVDMSDGSSSSQEBEPESKAKAPQEEGPKGVDEQS DSSESEEEKPPEEDKEEEEEKAPTQEKRRKDSSESSESSE ESDIDSEASSAFFMAKKKTPPKRERKPSGSSSRGNSRPGTPSAE GGSTSSSTLRAAASKLEQKRVSEMPAAKRLRLDTGPQSLSGKST PQPPSGKTTFNSGDVQVTEDAVRRYLTRKPMTKDLLKKFQTKK TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE
6585	3	1678	GPINRSRIDDVGGDPRAEASCSVLHSPHAMADSRDPASDQMQHWKEQRAAQKADVLTTGAGNPVGDKNLNVITVGRGPILLVQDVVF TDEMAHFRDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVDRPRGFVAFKFTYEDGNWDL VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPMVWDFWSLR PESLHQVSFLFSDRGIPDGRHNMNGYGSHTFKLVNANGEAVYCK PHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSTFYYIQVMTFNQAEFFPNPFDLTKVWPHKDYPLIPVGKLVNRRN FVNYFAVEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR LGPNYLHIPPVNCYPYRVRVANYQRDGPMDQDQGGAPNYYPNSF GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLINE EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL DKYNAEKPKNAIHTFVQSGSHLAAREKANL
6586	32	804	PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGQESSGLNLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNRGRGSSQAGGSGSAGQYGSDDQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGETSGDQAGGEGKHTVFKTYISPWERAMGVDPQQXKMLGIDLLA YGAKAELPKYKSFNRTAMPYGGYBKASKRMTFQMPKV
6587	75	1117	RRVPSLGKMEPCWDGENDIETPYGLLHVIRGSPKGNRPAILTY HDVGLNHLKCFNTFFNFEDMQEITKHFFVCHVDAPGQVQV GASQF PQGYQFPMSEQLAAMLPSVVQHFQKYYVIGVIGVAGAYVLAKFA LIFFDLVEGLVLVNIIDPNGKWIDWAATKLSGLTSTLPDVTLSH LFSQEEHLVNNTLVQSYRQQIGNVVNQLQLFNNMYNSRRDL D INRPGTVPNAKTLRCVPMVLVVDNAPAEEDGVVECNKLDPTTTT FLKMADSGGLPQVTQPGKLTFAFKYFLQGMGYMPSASMTRLARS RTASLTSASSVDGSRPQACTHSESEGLQGVNHTMEVSC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6588	137	501	LGLOAQLLELRITNNYQLSDELKNGVELTSLRQKVAYLDKEFSK AQKALS KSKKAQEVEVLLSENEMLQAKLHSQEEDFRLQNSTLMA EFSKLCSQMEQLEQENQQLKEGAAGAGVAQAGP
6589	2	1405	RPWGSAMATFSRQEFFQQLLQGCCLLPTAQOGLDQIWLILAICLA CRLWLRLGLPSYLKHASTVAGGFPSLYHFFQLHMMVWVLLSLLC YLVLFLCRHSSHRGVFLSVTILYLLMGEMHMDVTVTWHKMRGA QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGITVFGPW ISFHSYLQAVQGRPLSCRWLQKVARSLALALLCLVLSTCVGEYL FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFHFSNYFV GFLSEATATLAGAGFTEEKDHLWDLTVSKPLNVELPRSMVEVV TSWNLPMYSYWLNNYVFKNALRLGTFSAVLVTYAASALLHGFSFH LAALLSLAFITYVEHVLRLRLARILSACVLSKRCPPDCSHQHR LGLGVRALNLLFGALAI FHLAYLGSLEFDVDDTTBEQGYGMAY TVHKWSELWSASHWVTFGCWIFRYRLIG
6590	2177	656	VRAYEHVLSLLENVFTPMFCHRDYFRQLLRGAESPTRNSKLN GSLSLDDFRNTQKRGESEFGISRIGSKIKGVFKSTTMEGAMLPNY GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY VDFEDPSSERKEKKERIPVFCIDVERNDRAVGHEPEHWSVYR RYLEFFVLESKLTEFHGAFFDAQLPSKRIIGPKNYEFLKSKREE FQBYLQKLLQHPELSNSQLLADFLSPNGGETQPLDKILPDVNLG KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL SPTSENNKKLFNDLFKNANRAENTERKQONQYFMEVMTVEGVY DYLMYVGRVVFQVPDWLHLLMGTRILFKNTLEMYTDYYLQCKL EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKAKQTFEEM MNYIPDLLVKCIGEEKYESIRLLFDGLQQPVLNKQLTYYVLLDI VIQELFPELNKVQKEVTSVTSWM
6591	2177	656	VRAYEHVLSLLENVFTPMFCHRDYFRQLLRGAESPTRNSKLN GSLSLDDFRNTQKRGESEFGISRIGSKIKGVFKSTTMEGAMLPNY GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY VDFEDPSSERKEKKERIPVFCIDVERNDRAVGHEPEHWSVYR RYLEFFVLESKLTEFHGAFFDAQLPSKRIIGPKNYEFLKSKREE FQBYLQKLLQHPELSNSQLLADFLSPNGGETQPLDKILPDVNLG KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL SPTSENNKKLFNDLFKNANRAENTERKQONQYFMEVMTVEGVY DYLMYVGRVVFQVPDWLHLLMGTRILFKNTLEMYTDYYLQCKL EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKAKQTFEEM MNYIPDLLVKCIGEEKYESIRLLFDGLQQPVLNKQLTYYVLLDI VIQELFPELNKVQKEVTSVTSWM
6592	3	1861	APFPLGSTISSGSMIDANLKLQBAEQRLKAIVAEKFAIATKEG DLQPVERFFKIFPLLGLHEEGLRKFSEYLCKQVASKAENLLMV LGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGPGR LYTLIKYLQVECDRQVEKVDKFIKQRDYHQQFRHVQNLMRNS TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSEDFEVDGS MASEEVKQEHQKCLDKLLNCLLSCTMQELIGLYVTMEEFMRE TVNKAVALDTYEGQQLTSSMVDVFIIVKCCIGRALSSSIDCL CAMINLATTELESDFRDVLCNKLRMGFATTQDIQRGVTSAVN IMHSSLQOGKPDTKGIESTDCAKMSFLVTLNNVEVCSENISTLK KTLES DCTKLFSQIGGEQAQAFDSCLSDLAAVSNKFRDLLQE GLTELNSTAIKPVQWPWINSFFSVSHNIEEEFNDEYANDPWVQ QFILNLEQQMAEFKASLSPVIYDSLTLGLMTSLVAVELEKVVLS TFNRLGGLQFDKELRSLIAYLTVTWTWTRDKFARLSQMATILN LERVTEILDYWPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR LRL
6593	3	1837	EAFSAGSRRRRGLALQRGVLGGYCPCCRRRRGRLLVLLLLVR RGGBGGGRGRGDKRRRRQARRRRPEAEARGGKMADVLSVL RQYNIQKKEIVVKGEVIFGEFSWPKNVKTNVYVWGTEGEGQPR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EYTLDSILFLLNNVHLSHPVYVRRRAATENIPVVRPDRKDLLG YLNGEASTSASIDRSAPLEIGLQRSTQVKRAAEVLAEAKKPRI EDEBCVRLDKERLAARLEGHKEGIVQTEQIRLSSEAMSVEKIAA IKAKIMAKKRSTIKTDLDDITALKQRSFVDAEVDVTRDIVSRE RVWRTTTLQSTGKNFSKNIFAILQSVKAREEGRAPEQRFAPN AAPVDPTLRTKQIPAAAYNRVDQERFKGKEETEGFKIDTMTGYH GMTLKSVTGASARKTQTAAQPVPRPVSQARPPPNQKKGSRT IIIPAAATSLITMLNAKDLQDLKFVPSDEKKKQGCORENETL IQRRKQMQPGGTASVTVPYRVVDQPLKLMQDWDVAVVAVFQ GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQKW DVTVLELSYHKRHLDRPVFLRVWETLDRYVMVXKXSHLRF
6594	1	1096	EFFRRFRGSSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWSA DILSTIGYDNIHQHLNNGRNCKEFEDPLKRAAIBERYGKDLL NLSRKPCGQSEINTLKRALEVFQKQVDNVAQCHIQLAQSLREE ARKMEEFREKQKLQRKKTTELIMDAIHKQKSLQFKKTMADAKNYE QKCRDKDEAEQAVSRANLVNPKQKEKLFVKLATSKTAVEDSDK AYMLHIGTLDKVBREBQSEHIKACEFAEAQECERINFFRNALWL HVNQLSQQCVTSDEMYEQVRKSELMCSIQRDIEYFVNQRKTGQI PPAPIMYENFYSSQKNAVPAGKATGPNLARRGPLPIPKSSPDDP NYSLVDDYSLLYQ
6595	57	781	PLGTMSDDLGEDEGLLSLAGKRRGRGNLPKESVKILRDWLYLH RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRLPDMLRKD GKDPNQFTISRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS VCSMPLHSGQGEKPAAPFPRGELESFKPLVTPGSTLTLLTRAEA QSPTGGLFNTPTPTPEQDKEDFSFQLLVEVALQRAAEMELQK QDPSLPLLHTPIPLVSENPO
6596	2	1026	PLPVRRYHGRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAY GEEWCVIDDCAKIFCIRISDDIDDPKWTLCQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNLSLEEIIYQNGESILYLWVEKIRD VLIQKSQMTPEGPDVKKKTEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPFIDHGIPITDRRSTFQAHLPVVCQKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFQDCEDDGETA AGGRLHLMEILNVKNVMVVSRYGGILLGPDPRFKHINNCAIN ILVEKNYTNPSPESSKALGKKNKKVRKDKKRNEH
6597	2	1026	PLPVRRYHGRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAY GEEWCVIDDCAKIFCIRISDDIDDPKWTLCQVMLPNEYPGTAP PIYQLNAPWLKGQERADLSNLSLEEIIYQNGESILYLWVEKIRD VLIQKSQMTPEGPDVKKKTEEDVECEDDLILACQPESSVKALD FDISETRTEVEVEELPFIDHGIPITDRRSTFQAHLPVVCQKQV KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFQDCEDDGETA AGGRLHLMEILNVKNVMVVSRYGGILLGPDPRFKHINNCAIN ILVEKNYTNPSPESSKALGKKNKKVRKDKKRNEH
6598	1099	419	PRVRWATTMAMSFEPWPQYRFPFFFTLQPNVDTRQQLAAWCSL VLSPFCRLHKQSSMTVMEAQESPLFNNVKLQKRLPVESIQIVLEE LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSQNNNSV FTLYELTNGEDTEDEEFHGLDEATLLRALQALQEQHKAEIITVS DGPRRQVLLAGTCLPLLLTSHLSRAFKRRRTQCPPKTGTVTPPD SKGLQS
6599	164	1593	KMAALTTLFKYIDENQDRYIKKLAKWVAIQSVSAWPEKRGIEIR MMEVAAADVQKLGGSVELVDIGKQKLPDGSEIPLPILGRLGS DPQKKTVCITYGHLVDQPAALDGDNDSEPFVTLVERDGKLHGRGST DDKGFVAGWINALEAYQKTGOEIPVNVRFCEGMEESSGSEGLDE LIFARKDTFFKDVVDYVCISDNYWLGKKKPCITYGLRGICYFFIE VECSNKLHSGVYGGSVHEAMTDLILLMGSVDKRGNIIIPGIN EAVAAVTEEHKLYDDIDFDIEFAKDVGAQILLHSHKIDILMH RWRYPSSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVNMTPE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VVGEQVTSYLTKKFAELRSPNEFKVYMGHGGKPVVSDFSHPHYL AGRRAMKTVFGVEPDLTREGGSIPVTLTFQZATGKNVMLLPVGS ADDGAHSQNEKLNRYNYIEGTMKLAAYLYBVSQDKD
6600	2	934	PGRLFRVAAMESAGLEQLRELLLPDTERIRRATEQLQIVLRAP AALSALCDLLASAADPQIRQFAAVLTRRLNTRWRRLAAEQRES LKSLILTALQRETEHCVSLSLAQLSATIFRKEGLEAWPQLQLL QHSTHSPHSPEMGLLLSVVTSRPEAFQPHRELLRLNET LGEVGSFGLLFYSLRTLTTMAPYLSSTEDVPLARMLVPKLIMAMQ TLIPIDEAKACEALEALDELLESEVPVITPYLSEVLTFCLEVAR NVALGNAIRIRILCCLTFLVKVSKALLKNRLLATLAHPFPHC GC
6601	529	1420	PRAAARAPPPAVLRDRRAATAPGAGEMTLHGPLAQRYFLNHIE KITTWQDPRKAMNQFLNHNMLHPAVSSTFPVQSRMAVSQPNLVM NHQHQQQMAPSTLSQQNHPTQNPAGLMSMPNALTTQQQQQKQL RLQRIQMERERIRMRQEELMRQEAALCRQLPMEAEATLAPVQAAV NPPTMTDPMRSITNNSSDPFLNGGPHYHSEQSTDSGLGLGCYSV PTTPEDFLSNVDEMDTGENAGQTPMNINPQTRFPDFDCLDCLPGT NVDLGTLESEDLIPLFNDVESALNKSEPFLLTWL
6602	127	617	LLDFPALPKFVLAQSPKAGKPSMTSMTQSLREVIKAMTKARNF ERVLGITLVSAAPGKVICEMKVEEHTNAIGTLHGGLTATLVD NISTMALLCTERGAPGVSDMNITYMSPAKLGEDIVITAHVLKQ GKTLAFTSVDLTNKATGKLIQAQRHXTKHLGN
6603	79	660	PVGFSSLAARTGLGHLFPFLHRLASSRGLDMDLLQFLAFLFVLLL SGMGATGTLRTSLDPSLEYKKMFVKKRREQLLALKNLAQLNDI HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGFPPQDEKLD AFSHVVENTAFFGDVVLRFPRIVHYFDHNSNWNLLIRWGISFC NQTVGFNQGPSPILSLM
6604	3	686	TSTAQRQGGGRMSFRGGGRGGFNRGGGGGFFNRGGSSNHFRGGG GGGGGGNFRGGGRGGFGRGGGRGGFNGQDQGGPPERVVLLGEFL HPCEDDIVCKCTTDENKVYPFNAPVYLENKEQIGKVDEIFGQLR DFYFSVKLSNEMKASSFKKLQKFYIDPYKLLPLQRFLLRPPGEGK GPPRGGGRGGGRGGGRGGGRGGGRGGGRGGGGGGFRGGGRG GGFRGRGH
6605	7	848	SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV ALVAVAEHSGEFEKIMQLSERYNGFVLPCLGVHPVQGLPPEDQR SVTLKDLDAVLPFIENYKDRLLAIGEVGLDFSPRFAQTGEBQKEE QRQVLIRQIQALAKRLNLPVNVHSRSAGRPTINLLQEQAELVLL HAFDGRPSVAMEGVVAGYFFSIPPSIIRSGQQLVKQLPLTSIC LETDSPALGPEKQVRNEPWNISISARYIAQVKGISVEEVIEVTT QNALKLFPKLRHLLQK
6606	2	1682	FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS KSLGLIEGYGGRGKGLPATLSPAEEEKAGPHEKYGYNSYLSE KISLDRSIPDYRPTCKCEKYSKDLQISIIIFIVNEALSILR SVHSVNHPTTHLLKEIILVDDNSDEBELKVPLEEYVHKRYFGL VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAE VLSRIQENRKRVLPSIDNIQDNFEVQRYENSAHGYSWELWCM YISPPKDWWDAGDPSLPIRTAMIGCSFVVRNKKFGEIGLLDPG MDVYGGENIELGKIVWLCGGSMEVLPCSRVAHIERKKKPYNSNI GFYTKRNALRVAEVMDDYKSHVYIAWNPLENPGIDIGDVSER RALRKSLSKCKNFQWYLDHVPYEMRRYNTVAYGELRNNAKDV LDQGFLENHTAILYPCHGWGPOLARYTKEGFLHLGALGTTTLLP DTRCLVDNSKSRLPQLDCKVKSSLYKRWFIQNGAIMNKG RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK
6607	137	986	VPACAGLKKEARSLASPPRLNLTKLQASCRALFSPPIQSRQTT GISFQGRGGAGPGVPTRTQVPAAMGAVMGTFFSSLTQKRRPSKD KIEDELEMTMVCHRPEGLEAQTNFTKRELQVLYRGFKNECP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SGVFNEDTFKQTYAQQFFPHGDASTYAHYLFNAFDITQTGSKVFE DFVTALSILLRGTVHEKLRWTFNLYDINKDGYINQEEMMDIVKA IYDMMGKYTYPVLKEDTPRQHVDFVFFQKMDKNKDGIVTLDEFLE SCQEDDNIMRSLQLFQNVN
6608	224	1140	RPCFSSPTGLCPRLSYPMILLQHAVLPPPKQSPSPPMVSATRS TGTLQLPPQKPFQGEASLPLAGEEELSKGGEQDCALEELCKPLY CKLCNVTLNSAQQAQAHYQGNHKKLRNYAANSPPPARMSN VVEPAATFVVPVPPQMGSKPGGRVILATENDYCKLCDASFSSP AVAQAQHYQGNHAKRLRLAEASNSFSSESELGQRRARKEGNEF KMMPNRRNMYTVQNNSGPYFNPRSRQRIPRDLAMCVTFSGQPYC SMCNVGAAGEEMEPROHLESQKHKSQVSEQRYNEMENLGIV
6609	1	443	FRLCRRFRFVAGGRLAGAGLRESRVPAPEQRLSALTLLSWSAVT PAAEPGNFQLSPAEPGRGLASPVRAAPRACPAEMSELNTKTS PATNQAAGQEEKGKAGNVKKAEEEEIDILDTAPETEKAAALAIQ GKFRRFQKRKKDPSS
6610	319	881	GRKSLCNLHIFIRFLTYPDYMGMMCTAKKCGIRFPQPPAILI YESEIKGKIRQIMPVRNFSKFSQDTRAAEQKNNPRHKSYLEQ VSLRQLEKLPFLRGYLSGQSLAETMEQIQRETTIDPEEDLNKL DDKELAKRKSIMDELFEKNQKKDDPNFVYDIEVEFPQDDQLQS CGWDTESADEF
6611	978	212	PGCSGAGSRVWVLPALRHLAMGSTESESGRRVSVFGVDEEVRV LQGVRLSENVNRMKEPSSPPAPTSTFGLQDGNLRAPHKEST LPRSGSSGQQPSGMKEGVKRYEQEHAAIQDKLFQVAKREREAA TKHSKASLPTGEGSISHBQKSVRLARELESREABLRRTDFYK EQLEIRIERKNAEMYKLSSEQFHEAASKMESTIKPRRVEPVCSGL QAQILHCYDRDPHEVLLCSDLVKAYQRCVSAAHKG
6612	1724	992	VSTHASALSRTQGPQRPRAAASGAGAGTAGGGGSGGAGBSKM STEAQRVDDSPSTSGSSSDGQRESVQGEPEREQVQPKKKEGKI SSKTAALKLSTSAKRIQKELAEITLDPNPNCAGPKGDNIYEWRS TILGPPGSVYEGGVFFLDITFSPDYPPKPPKVTFRTRIYHCNIN SQQVICLDILKDNWSPALTISKVLLSICSLTDCNPADPLVGS IATQYMTNRAEHRMARQWTKRYAT
6613	130	748	ELELSNNPEQSNDRVAVFVAGGVGKSSLVLRVFKGTRESYI PTVEDTYRQVISCDKSICTLQITDTTGSHPFAMQRLSISKGHA FILVYSITSQSLEELKPIYEQICEIKGDVESIPIMLVGNKCD SPSREVQSSEABALARTWKCAFMETSAKLNHNVKELFQELLNLE KRTVSLQIDGKSKQKQKKEKLKGCIVM
6614	3	1191	SSAAEAMRVLVRRCWGPPLAHGARRGRPSQWRALARLWGEDCR DSRVREKPPWRVLFPGTDQFAREALRALHAARENKEEELIDKLE VVTMPSPSPKGLPVKQYAVQSOLFVYEWPDVGSGEYDVGVASF GRLLNEALILKPPYGIINVHPSCLPRWRGPAPVIHTVLHGDTVT GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELEAVLSRIGAN MLISVLKNLPESLSNGRQPMEGATYAPKISAGTSCI KWEEQTS EQIFRLYRAIGNIIPLOTLMANTIKLLDLVEVNSSVLADPKLT GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKSLTATDFY NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTAMQQCIE
6615	832	35	GRVGAGASAMSELPDVRAPLREHPSLRITDARKVRCILTGHE LPCRLPELQVYTRGKKYQRLVRASPAFDYAEFPHIVPSTKNPH QLFCKLTLRHINKCPEHVLRTQGRYQALCKYBECQKQGVY VPACLVHRRRRREDQMDGDPREPFAFWPTSSDEGGAASDDSM TDLYPPELFTRKDLGSTEDGDTDDFLTDKEDEKAKPPREKATD EGRRETTVYRGLVQKRGKKQLGSLKKKFKSHHRKPKSFSSCKQS G
6616	347	1886	LLPPCQGARPLSSPHASEDNLFWNCILCAFPHPSPQPLQYP VWPLLLVITQIPAPRHLNRNPFSSRGGLDSSGSLSTPSICRS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPPIWLQSPPPQSSP PPQHPCHTCRGLVDSFNKGLERTIRDNFGGGNTAWEEENLSKY KDSETRLVELEGVCSKSDFECHRLLELSELVESWWFHKQQA PDLFQWLCSDSLKLCPPAGTFGPSCLPCPGGTERPCGGYQCEG EGTRGGSGHCDQCAGYGGGACGQCGLGYFEARNASHLVCSACF GPCARCSGPESNCLQCKKGWALHHLKCVDIDECGETEGANCGAD QFCVNTESGYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKC LDVDECETEVCPEGNKQCENTEGGYRCICAEGYKQMEGICVKEQ IPESAGFFSEMTEDELVLVQQMFPGIIICALATLAAKGLVFTA IFIGAVAAMTGYWLSERSDRVLEGFIKGR
6617	118	673	VWMAWQVSLLELEDRLQCPICLEVFKBSLMLQCGHSYCKGCLVS LSYHLDTKVRCPMCQAVDGGSSSLPNVSLAWVIEALRLPGDPEP KVCVHHRNPLSLFCEKDQELICGLGGLGSHQHHPVTPISTVCS RMKEELAAFLSELKQEQKKVDELIKLVKNRTRIDGSAPSLCPC LGPATFTFL
6618	548	136	DGKVARRAPNSPAFQNDIYPLVSAPRATTAESPSWKVLQNTQCR NVPKMTSERSIPCLSAAGGTGKKQEQGRAMATLDRKVPSP AFLGKPSWSSWIDAAKLHCSNDVLEEAGKEGKSRVEMRLNKEA WKYGT
6619	246	842	PASSEVLTAAMVFLLLNCIVAVSONMGIGKNGDLRPPPLRNEFR YFQRMTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDRINLVLS RELKEPPQGAHFLARSLDDALKLTERPELANKVDMIWIVGSSV YKEAMNHLGHLKLFVTRIMQDFESDTFSEIDLEKYKLLPEYPG ILSDVQEGKHIKYKFEVCEKDD
6620	3	1879	NSRVDDFVARARMAAENASQESALGAYSVPDYSITSFPRLP DEPAPAAPLRGRKDEDAFLGDDPTDPSFLKSARLQRLPSSSE MGSQDGSPLRETRKDPFSAACSCQDGLTVIVTACLTFATG VTVALVMQIYFGDPQIFQQGAVVTDAACTSLGIEVLSKQSSV DAVAALCLGIVAPHSGLGGGVMLVHDIRNESHLDIFRES APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHLQYGRLPWS QVLFAAAVAQDGFNVTHDLARALAEQLPPNMSERFRETFLPSG RPPLPGSLLHRPDLAELVDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPHTPGALI SALNILEGFNLTSLSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLFPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFSGSLITPSGILLNSQMLDFS WPNRTANHSAPSLNSVQPGKRPLSFLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCLDCRCLSYLWLV SIPHAANMG
6621	1	662	VQGITSVQORLQALRKEKSRDAARSRRGKENFEFFELAKLLPLP AAITSQLDKASIIRLTISYLMKMRDFANQGDPPWNLRMEGPPNT SVKVIGAQRSSPSALAEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGSLQVELTGSSVFDYVHPGDHVEAEQLGMK LPPGRGLLSQGTAEAGASSASSSSQSETPEPVVCFPPASDQFLL
6622	2	319	GRASQAQEBETEAGGPERARAMEANMPKRKEPGRSLRIKVISMG NAEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVDRREIKVN IFDMAGHPFFYEVKPF
6623	1886	189	KALFEKVKFRLHVEEGDILYAMYVRQTVLKVIFLIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTYLWLFYRSLREYSFEYVRQETGDFDDIPDVKNDF AFMLHMDIQYDPLYSKRFVFLSEVSENKQLQNLNNEWTDPKL RQKLQTNANRLELPLIMLSGLPDTVFETELQSLKLEIIKVM IPATIAQLDNLQELSHQCSVKIHSAAFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVLTLESRLDLKSLKI LSIKSNVSKIQAQVVDVSSHQKMCIHNDGTLKMLNLLKMTN LTELVLVCDLERIPHAVFSLLSLQELDLKENNLKSIIEIVSFQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP DELYFCKKLKTLKIGKNSLVSPKIGNLLFLSYLDGKGNHFEI LPPELGDCRALKRAGLVVEDALFETLPSPDVREQMKTE
6624	218	1786	GSRRGGGSRIPAVSTHVAPGRSVLRPPFASGALRLRLSVLKALGGC RGRPSGLAHLSEQETSHWRAKRSGRACLDGFPGEILRSFIMCKTA REWLRTVTTLFMARAIAMVVPNATLLEKLEKYMDEDEGEWWIA KQKGKRAITDNDMQSILDLHNKLSQVYPTASNMEYMTWVDELE RSAESWAESCLWEHGPASLLPSIGQNLGAHWGRYRPTTFHVQSW YDEVKDFSPYPEHECNPCPFRCSGPVCTHYTQVWVATSNRIGC AINLCHNNNIWQIWPKAVYLVNYSFKGNWGHAPYKHGRPCS ACPPSFGGGCRENLCKEGRSDRYPPREBEETNEIERQQSQVHDT HVRTRSDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNRYEC PAGCLDSKAKVIGSVHYEQSSICRAAIHYGIIDNDGGWVDITR QGRKHFIKSNRNGIQTIGKYQSANSFTVSKVTQAVTCETTVE QLCPFHKPASHCPRVYCPRLYASKSTLCSNWNSSLF
6625	1124	543	PGPRGGGSGLLSTKALGRSRGLGMHPGSSGGTEGGVPTALRPP GPLVPSTSDNLLKNIELFDKLALRFHGRLLFLKDLVLDGDECCW SFYGGQGRKIAEVCCTSIYATEKKQTKVFPEARIPEETLNILI YETPRGPDPALEATGGAAGAGGAGRGEDEENREHRVRRIHVRR HITHDERPHGQQIVFKD
6626	3	1498	SAVEFVYTRDFHLILGISVEFLCSLRSDATMESITACLHALQAL LDVPWPRSKIGSDQDSGIELLNVLHRVILTRESPSIQLASLEV RQIIICAAQEHVKEKRRSAEVDGAAEKETLPEFGEKDTGGILVP GKSLVFATLELCVCILVRQLPELNPKLITGSPGVKATKPKIILED GSRVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRGTAV KLPGGQLSSTVAASLQALKGILSSPMARARKSRTATWDLRLSAL TTILDCWDVDPVDETHQELDEVSLTITVFIILSTSPEVTTIPCLQ KRCIDKFATLEIKDPVVQIKTYQLLHSIFQYPNPVSPYPIYS LASCIMEKLQEIHKRPENTAELEIFQEGIKVLETLVTVAEHH RAQLVACLLPILISFLDENSLSGATSIMRNLHDFALQNLQMIG POYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS PGKNSSIQKTSFL
6627	1	697	GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSFSDLTGKVMLL GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV KLQIWDTAGQERFRSVTHAYYRDAQALLLYDITNKSSFDNIRA WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV PFLETSKTMNVELAFLAIAKELKYRAGHQADEPSFQIRDYVE SQKRSSCCSFM
6628	1	1861	QCAEFGGGSGGGGGSGGGSGGGGAGGEEENKENERPSAGSKAN KEFGDSLSEILQIIKESQQQHGLRHGDFQRYRGYCSRRQRRLR KTLNFKMGNRHKFTGKKVTEELLTDNRVLLLVLMDAERAWYAM QLKQEBANTEPRKRPHLLSRLRKAVKHAELERLCSNRVDAKTK LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE EQAVLYNQRVEEISPNIYCAYNIGDQSAINELMQMLRSGGTE GLLAEKLEALITQTRAKQAATMSEVWGRTPVPVKIDKVRIFLL GLADNEAAIVQAESEETKERLFESMLSECRDAIQVREELKPDQ KQRDYILEGEPKVSNLQYLHSYLYTYIKLSTAIKRNNMAKGLQ RALLQQQPEDDSKRSRPPQDLIRLYDIIILQNLVELLQLPGLBED KAFQKEIGLKTIVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK YANBVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAILDA NDAHQTETSSQVKONKPLVERFETFCLDPSLVTKQANLVHFPF GFQPIPKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF GFRS
6629	5653	4549	GATFLGSGGRTGKMDAATLTIDTLRFAEFEDFPETSEPVWILG RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MLRCGQMIFAQALVCRHLGRDWRWTQKQKQPDYSYFSVLNAFIDR KDSYYSIHQIAQMGVGEKSGISQWYGPNTVAQVLKKLAVFDTWS SLAVHIAMDNTVMEEIRRLCRTSVPCAGATAFPADSDRHCNGF PAGAEVNTNRPSRWRPLVLLIPLRLGLTDINEAYVETLKHCFMMP QSLGVIGGKPNASAHYFIGYVGEELIYLDPHTTQPAVEPTDGCPI PDES FHCQHPPCRMSIAELDPSIAVVRGGHLSTQAFGAECCLGM TRKTFGFLRFFFSMLG
6630	2	423	LVQCGGIRRRSAWGAAMPGRHVSRRVRLYKRVQLHRVLPDDLKS LGDQYVKDEFRRHKTVGSDAQRFLEWEVYATALLQOANENRQ NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI SESMPKPF
6631	2	423	LVQCGGIRRRSAWGAAMPGRHVSRRVRLYKRVQLHRVLPDDLKS LGDQYVKDEFRRHKTVGSDAQRFLEWEVYATALLQOANENRQ NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI SESMPKPF
6632	1273	588	WNSRGRTRQGAAPLAPAAAMKAVVQVRVTRASVTVGGEQISAIGR GICVLLGISLEDTQKELEHMRKILNLRVFEDESGKHWKSVMD KQYEILCVSQFTLQCVLKGKNDPFLHAMPTEBAEGFYNSFLEQL RKYRPELIKDGKFGAYMQVHIQNDGPVTIELESAPGTATSDP KQLSKLEKQQKKEKTRAKGPSESSKERNTPRKEDRSASSGAEG DVSSEREP
6633	1145	617	ATGRHEGVPTLEGIIQQLVNGIITPATIPSLGPWGLVHSNPMY AWGANGLDAIITQLLNQFENTGPPPADKEKIQALPTVPVTEHV GSGLECPVCKDDYALGERVRLPCNHLFHDGCIWPLEQHDSCP VCRKSLTGQNTATNPGLTGVSFSSSSSSSSSSSPSNENATSNS
6634	1	1134	CGGIPRKSGSPRRRLPMARLDRCLPRLMLTLRSLLFWSLVYCYC GLCASIHLLKLLWSLKGKPAQTFRPAREHPPACLSDPGLGTHC YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYWRVYQLREF KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY SKCVLIGHDWGGMIAWLLAICYPEMVMKLVINFPHPNVFTEYI LRHPAQLLKSSYYYFQIPWFPEFMFSINDFKVLKHLFTSHSTG IGRKGCCQLTTDELEYIYVFSQPGALSGPINHYRNIFSCPLPKH HMTTPTLLLLWGENDAFMEVEMAETVRFYVKNYFRLTILSEASH WLQDQDPDIVNKLIWTFLEETRKD
6635	1420	470	EMRAGQQLASMLRWTRAWRLPREGLGPHGSPFARVPVAFSSSSG GRGAEPRLPLSYRLLDGEAALPAVVFHLGLFGSKTNFNSIAK ILAQTGRRLTVDARNHGDSPHSPDMSYEIMSDQLQDLLPQLG LVPCVVVGHSMGGKTAMLLALQRPVELVERLIAVDISPVESTGVS HFATYVAAMRAINIADLPSSRARKLADEQLSSVIQDMAVRQHL LTNLVEVDGRFVWRVNLDAITQHLDKILAFPPQROESYLGPTLFL LGGNSQFVHPSHHPEIMRLFPAQMOTVPNAGHWIHADRPQDFI AAIRGFLV
6636	1514	1801	SFCMFSHKQDSHFQAVPVQEKKKRLRRAPWRAFAQOPRLKHPAE QPIVRQCLQRPPFCGLGVLPVQQQLPPSLGPVLSPHSDPGWCRVD DGGDGVF
6637	2	1501	CSSSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEAGSKSI KASEDSLVSLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT VVSFFCNNSYVLSGNEKRTCCQNGEWSGKQPIKICAKREPKISD LVRRRVLPQVQSRETPLHQLYSAAFSKQLQSAPTCKPALPFG DLPMGYQHLHTQLQYECISPFYRRLGSSRRCLRTGKWSGRAPS CIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSLHKGAW FLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKFYR DDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARIS TRVQPICLAASRDLSFQBSHITVAGWNVLADVRSPGFKNDL RSGVVSVDSSLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC TAETGGIAAVSFPGRASPEPRWMLMGLVSWSYDKTCSHRLSTAF

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
			TKVLFPKDWIERNMK
6638	1391	224	GGIPQAGGKMAAPWWRAALCECRRWRGFTSAVLGRRTPLPLGPM PNSDIDLSNLERLEKYRSFDRYRRRAEQEAQAPHWRTYREYFG EKTDPKKIDIGLPPPKVSRTOQLLERKQAIQELRANVEEERAA RLRTASVPLDAVRAEWERTCGPYHKQRLAEYYGLYRDLFHGATF VPRVPLHVAVAVGEDDLMPVYCGNEVTPTEAAQAEVITYEAEEG SLWTLTLLSLDGHLLLEPDAEYLLHWLLTNIPGNRVAEQVTCYPYL PPFPARGSGIHLAFLFLFKQDOPIDFSEDARPSPCYQLAQRTPR TFDFYKKHQETMTFAGLSFFQCRWDDSVTYIFHQLLDMREPVFVE FVRPPPYHFKQKRFPHRQPLRYLDYRDSHEPTYGIY
6639	2046	1268	IGCFIMDGGDDGNLTIKKRFVSEALDERRRKRQEEWEKVRKPE DPBECPEEYVDPRLSYERLQEQKDRKQEQYEEQFKFKNMVRGLD EDETNFLDEVSROQELIEKQRREBELKELKEYRNLLKKVGISQE NKKVEVEKLTVPKPIETKNKFSQAKLLAGAVKHKSSSEGSNSVKRL KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPAAVCIGILPGL GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP
6640	117	1043	VLEPPDVSMASEDRSLRVLVVGKTSKGSATANTILGEEIFDS RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE ISRCIISCPGPHAIVLVLLGRTYEEQKTVALKAVFGKSAM KHMVILFTRKEELEGQSFHDFIADADVGLKSIKCEGNRCCAFS NSKKTSAEKESQVQELVELIEKMQCNEGAYFSDDIYKDTTEER LKQREEVLRKIYTDQLNEEIKLVEEDKHKSEKKEIKLLKLLK YDEKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS
6641	1	894	SAAVGRRSEVRGCAPRPLRRSARRMDPVPGTDSAPLAGLAWSS ASAPPPRGFSAISCTVEGAPASFGKSAQKSGYFLCLSSLSGLE NPQENVVADIQIVVDKSPPLPGFSPVCDPMDSKASVSKKRMV KLLPLGATDTAVFVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS TLRRNDISIYEASSLYGISAMDGVPTLHPRFEGKSCSPLAFSAF GDLTIKSLADIEEYNYGVFVEKTAARLPSSVS
6642	22	1296	PLEERMMTKMDPNDQAQRDIIFELRRIFAFAESDPSNAPGSGTE KHKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV HQDTYIRIVLENSREDKHECPFGSAIELTKMLCEILQVGLP NEGRNDYHPMFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER MSQDDFQSPPIVELREKIQPEILELIKQQLNRNLCEGSSFRKIG NRRRQERFWYCRALNHNKVLHYGDLDNPNQGEVTFESLQEKIPV ADIKAVTGKDCPHMKESALKQNKVEVLELAFSILYDPDETINF IAPNKYEYCIWIDGLSALLGKDMSSSELTKSDDLTLSSMEMKLRL LDLENIQIPEAPPPPIKBPSSYDFVYHYG
6643	3049	2265	SLHAPAEGRTRGRLAEPKMLTRKIKLWDINAHITCRLCSGYLI DATTVTECLHTFCRSLVKYLEENNTCPTCRIVIHQSHPLQYIG HDRTMQDIVYKLVPLGQBAEMRKQREFYHKLGMVEVPGDIKGETC SAQHLDSDHRNGETKADDSNKEAAEEKPEEDNDYHRSDEQVSI CLECNSSKRLGLKRWIRCSAQATVLHLKKFIAKKLNLSSFNEL DILCNEEILGKDHTLKFVVVTRWRFKAPILLHYRPMKMDLL
6644	1489	290	FRPLATEPRGSSPVQLVSSVTSVRLPLFLNLGGEMLYILDQR LRAQNI PGDKARKVLNDIISTMFNRKFMEELEFKPQELYSKKALR TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL LVTFNHLDTIKGFIRDSPTILQVDETLRQLTEIYGGLSAGEFQ LIRQTLTIFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT EVPGLIRMFNNKGEVVKRIEFKHGGNYVPAPKEGSFEYGDVRL KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF LARLMGMEIKKPSGPEPGFRLNLFITDEEEQAALTRPEELSY EVINIQTQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAM DEL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6645	6530	4646	FVEGLAGVYVYKAASEGKVLTLAALLNRSSEDIRYLLGYVSQOG GQRSTPLIIAARNGHAKVVRLLLEHYRVQQTQGTVRFDGYVID GATALWCAAGAGHFVVKLLVSHGANVNHTTVNSTPLRAACFD GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLE QRADPNKAKHCGATALHFAEAGHIDIVKELIKWRAAIVVNGHG MTPLKVAESCKADVVELLLSHADCDRRSRIEALLEGASFAND RENYDIKTYHYLYLAMLERPDGDNILEKEVLPPHAYGNRTE CRNPQELESIRQDRDALHMEGLIVRERILGADNIDVSHPIIYRG AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM IHLNETVKAPDIECVLRCSVLEIEQSMNRVKNISDADVHNAMDN YECNLYTFLYLVCISTKTQCSBEDQCKINKQIYNLIHLDPRTE GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLDCGAEVNA VDNEGNSALHIIQYQNRPISDPLTLHSIIISLVEAGAHTDMTNK QNKTPLDKSTTGVS EILLKTQMKMSLKCLAAARAVRANDINYDQD IPRTLEEFVGFH
6646	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY EGREKKGISDVRRTFCLFVTFDILLFVTLWIIELNVNGGIENL EKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL TTAVTSAPLLAKVILSKLFSQAGFYVLPPIISFILAWIETWFLD FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA GSEEAEEKQDSEKPLLEL
6647	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY EGREKKGISDVRRTFCLFVTFDILLFVTLWIIELNVNGGIENL EKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL TTAVTSAPLLAKVILSKLFSQAGFYVLPPIISFILAWIETWFLD FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA GSEEAEEKQDSEKPLLEL
6648	413	897	RNCWNCFTKYFNSPPEIDHKDSYLI TRSMAEPDYIEDDNPEL IRPQKLINPVKTSRNHQLHRELLMNQKRGAPQNKPELQKVME KXKRDQVIKQKEEAQKKSDLEIELLKRQKLEQLELEKQKQLQ EEQENAPEFVKVGNLRRTGQEVAAQES
6649	1357	832	WIPRAGIRHEVKWDVKEIMSQHNIYVDALLKEFEQFNRLNEV SKRRVIRPLVSNILWEHCIRLANRTIVEGYANVKKCSNEGRALM QLDFQQFLMKLEKLTDIRPIPDKEFVETIYKAYLTENDMERWI KEHREYSTKQLTNLVNVLGSHINKKARQKLLAADDIDRPKR
6650	32	765	LVPLVFSLLVQSCQVYRSIAMKFVPCLLVLTSLGLTGLQAPR QKQGSTGEEFHFQTTGGRDSCMRPSSLGQAGVWLRVDCRNTD QTYWCEYRGQPSMCQAFADPKSYWNQALQELRRLHHACQGAPV LRFSVCREAGPOAHMQQVTSLSLKGSPENQQPEAGTPSLRPKAT VKLTEATQLGKDSMEELGKAKPTRPTAKPTQPGPRPGGNEEAK KKAWHCWKPFQALCAFLISFFRG
6651	3425	1353	AKELLKVGDFSLCAGPYQNTADTMENLSKEFLASFVSEFDSA CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG DSDLDLLGDCRNPRDLSDSYTLRGSYTRKKDVPTDGYESSLNF HNNQEDWGCSSWVPGMETSLPPGHWAATAVKKEKCVPPYVQIR DLHGILRTYANFSITKELKDTMTSHGLRRHPSFSANCGLPSSW TSTWQVADDLTQNTLDLBYLRFHAKLKQTIKNGDSQHSASSANV FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSLPLVTVESDP RPQGGPRRGYTASSLDSSSSWRERCCHNRDLRNSQRNHTVSFHL NKLKYNSTVKESRNDISILNEYAEFNKVMKNSNQFIQDKELN DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA CKSTFLFYLVETEDKSFVVRTKNLLRKGHTEIEPQHFCAQFHR ENDTLIIIRNEDISSHLHQIPSLLLKLKHFPSVIFAGVDSPGDV LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNHG RWKLLHYRENKCLKEDERVDSHTAHKNIMLKSQSANIIELH YHQCDSSSTKAEILKCLNLQIQHIDARFAVLLTDKPTIPREV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FENNGILVTDVNNFIENIEKIAAPFRSSYW
6652	2	1343	IPGSTISCSCHSRRLRGSSPAPRLSLGAASPRPRPSSLPLPLPLPPLFLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPCEVVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNITCDSFKISWEMDSKSKDRITHYFIDLNNKENKNSNFKHKDVPVTKLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVSEWSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHKEFYDYVREHHGNAMQPSVKDNGSGSHGSPISGKLEGIFSCSTEFNTGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDFYCMYTAYHYVILVIAPVSGPGDEFCKQRLPQLNSKDNKFLTCTEEDGVLVYHHAQDVILEVIYTDVVDLSLGTVAEITGHQLMSLSTANAKKDPSCCKT CNISVGR
6653	170	1910	FFLEPRLRPFASRARFVFPARTRPSPLHPCCFEGGGMSLSQ RVAAAAARGADDAMESSKPGPVQVVLVQKDQHSFELDEKALASILLQDHIRDLDVVVSVAGAFRKGKSFILDFMLRYLSQKESGHS NWLGDPEEPLTGFSWRGSDPETTGIIQIWSEVFTVEKPGGKKVAVVLMDTQGAQFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED DLQQLQLFTEYGRLAMDEIFQKPFQTLMPVLRDWSFPYYSYGL QGGMAFLDKRLQVKEHQHEEIQVNRNHIHSCFSDVTCFLLPHPG LQVATSPDFDGKLDIAGEFKEQLQALIPYVLNPSKLMKEKEING SKVTCRGLLEYFKAYIKIYQGEDLPHPKSMLQATAEAYNLAAA SAKDIYNNMESEVCGGEKPYLSPDILEEKHCEFKQLALDHFCKT KMGKGKDFSFYQQBLEEEIKELYENFCKHNGSKNVFSTFRTPA VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY IRYSGQYRELGGGIDFGAAYVLEQASSHIGNSTQATVRDAVVG RPSMDKKAQ
6654	1	705	RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM WKVTAFIGNSIVVAQVWVEGLWMSCVVQSTQGMQCKVYDLSLLAL PQDLQAARALCVIALLVLFGLLVYLAGAKCTTCVEEKDSKARL VLTSGIVFVISGVLTLPVCWTAHAVIRDFYNPLVAEAQKRELG ASLYLGWAASGLLLLGGLLCTCPSGGSQGP SHYMARYSTSAP AISRGPSEYPTKNYV
6655	341	16	KDAYMPKKGLLALALVFLPVFAAEHWIDVRVPEQYQEHVQGA INIPLKEVKERIAVAPDKNDTVKVYCNAGRQSGQAKEILSEMG YTHVENAGGLKDIAMPKVKG
6656	2	1212	TELPFRPANLAIQPLSPLRALAPLPEKPGAVPPPPQKMAKVAK DLNPGVKMSLQQLQSARGVACLGCKGTCSGFEPHSWRKICKSC KCSQEDHCLTSDLEDDRKIGRLMDSKYSTLTARVKGGDGIRIY KRNRMIMTNPATGKDPTFDITITYEWAPPVGTQKLGLQYMLIP KEKQPVGTGTEGAFYRRRLMHQLPIYDQDPSRCRGLLENELKLM EEFVKQYKSEALGVGEVALPGQGGLPKEEGKQEKPEGAETTA TTNGLSLSDPSKEVEYVCLCKGAAPPDSPVVYSDRAGYNKQWHP TCFVCAKCEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI IFAEDYQRVEDLAWHRKHFFVCEGCEQLLSGRAYIVTKGQLLCPT CSKSKRS
6657	830	2120	LLTCQERAGDCLLSASTMKEVVYVWSPKKVADWLLLENAMPEYCEP LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLMEH HLEAHKNGHANGHLNIGVDIPTDGSFSIKIKPNGMPNGYRKEM IKIPMEPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER VPPKEVQPPLEDFTFDHFNVRVQWAFSICEINGMILVGLWLIQWL LLKYKSIISRRFFCIVGTLYLYRCITMYVTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMGDYLVSHTVMTL TLTYLFIKEYSPRRLWYWHICWLLSVVGI FCILLADHXYTVDVVV AYYITTRLFWYHTMANQQVLKEASQMNLLARVWVYRPFQYFEK NVQGI VPRS YHWPFPWPVHL SRQVKYSRLVNDT
6658	35	855	HCCALGAPGSPYRGYFSSAAPCTAPRKAKHQSTLEGLTKRMLM

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FDPVPVKQEAMDVPVSVPSPNYMESMKPNKYGVYISTPLPEKFF QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSLKFPSSHRRASPGLSMPSSSPPIKKYSPSPGVQPPGVPLSMPPVMAAALSRHG IRSPGILPVIQPVVQPVFPFMYTSHLQQPLMVSLEEMENSSSS MQVPVIESYEKPISQKKIKIEPGIEPQRTDYYPEEMSPPLMNSV SPPQALLQE
6659	18	523	EPQRGDCETWFQNCSLPKFVCFWCWGFWLWRAHMSNLHSLPGL RGLTSISRNLQCTNAMRVINNYQRRWKNQNTFLLATFANVVNV CGNPTITCPHNRTLNNCHSGVQVPLMYCNLTTPSPQINISNCRY AQTTPANMFYIVACDNRDQRRDPQYVVPVHLHTII
6660	514	1707	CAASLDCRHHLCEDPMKLVWPSAKLLQAAAGASARACDSVTSNV LPLLEQFHKHSQSSQRRITILEMLLGLKLQKWSYEDKDQRL NGFKDQQLCSLVFMALTDPTQLQVLGIRTTLTVLGAQPDLLSYED LELAVGHLYRLSFLKEDSQSCRVALEASGTLAALYPVAFSSHL VPKLAEEELRVGESNLITNGDEPTQCSRHLCLQALSASTHPSIV KETLPLLLQHLWQVNRGNMVAQSSDVIACQSLRQMAEKCCQDP ESCWYFHQTAIPCLLALAVQASMPKEKPSVLKVLLEDEVLAAM VSVIGTATTHLSPLAAQSVTHIVPLFLDGNVSLPENSFPSPRF QPFQDGSQRRLLIALLMAFVCSLPRNVSEHIWEVLLFNLDKVT PG
6661	179	430	GVHAASGTLSATWLAEAKMFDLSLAKAGKYLQAAKLMIGMPDYD NYVEHMRVNHDPDQTPMTYEEFFRERQDARYGKGARCC
6662	185	423	RSLPKPAPAQPASIHCFRSGVTPPTAKTAMSDGNTAFNALMYC GPKADDGNI FSACAPASSAVKASVSVAQPPQAVIP
6663	3	1005	RPVLSRRVDDFVPLPETSGRRKKLERMYSVDRVSDDIPIRTWF PKENLFSFQTASTTMQATSNFRKHLRMVGSRRVKAQTFERRER SFSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAFEDLDWDT EKGLEAVACDTEGFVPKVMLISSKVPKAEYIPTIIRDDPSII PILYDHEHATFEDILEEIERKLVYHKGAKIWKMLIFCQGGPGH LYLLKNKVATFAKVEKEEDMIHFWKRLSRLMSKVNPEPNVIHM GCYILGNPNGEKLFQNLRTLMTPYRVTFBSPLELSAQGQMIET YFDRLRLWKSQRHSLKLLDFDDVL
6664	58	968	PLRLRLPRSVVVMDSPWDLALAFSRTSMPPFFDIAHYLVSVMA VKRQPGAAALAWKNPISWFTAMLHCFGGILSCLLLAEPPLKF LANHTNILLASSIWIYITFFCPHDLVSQGYSLPVQOLLASGMKEV TRTWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIITNFERL VKGDWKPEGDEWLKMSYPKVTLLGSVITFTFQHTQHLAISKHNL MFLYTI FIVATKITMTTQTSTMTFAPFEDTLSWMLFGWQQPFS SCEKKSEAKSPSNGVGLASKPVDVSDNVKKKHTKKNE
6665	171	1278	DERRLACRQVVTTQRSELYPGFQKRQRFPLKAGEEAAAQGGRL PGRWLGPQGTQNPSCSVHTATGPEPRKLPLLPDPSNPGYPKEPA ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCVFPIDLAK TRLQNHQKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP EKAIKLAANDFFRLLMEDGMQRNLKMEMLAGCGAGMCQVVVTC PMEMLKIQQLDAGRLAVHHQGSASAPSTSRSYTTGSASTHRRPS ATLIAWELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLFANLNN LCFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK KGLGEDMYSGITDCAR
6666	498	2868	MTTFLPVPMAGFSFGTFGNPPMESPSAWQTIHQPFIVSCLTL WSPGWCWPQIQKEGVGLWDIRKQSSLLRYGGNLSLQASMSVRF NSNGTQLLALRRLLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC CFAGDRDQYILSGSDDFNLYMWRI PADPEAGGIGRVVNGAFMVL KGHRSIVNQVRFPNPTYMICSSGVEKIKIWSPPYKQPGCTGDLG GRIEDDSRCLYTHEEYISLVLSNGSGLSHDYANQSVQEDPRMMA FFDLSLVRREIEGWSSDSDSSESTILQLHAGVRSERSGYTDSSES SASLPRSPPTVDESADNAFLGLPLRVTTTNTVASTPTPTCED

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AASRQQRLSALRRYQDKRLALSNESDSEENVCEVELDTDLFPR PRSPSPPEDESSSSSSSSSEDEELNERRASTWQRNAMRRRQKT TREDKPSAPIKPTNTYIGEDNYDYPQIKVDDLSSSPTSSPERST STLEIQPSRASPTSDIESVERKIYKAYKWLRYSYISYSNNKDGE TSLVTGEADEGRAGTSHKDNAPAPSSSKEACLNIAAQRNQDLPP EGCSKDTFKEETPRTPSNGPGHESSHAWAEVPEGTSQDTGNSG SVEHPFETKKLNGKALSSRAEPPSPVPFKASGSTLNSGSGNCP RTQSDDEERSLETICANHNNRGLHPRPFPHNNGQNLGELEV AYSSPGHSDTDRDNSSLTGTLLHKDCCGSEMACEPTNAGTREDP TDTPATDSSRAVHGSHGLKRORIELEDTSSENSSEKKLKT
6667	171	1310	ABEERLAAMRSDSLVPGTHTPPIRRKSKFANLGRIFKPKWKRR KSEKFKHTSAALERKISMRSREELIKRGVLKEIYDKDGELSI SNEEDSLENGQSLSSSLSLPALSEMEPVMPRPDPCSYEVLQPS DIMDGPDPGAPVKLPCLPVKLSPLPPKKVMICMPVGGPDLVSLV SYTAQKSGQGGVAQHHTVLP SQIQHQLQYQSHGQHLPS TTGSL PMHPSGCRMIDELNKTAMTMQRLESSEQRVPCSTSYHSSGLHS GDGVTKAGPMGLPEIRQVPTVVIECDDNKENVPHESDYEDSSCL YTREEEEEEDEDDSSLYTSSLAMKVKCRKDSLAIKPSNRPSKR ELEKNILFRQTDEERLELRQIGTKL
6668	714	358	TLAVATGPALTLRCHVCTSSNCKHSVVCFASSRFCKTTNTVEP LRGLNVKKDCAESCTPSYTLQGGVSSGTSSTQCCQEDLCNEKLH NAAPTRTALAHSAALSGLALSLLAVILAPSL
6669	459	1207	KDEETRKYDYMLDHPPEYSHYHYYSRRLLAPKVDVRVILVS VCAISVFQFFSWWNSYNKASISLATVPKYRIQATEIAKQQGLLK KAKEKGKNNKSKKEIRDEEENIKNIIKSKIDIKGGYQKPKQICD LLLFQIILAPPHLCYIVWYCRWYFNFIKGEYGEERLYIIR KSMKMSKSQFDSLEDHQKETFLKRELWIKENYEVYKQEQEELK KLEKNILFRQTDEERLELRQIGTKL
6670	184	594	VARI*GEAAKMSSEPPPPYPGGPTAPLLEEKSGAPPTFGRSSPA VMQPPPGMPLPPADIGPPPYEPGHPMPQPGFIIPPHMSADGTYM PPGFYPPGPHPPMGYYPGPYTPGPYPGPGGHTATVLPVSGAA TTVTV
6671	1	763	LPAEKPRAPNMAGGRCGPQLTALLAAWIAVAATAGPEEAALP PEQSRVQPMASNWTLMVEGEWMLKPYAPWCPCSQQTDSWEAF AKNGEILQISVGKVDVIEPGLSGRFFVTTLPAFFHAKDGIFRR YRPGGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFS ISGKIWHLHNYFTVTTLGIPAWCSYVFFVIATLVFGLSMDLVL*V ISQCNWDPPYRHVS*/RPSTNLGVHTAHTSEHLRL
6672	304	1089	APGSKPVQFMDFEKTSFGMSVFNLSNAINMSGIILGLAYAMAHT GVIFFLALLLCIALSSYSIHLITCAGLAGIRAYEQLGQRAFG PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG DWFLKGNLLIIIVSVLIILPLALMKHLGYLGYTSGLSLTCLMFF LVSVIYKKFQLGLCYRATMKQWESEALVGTPOPRDSTA AVKAQ MFHS*LTGVLTPQWPIMAFAFVCHPGGAGPSITELCRAFOAQD
6673	1116	1963	LQIQTHHTHVGARVTHLGSHQLLANAGTMLCRQSSSMAPAFSQ SVTCGSPCVRKQESATKCLHIGACGSDLWARGWEQG*G*GLNV WLCPCVAFHRGARPOAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSSGQERQS\WVLPVPVGEPLKLPGLPG*NK SFSRV/SGSKGWILPRQLM*AS*R\TPRFVPGTQWVPI TW/PL ITWH*SAPTPLKACPAPRESDPCCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG
6674	1	440	LEFDYMCQYDYVEVRDGDNRDQIIKRVCGNERPAPIQSIGSSL HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ PTPC*IGTRVAFFLT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
6675	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKIHPSPMPGDSGSEIQSGNGETQGYVYAQSVDTSSWDFGIR RRSNTAQRLERLRKERQNIKCKNIQWKERNKQSAQELKSLFE KKSLEKEPPISGKQSILSVRLEQCPLQLNPNFNEYSKFDGKGHV GTTATKKIDVYLP LHSSQDRLLPMTVVMTASARVQDLIGLICWQ YTSEGREPKLNDNVSAAYCLHIAEDDGEVDTFPPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSIMHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWREQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE
6676	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKIHPSPMPGDSGSEIQSGNGETQGYVYAQSVDTSSWDFGIR RRSNTAQRLERLRKERQNIKCKNIQWKERNKQSAQELKSLFE KKSLEKEPPISGKQSILSVRLEQCPLQLNPNFNEYSKFDGKGHV GTTATKKIDVYLP LHSSQDRLLPMTVVMTASARVQDLIGLICWQ YTSEGREPKLNDNVSAAYCLHIAEDDGEVDTFPPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSIMHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWREQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE
6677	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD LEKIHPSPMPGDSGSEIQSGNGETQGYVYAQSVDTSSWDFGIR RRSNTAQRLERLRKERQNIKCKNIQWKERNKQSAQELKSLFE KKSLEKEPPISGKQSILSVRLEQCPLQLNPNFNEYSKFDGKGHV GTTATKKIDVYLP LHSSQDRLLPMTVVMTASARVQDLIGLICWQ YTSEGREPKLNDNVSAAYCLHIAEDDGEVDTFPPPLDSNEPIHKF GFSTLALVEKYSSPGLTSKESLFVRINAAGFSLIQVDNTKVTM KEILLKAVKRRKGSQKVSGRADGVFEEDSQIDIATVQDMLSSH HYKSFKVSIMHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS ADTWREQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ KASTKFWIKQKPISIDSDLLCAC\DLAEE
6678	221	865	GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRLVSSNFGRO*LR PFPCSQLPMSQGLWHLDCPCPWVPIPGQWRKGRQMRN*QS LLGSDQESVGLDLCVFNFLHVLGLFP*PHELFLLPVVDLG FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCLRLQTHDLEGSRN HHPLFLVVGWRDAVKHLETQVQSLASLGFVGQHTSHGPP
6679	2	786	LEFARGAMPFLGQDWS PGQNWVKTVDGWRFLDEKSGSFVSDL SSYCNKEVYNKENLFNLSLNYD/SCSQEEKEGHAE*QNQNS\DPH QEKWIYVHKGSTKERHGYCTLGEAFNRDLDFSTAILDSRRFNYV RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR ELLQTLTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEPTPVTEESGLF
6680	1498	2951	PLCTPLMPALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE PARKNEPDTHCPRGEARPEV*HLPKPHSPGSEAEIQTSA*ALP /NOVSPPPQM*GAENGDRQGGKERAGEELHRSSSGLTAAPGFP EVHRNLQTFPGLPSRGGGP/GGACTQGSWAPGEP/SPLLPAS MQRSAQGLPGWEAGLVESPTTHI PALRPSGTNATGEAFSTTCS SGF/PAPPGFTGLRPGGSSSGGHG*PGLPVGKV\GALGAAQD PQSQRGPTQGTGTEMLLSGLGSAKACPAARPAVP*LPSPDAS TIPKKGTRGFGGPGVLQERNRWVVGRAQGFSTADAAGTAPPGV *LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVWGRHGPQV AQGCPPGAGCWGQPRGSQRCPRTYTHSLPHGGRAPCPRCWH* WQDPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR FQGGGGG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6681	1169	511	INIIYYNQQRAPHELK\EKLMSAPALGLPDLTKLFTLHVSERE KMTVGVLTTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL LAQEADELTLRQNLNRKSPHA\VVTLLINTKGHH*LINARLTRYQ TLLCENPHKTIEVSNT/LNPATLLLVTRSPVKHNCLEVLDSVYS SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETS PAPVTPR S
6682	109	1238	TVLCGAMQVSSLSNEVKIYSLSCGKSLPEWLSDRKKRALQKKD VD VRRRIELIQDFEMPTVCTTIKVS KDQYILATGTYKPRVRCYDT YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG FYYKTRIPKFGDRFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN PLQTDAAENNVCDINSVHGLFATGTIEGRVECDPRTRNRVGLL D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAGTTTGQVLLY DLRS DKLPLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK NSGKIFTSLEPEHDLNDVCLYPNSGMMLTANETPKMGIYYIPVL GPAPRWCSFLDNLTELEENPESNE
6683	109	1238	TVLCGAMQVSSLSNEVKIYSLSCGKSLPEWLSDRKKRALQKKD VD VRRRIELIQDFEMPTVCTTIKVS KDQYILATGTYKPRVRCYDT YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG FYYKTRIPKFGDRFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN PLQTDAAENNVCDINSVHGLFATGTIEGRVECDPRTRNRVGLL D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAGTTTGQVLLY DLRS DKLPLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK NSGKIFTSLEPEHDLNDVCLYPNSGMMLTANETPKMGIYYIPVL GPAPRWCSFLDNLTELEENPESNE
6684	111	527	GLRGGTSRGRAGREPEFAAGVLCVVGFCQSPCPPGGRGREAPA PP\SGRRHA* RPA*WLGPGGDSGGREEGGS/GELQRAMESKMG ELPLDINIQEPRWDQSTFLGRARHFFTVDPRNLLLSGAQLEAS RNIVQNYR
6685	258	1473	KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPPDPQKVL QGVIDMKNAVIGNNKQKANLIVLAGVPRLLYLQQTSSSTELKT ECAVVLGSLAMGTENNVSLLDCHIIIPALLQGLLSLDLKFI EAC LRCLRTIFTSPVTPPELLYTDATVIPHLMALLSRSRYTQEYICQ IFSHCCKGPDHQTILFNHGAVQNIHLLTSLSYKVRMQUALKCF S VLA FENPQVSM TLVNVLDGELLQPIFVKMLQRDKPIEMQLTSA KCLTYMCRAGAIRTDNCIVLKTLPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK RLDHDLKHAHELQAAPKLYASLGANDEDIRKKVSLGEGRPVVL TASRQGVTS
6686	310	927	DSVTFDDLAVDFTPKWTLTDPTQRLYRDVMLENYKNLATVGY QLFKPSLISWLEQEESSERTVQRGDFQASEWKVQLKTKELALQD V LGEP TSSGIQMI GSHNGGEVSDVKQCGDVSSEHSC LKTHVRTQN SENTFECYLYGVDFLTLHKKTS TGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT
6687	181	915	EAMLEAPYKKEDEQQRKEVKDYPSNTTSSTSNSGNETSGSST IGETSNRSDRDRYRRNRSRSPGRQCRHRSRSDRRHGSER SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMLAAR IRPDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLGVPIIVQASQAEKNRLAAMANNLQKNGGPMR LYVGS LHFNITEDMLRGIFEPFGKV
6688	1025	1	AEVNYPRVFHKKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPLPR/SATARMATAAAPNSSIDLPSDSGMGFI SPAGDSLD LPSDGGTGFFSLAGDSSSTRLSLAFISFSLSSVSVGSAGTTS STSVGSVVAAPTSSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE VAVICGSXGAGASGSASCSSRAGKTTEATAASSMPSGTSSFTC TMSELEELFSLFSPAPLLSKLFTSSGSIACCQDSGPSDTGRLS VCQLWLADSDTGKLSDCQEVVTVGDSGGLTCPELSLGRM*MSLL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SSAIVIPGYSSSSDSRLNTVPTVDLLCPPTKSST
6689	640	1299	SSSASYATSATISISDTAFSGSLKLKHGLLSALDSSSRST*STSS AEDSTFRICSPSVSDTSSDSSGSKDNVILFISKVSI*SCFSLSS FFSDSISFCFSSSSFCR*FVSSKVSQNALSSRLSNGPGGSSK QRNSLTARQLAMSL*ATKF*RNACNPCLSSKKSAL*LSLNQRF GGSASRKPGNISFNSQKCSALSYYCCNFVIKPREVSVSSENYPAF
6690	1	442	GTRGKMAATLGLGSGWQWRRLSARDGSRMLLLLLLGSGGQP QQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQ YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFQKHGQGGKKNL/H GDGLAIWYTKDRMQP
6691	287	1401	LKTETSEEKARRYKDRPSQLNAVFQEQKMIQAQESITLEDVAV DFTWEEWQLLGAQAQDLYRDVMLENYSNLVAVGYQASKPDALFK LEGGEQLWTIEDGIHSGACSDIWKVDHVLRLQSESLVNRKPC HEHDAFENIVHCSKSQFLLGQNHDFDLRGKSLKSNLTLVNQSK GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASQKLSTKSQF ISPKHQKTRKLEKHHVCSECGKAFIKKSWLTDHQMHTGEKPHR CSLCEKAFSRKFMLEHQRHTHTGEKPYECPEGKAFLLKKSRLNI HQKTHTEKPYICSECGKGFIOKGNLIVHQRIHTGEKPYICNEC /GKGFIQKTCIAHQRFHTER
6692	178	939	WIKGELSLWERFCANI IKAGPMPKHIAFIMDGNRRYAKKQVE RQEGHSQGFNKLAECLRWCNLGILEVTVYAFSIEFNRKSKSEV DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL IAQAVQATKNYNKCFNLVCFAYTSRHEISNAVREMAWGEQGLL DPSDISESLDKCLYTNRS PHPDILIRTSGEVRLSDFLLWQTSH SCLVFQPVWLWPEYTFWNLFMAILQFQMNHSLVQK
6693	178	939	WIKGELSLWERFCANI IKAGPMPKHIAFIMDGNRRYAKKQVE RQEGHSQGFNKLAECLRWCNLGILEVTVYAFSIEFNRKSKSEV DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL IAQAVQATKNYNKCFNLVCFAYTSRHEISNAVREMAWGEQGLL DPSDISESLDKCLYTNRS PHPDILIRTSGEVRLSDFLLWQTSH SCLVFQPVWLWPEYTFWNLFMAILQFQMNHSLVQK
6694	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAESRQHELPRV EVHSLGQILPDGLTAEAGPPEAQDPWGS PGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHV NAAAGKFQVDTGAKFYRGMSLEYGIEADDNPFDFLSVYFLP
6695	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAESRQHELPRV EVHSLGQILPDGLTAEAGPPEAQDPWGS PGISLPAAHIGFAAA LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHV NAAAGKFQVDTGAKFYRGMSLEYGIEADDNPFDFLSVYFLP
6696	1	782	PRVRGRVGERWAFSLVPAAMSSEMEPLLAWSYFRRRKFQCAD LCTQMLESXPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMML DENAIQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPIITGFL RPSTQSGRPGTMEQARTPTATYARPIITSSGRFVRLGTASML TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVK TALD LAALSTEHSQYKDWK/DQIEKCYRVGMRYAEKQIKSS
6697	3	782	PPLFLRLNSRALRPGSRKVMVVPASLSGQDVGSFAYLTIKDR IPQILTKVIDTLHRHKSEFFEKHGEGVEAEKKAISLLSKLRNE LQTDKPFIPLEKFDVDIWNQYLEYQQSLNESDGKSRWFYSP WLLV\ECYMYRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQES IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL SL\SGGESSQNTNVLSLEDLKPFI LLNDMEHLWLSLSNCK
6698	668	754	VGSCACAGSCKCKECKTSCCKSECRAPP
6699	325	492	EGELF/PARRVLPRAMTASAQPRRRPGVGVVVTSCKHPRCV LLGKRKGSVAGSFQLPGGHLEFGETWEECAQRETWEEAALHLK NVHFASVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, **=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ESKRIIYNHAFFQESKWSGGILQ
6700	1098	1392	TQCWRSSSTPGMRTHFRTQF/RLECGQGFSQQENGHCMDTNECIQ FPFVCPDRDKPVCVNTYGSYRCRTNKKCSRGRYEPNEDGTACVERT LLGLCNLLGK
6701	2	1485	AAAGPRTRVRRAAAFEQGQSPSPGLGPTSDKAAAPRTPKRRRLW RQRQ/HPAMLCYVTRPDVLMVEVEVEAKANGEDCLNQVCRRLGI IEVDYFGLQFTGSKGESLWNLNRNISOQMDGLAPYRLKLRVKF FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA QTKFGDYNQNTAKYNYEELCAKELSSATLNSIVAKHKELEGTSQ ASAELYQLQIVSAMENYGIWHSVRDSEGGQLLIGVGPBGISIC KDDFSPINRIAYPVVQMATQSGKNVYLTVTKEGNSIVLLFKMI STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHLSLF LNENINLGGKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRRNQ SPSHSPKSSSESMNCSSCEGLSCQQTTRVLQEKLRKLKEAMLCM VCCBEBINSTPCPGHTVCCESCAAQLQVGESAAHFCLQPHLSL LLTGSRSQVLAR
6702	397	1971	PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK RAEALLCSRKATVVRLDVAVRMAEEQEFTQLCKLPAQPSHPHCV NNTYRSAQHSQALLRGLLALRDSGILFDVVLVVEGRHIEAHRIL LAASCDYFKGMFAGGLKEMEQUEVLIGHVSNAMCQILHFIYTS ELELSLNVQETLVAACQLQIPEIHFCCDFLMSWVDEENILDV YRLAELFDLSRLTEQLDTYILKNFVAFSRTDKYRQLPLEKVYSL LSSNRLEVSCETEVEGALLYHYSLEQVQADQISLHEPPKLEET VRFPLEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ SPQTELRSDFCVVGFGGIHSTPS\MSSATRPKYLNPGLGEWKH FTASLAPRMSNQGI AVLNNFVYLIGDNNVQGFRAESRCWRYDP RHNRWFQIQSLQQEHADLSVCVVGRIYIYAVAGRDIYHNDLNAVER YDPATNSWAYVAPLKREYVAHAGATLEGKMYITCGRKGRIIT
6703	45	1244	GVGFRAAAMPLELELCFGRWVGQHPCFIIAEIGQNHQGDLDVA KRMIRMAKECGADCAKFOKSELEFKFNKALERPYSKHSWGT YGEHKKHLEFSDQYRELQRYAEVGIFFTAGSMDMAVEFLHE LNVFFFKVSGDNTNFPYLEKTAK/TRGWHSVLRDVCVQQLNDE TSSWDVLGRVRSKEKVLMLVLDYSGRPMVSSGMQSMQMDTMKQ VYQIVKPLNPNFCFLQCTSAIPLQPEDVNLRVISEYQKLPDIP IGYSGHETGIAISVAALGAKVLERHITLDKTWKGSDHSASLE PGLAELVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKV KIPEGTILTMDLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDD TIMEE
6704	82	1007	TMNTRNRVVNSGLGASPASRPTRDQDPFSGRQGELESPVEDQREG LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNBIQRIAEQE LANLEKWKQNRAPVHLVPRRLGGSQSETEVRQKQQLQLMQSK YKQKLKREESVRIKKEAEAEALQKMKAIQREKSNKLEKKRLQE NLRREAFREHQYKTAEFL/ROTEHRIARQKCLSKCCLWPTILN MGQKLGLO\DSLKAEENRKLQKMKDEQHQKSELLELKRQQQE RAKIHQTEHRRVNNAFDLRLQGGKSQPGGLEQSGGCWNMNSGNSW GI
6705	2	786	RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT SYKRKGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSPD LKVIYILVRPKAGQTLQHRVFQILDSKLFKVEVIRPNVHEKIR AIYADLNQNDFAISKEDMOELLSCTNIIFHCAATVRFDDTLRHA VQLNVTATRQLLLMASQMPKLEAFIHISTAYSNCNLKHIDEVIY PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
6706	130	531	FTHSSSSHSQEMGLKLNMLRNDGHFCDDITIRVQDKIFRAHKVVL AACSDFFRTKLGVQAEDENKNVLDLHHVTVTGFIPPLEYATAT LSINTENIIDVLAASYSQMFSVASTCSEFMKSSILWNTPNPSQP EK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6707	2233	1343	YWSGIGYELQHFHWRKFHFEKKGPPSTCQERLYESRSRWPCIS* GMVVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSQRASKCHS FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NV SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNLLC NRRVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEH TD*LPK*GPGYIQHFHCDNLCILYNISFNLFYSYF*GVARYA C*RWYFEWLLYNHCGDILVACL*RRQL*SSQ
6708	115	1729	TVGSWSRSGRSPPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT GEIRRVVPHRPPCKLALGSDGVRVTMESALTARDRVGVQDFVLL ENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVPYRDLQIYYSR QHMERIRGVSYFEEPPHLLAVADTVYRALRTERRDQAVMISVES GAGKTDATKRLQLYAETCPAPQRGGAVRDRLQSNPVLEAFGN AKTLRNDNSSRFGKYMDVQDFDKGAPVGGHILSYLLEKSRVVHQ NHGERNFHIFYQLLEGGEEETLRLGLERNPQSYLYLVKGQCAK VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNH FAANESNAQVTENQLKYLTRLSSVEGSTLREALTHRKIIAKG EELLSPLNLEQAAYARDALAKAVYSRTFTWLVGKINRSLASKDV ESPSWRSTTVLGLLDIYGFVFOHNSFEQFCINYNCKLQQLFI ELTLKSEQEEYEAGIAWEPVQYFNNKIICDLVEEKFKGII\SI LDE\ECRLPGE
6709	3	894	PPHEHLFPSEGERGPFSSFLVSRRGLGPGKMGKKGKEKKGRGAEK TAAKMEKKVSRKSRKEEEDLEALIAHFQTLDAKRTQTVELPCPP PSPRLNASLSVHPEKDELILFGGEYFNGQKTFLYNELYVYNIRK DTWTKVDIPSPPPRRCAHQAVVVPQGGGQLWVFGGEFASPNGEQ FYHYKDLWVLHLATKTWEQVKSTGGPSGRSGHRMVAWKROLILF GGFHSTRDYIYNDVYAFNLDFTTWSKLSPSGTGPTPRSGCQ\ IPSPRAASSVYGGYSKQVRKDKVDKGRHSDMF
6710	158	980	RHKMTNYRVESSSGRAARKMRLALMGPAFLAAGYIDPCNFATN IQAGASFGYQLLWVWVWAMLIQILSAKLGATGKNLAEQI RDHYPRPVVWFYVWQAEIIAMATDLAEFIGAAIGFKLILGVSL QGAVLTGIATFLILMLQRRGQKPLEKVIGGLLFLVAAAYIVELI FSQPNLAQLGKGMVIPSLLTSEAVFLAAGVL\GATIMPHVI/YI WHSSLTQHLHGSRQORYSATKWDVAIAMTIAGFVNLAIMATAA SELNFYGTGVA
6711	3	347	VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK ELVRTDLHNILMKENKNDQAI*HIMEDLDITNAHQIIFKELIML MAMLTWSYHDNMHDADYGPQQHRPG
6712	118	578	PHGQKRTRYQVRAPGQQPQAQLAMALCLKQVFAKDKTFRPRKR FEPGTQRFELYKKAQASLSGLDLRSVVRLLPGENIDDWIAVHV VDFFNRIINLIYGTMAERCS*TSFVPMAGGPRIEYRWQDERQYRR PAKLSAPRYMALLMDWIESLI
6713	2485	3	QARGSDSEGEFEIQAEDDARARKLGPGRPLPTFPPTSECTSDVE PDTREMVRAQNKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI QRKTIPIVILDGKDVVAMARTGSGKTACFLPMFERLKTHSAQTG ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF AALHENPDII IATPGRLVHVAVEMSLKLSVEYVVFDEADRLPE MGFAEQLEI IARLPGGHQTVLFSATLPKLLVEPARAGLTEPVL IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVRPQDQTV VFVATKHAEYLTETLTQTVSCAHIYSALDPTARKINLAKFTL GKCSLTIVTDLAARGLDIPLDNVINYSFPAKGKFLHRVORVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVDDEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESI KRAKEMDLVGLGLHPLFSSRFEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKQKDRKAIARFQQ GQQGRQEQEGPVGPAAPSRPALQEQPEKEEEEAGESVEDIFS EVVGRKQRSGPNRGAARRRREARQDQEFYIPYRPKDFDSERG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LSISGEGGAFEQQAAGAVLDLMGDEAQNLTGRQQLKWRDKKKR FVGSGQEDKKIKTESGRYISSYKRDLYQKWKQKQKID*S*L GRRRGILTRRRPTEEVGEARPLAQAGCIPGPHAPRHPPLQAESA LELKTQKQILKQRRRAQKAALSQRWWPQAALCPQ
6714	169	1416	NNQCELLPPPPAPMAHIPSGGAPAAGAAPMGFQYCVCKVELSVS GQNLDDRDTVSKSDPFCVLTENNNGRWIEYDRTETAINNLNPAF SKKFVLDYHFEEVQKLKFAFDQDKSSMRLEHDFLGQFSCSLG TIVSSKKITRPLLLNDKPAKGKITIAAQLSDNRVITLSLAG RRLDKKDLFGKSDPFLEFYKPGDDGKMWLVHRTVIKYITLDPVW KPFTVPLVSLCDGDMCKPIQVMCYDNDGGHDFIGEFQTSVSQ MCEARDSVPLEFECINPKKQKQKKNYKNSGIIILRSCKINRDYS FLDYILGGCQLMFTVGIDFTASNGNPLDPSSLHYINPMGTNEYL SAIWAVGQIIQDYDSDKMFPALGFGAQLPPDWKVSHEFAINFNP TNPPCSGVDGIAQAYSACLP
6715	32	493	GPAGAESGSLHCLPATVQALAGAASPHGGQPPRRGPLIGSGMP GKPKHLGVPNGRMVLAVSDGELSSTTGPOGGEGRGSSLSIHS PSGPSSFPFTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEFS AENVTFWKACERFQQIPASDT
6716	1	176	GAGGPAPRSFGSEEPRAALERDKMSARAAAAXSTAMEETAWEQ HTVTLHRVSLCCSK
6717	115	896	LFAMSGFENLNTDFYQTSYSIDDSQQSYDYGGSGGPYSKQYAG YDYSQOGRFVPPDMMQPPQPYTGQIYQPTQAYTPASQPPFYGNN FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLG PMVFCIAFGATLLLAGKIQFGYVYGISAIIGCLGMFCLLNLSMT GVSFGCVASVLGYCLLPILLSSFAVIFSLQGMVGIILTAGIIG WCSFSASKIFISALAMEGQQLLVAYPCALLYGVFALISVF
6718	290	599	KQSTVTPGTILPSLKHNSGLCKFPETGGKMTTFKEGLTFKDVA VIFTEELGLLDPVQNRNLYQDVMLNFRNLLSVGHHPFKHDVFL LEKEKKLDIMKTATQ
6719	1	691	PTREEQDREDGKCHKMEMNPISGNLNCPIAMSCQSSDHGCET DLSDDDDKIEKPNFMKDSASQDNGLSRKISRKRVSSDSDSL QVVKKSSKARTGLLRITRCAATAANKIKLMSDVEDVSLNVHT RSKNGRKKPLHLACTAKKKLSOCEGSHCEVPSEQYACBGKPP DPDSEGSTKVLSQALNGDSSEDMLNSEKHRTNIHKIDAPSK RKSSSVTSSG
6720	3	822	HEVAEEAGGTVPQRGTMPGTRFQHVITPEPGKWELTGVEAA VPITEKSNPLTQDLDDKADAENIVRLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLEKPDGGLVVLSSGGTSGRMAF LMSVSFNQMLKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNTAVFLP VLVGFPNPMARHPFPPPRILRSLTVFPPSLRAPHYQITSLLFSM SVVTLISE
6721	3	822	HEVAEEAGGTVPQRGTMPGTRFQHVITPEPGKWELTGVEAA VPITEKSNPLTQDLDDKADAENIVRLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLEKPDGGLVVLSSGGTSGRMAF LMSVSFNQMLKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNTAVFLP VLVGFPNPMARHPFPPPRILRSLTVFPPSLRAPHYQITSLLFSM SVVTLISE
6722	1	390	RSWSKRTWQALPMAVLFLLFLCGTPQAADNMQAIVVALGEAVE LPCPSPTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLGNYSLNLEGSKEEDAGRYWCAVLGQHNYQNW
6723	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKIQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VEVKELQREPLTPBEVQSVREHLGHESDNL
6724	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKQLALT GNEGRVSVENIKQLLSAHKESSFDIILSLGVPGSTTLHSAEIL AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL VEVKELQREPLTPBEVQSVREHLGHESDNL
6725	356	722	RRRTTPVILATMDDDLMLALRLQEEWNLQEAERDHAQESLSLVD ASWELVDPTPDQLALFVQFNDQFFWGQLRAVEVKWSVRMTLCAG ICSYEGKGGMCSIRLSEPLLLKLRPRKDLVEVFFV
6726	98	714	HLQKMERKINRREKEKEYEGKHNSLEDTDQGNCKNSTLMTLVNG GYLYITQKQTLTKYPTDFLEGIVNGKILCPFDADGHYFIDRDGL LFRHVLNPLRNGELLPEGFRENQLLAQEAFFQLKGLAEVKS RWEKEQLTPRETTFLEITDNHDSQGLRIFCNAPDFISKIKSI VLVSKSRDLGFPPEFSISSNIIQFKYFIK
6727	1	831	FRGMGDERPHYYGKHTPQKYDPTFKGPIYNRGCTDIICCVFLL LAIVGYVAVGIIAWTHGDPKVIYPTDSRGFCGQKGTKNENKP YLFYFNIVKCAPLVLLLEFQCPTPQICVEKCPDRYLYTLNARSS RDFEYKQFCVPGFKNNKGVAEVLRDGDCPAVLIPSKPLARRCF PAIHAYKGVLMVGNETTYEDGHGSRKNITDLVEGAKKANGVLEA RQLAMRIFEDYTVSWYWDIISLGIAMAMSLFILLRFLAGIMG RGMIMGILVLGY
6728	486	935	FCSSWLRLSLADSSLSWKMLFLVLTGGIASGKSSVIQVFQQLGCA VIDVDVMARHVVPQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD LIFNQPDRRQLLNATHPEIRKEMMKETFKYFLREPTSPRGKK HVPSSALKEADSLMRDRT
6729	259	1191	VGLTGAQSGRTASMGDRQRAVAGPALRRWLLGTVTVGFQAQSV LAGVKKFDVPCGGRDCSGGCQCYPEKGGRGQPGVPGPQYNGPP GLQGFPGQGRKGDKGERGAPGVTPKGDVGARGVSGFPGADGI PGHPGQGGPRGRPGYDGCNGTQGDSPGQPPGSEGFTGPPGPGG PKGQKGEFYALPKEERDRYRGEPEPGLVGFQGPGRPGHVQGM GPVGPAPGRPGPPGPPGPKGQQGNRGLGFYGVKGEKGDVGPQPN GIPSDTLHPIIAPTGVTFHPDQYKGEKGESEPEGIRGISLKGE GIM
6730	784	1015	NMVDYEVVLGLQRYASPEDIKAYHKVALKWHPKNPNENKEEAE RKPFKEVAEAYEVLNDEKRDIDYDKYGTGLNEF
6731	1	446	GIRKRLHGAVVPRVEVGCFWETRESEGVHLERPTSFLKNNDEGS LDIYAGLDSAVSDSASKSCVPSRNCCLDLYEILTBEGTAKEATY NDLQVEYGGCQLQMKELMKKFKIEIQTNFSLINENQSLKKNISA LIKRTARVEINRKDEEI
6732	102	1205	GRWQRRPPPSPLWCLQPGGSDPQQLTLRHCLSHSPQDTPW AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPSRHRHRQEN LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSDAPAYRTPPSRQGRREVRFSDPEPPEVYGDPE PLVAKERSVPGKTRLEEFRRSDSAKEEVRESAYYLRSRQRRQPR PQTEEMKTRRTTRLQQQHSEQPPLQPSVPMTRRGLRDSHSSSE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSSEGETEEDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW
6733	613	1311	RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRLKTSGECKRTKKSLELSKEDLI QLLSIMEGELQAREDVHMLKTEKTKPEVLEAHYGSAAPEKVL VLHRDAILAQEKSIGEDVYEKPISELDRLLEEKQKETYRMLLEQL LLAEKCHRRTVYLENEKHKHTDYMNKSDFTNLLEQERERLKK LLEQEKAYQARKE
6734	189	551	SAAMFFVFGSCFQELQEKNSLELVSFEEVAVHFTWEEWQDLDD AQRTLYRDMLETYSLSVSLGHCITKPEMIFKLEQGAEPWIVBEE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TLNLRSLSGGSKKQVFSGICHRSLVELQEVHLV
6735	280	558	KSRAGVTKMSNPFLKQVFNKDKTFRPKRKFEPGTQRFELHKKA QASLNAGLDLRLAVQLPPGEDLNDWVAVHVDFNVRNLIYGTI XDGCT
6736	195	808	MNYELNFKREMPNISKGLTNLNLFLKRLSSVLPITDYVYPEN SSSNPYLIRRIEELNKTASGNVEAKVVCFYRRDISNTLIMLAD KHAKEIEBESETTVEADLTQKQKHLKRELFSLRQYESLPATH IRGKCSVALLNETESVLSYLDKEDTFFYSLVYDPSLKTLLADKG EIRVGPRYQADIPEMLEGTFFCFVFAVL
6737	150	1209	PVIMPLHFS PGDIVRPSCCVSSSPKLRNNAHSRLESYRPTDLS REDTGCNLQHSIDRENIDDLNMEFNPSPDHPRASTIFLSKQSQT DV REKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTIK CVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPDPYDKHN PEQKQIYRFVRTLSAAQLTAECAIVTLVYLERLLTYAEIDICP ANWKRIVLGAILLASKVWDDQAVWNVYDQCILKIDITVEDMNELE RQFLELLQFNINVPSSVYAKYFYDLRLSLRANNLSPFLEPLSRE RAHLEAISRLCEDKYKDLRRSARKRSASADNLTLPWSPAIIS
6738	148	653	CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLL WGAPWTHGRRSNVRVITDENWRELLEGDWMEFYAPWCPACQNL QPEWESFABWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHC KDGEFRRYQGPRTKKDFINFISDKEWKSIHPVSSWF
6739	3	631	SWPDMAEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRIHSAHKF VLAARSDSWSLANLSSKELDLSDANPEVMTMLRWIYDLEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TAEELNASTLMNYCAEI IASHWVSEVEGVNKAL
6740	3	631	SWPDMAEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRIHSAHKF VLAARSDSWSLANLSSKELDLSDANPEVMTMLRWIYDLEF REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ TAEELNASTLMNYCAEI IASHWVSEVEGVNKAL
6741	141	960	PLTLFFSSRARAGHTMNTSPGTVGSDPVLATAGYDHTVRFWQA HSGICTRTVQHQSQVNALEVT PDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIIHW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVFFSCLL PLAIGILQEGEFESLARRGLLFLACQGNVCVWNL TGGIGDEV TQ LIPKTKIP
6742	141	960	PLTLFFSSRARAGHTMNTSPGTVGSDPVLATAGYDHTVRFWQA HSGICTRTVQHQSQVNALEVT PDRSMIAAAVQPVSLGYQHIRM YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMTGGEDCTARI WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIIHW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVFFSCLL PLAIGILQEGEFESLARRGLLFLACQGNVCVWNL TGGIGDEV TQ LIPKTKIP
6743	1	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPRKM PKRISISKQLASVK ALRKCSDLKAIATTALIFRNSSDSGKLEKAIKDLLQTQFRN FAEGQETKPKYREILSELDEHTENKLD FEFMILLLSITVMSDL LQNIR
6744	95	1343	RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD RQKVSTVGYGMDEVEQDQHRARLKELFDSFDTTGTGSLGQBELT DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT LSNEEHFQEPDCSLEAPKPYVRGGKRYGRSLPEFQESVEEFPE VTVIEPLDEEARPSHIPAGDCSEHWKTQRSEYEAEQQLRFWNP DDNLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CEQYGLQNVGDGEMLEEVFHNLDPPDGTMSEVDFYGLFKNGKSLT PSASTPYRQLKRHLMSQSFDESGRRTTSSAMTSTIGFRVFSCL DDGMGHASVERILDWQEEGIENSQEIILKALDFGLDGNINLTEL TLALENELLVTKNSIHQACI
6745	1	588	TFRDQGWQRRRWLLGCASWESWEAAIAAGPLPSSTARQNNP AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP ELPVTSDCAVCEVLHQPVTRCGHVFCRSCIATSLKNNKWTC PYCRAYLPSEGVPATDVAKRMSYKNCACEDTLVCLSEMAHI RTCQKYIDKYGPLQLEETA
6746	110	492	GATGAMAESAPARHRRRRSTPLTSSTLPSQATEKSSYFQTTEI SLWTVVAIAQAVEKKMESQAARLQSLGRTGTAEKKLADCEKMA VEFGNQLGKQWAVLGTLLQYGLLQRRLENVENLLRN
6747	247	484	EAVTFKDVAVVFTBEELGLLDLAQRKLYRDMLENFRNLLSVGH QPFHRDTFHFLEEKFWMMDIATQREGNSVYAGVC
6748	201	665	MTTFKEAVTFKDVAVVFTBEELGLLDPAQRKLYRDMLENFRNL LSVGNQPFHQDTFHLGKEKFWKMTTSQREGNSGGKIQIEMET VPEAGPHEEWSQQIWEQIASDLTRSQNSIRNSSQFFKEGDVPC QIEARLSISXVQQXPYRCNECKQ
6749	95	719	RREVKGDDGVCPRARGSPQSQQFPSCAGGEGGLQSGEALDGAM SAGGPCPAAGGGPGGASCSVGAPGGVSMFRWLEVEKEFDKAF VDVDLLLGELDPQADITYEGRQKMTSLSSCFALCHKAQSVSQ INHLEAQLVDLKSLELTETQAEKVLEKEVHDQLQLQHSIQLQL HAKTGQSADSGTIKAKLSGSPVEELERELKAN
6750	3	428	SCESRRPGAKWVWASGALPRDITGLGSEQPSGDVAQSNRATMGT TAPGPIHLLLECDQKLMFELCNMDNLDLVLEEIQEBAERMFT BFSKEPELMPKTPSQKNRRKKRIRISYVQDENRDPIRRRLSRKS RSSQLSSRR
6751	152	1417	PTKATEMAGASVKVAVRVPFNSREMSRDSKCIQMSGSTTTIV NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEML QHAFEGYNVCI FAYGQTGAGKSYTMMGKQEKDQGGIIPQLCEDL FSRINDTTNDNMSYSVBVS YMEIYCERVRDLLNPKNGNLVRE HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS SRSHAVFNIIFTQKRHDAETNITTEKVKISLVDLAGSERADST GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNNKKKKT FIPYRDSVLTWLLRENLGGSRTAMVAALSPADINYDETSLTLR YADRAKQIRCNVINEDPNNKLIRELKDEVTRLRDLLEYAQLGLD ITDMTNALVGMSPSSSLALSSRN
6752	24	1834	RNCVPLGCRSRVKFHSDIKMQYSHHCEHLLERLNKQREAGFL CDCTIVIGEFQFKAHRNVLASFSEYFGAIYRSTSENNVFLDQSQ VKADGFQKLEFIYTGTLNLD SWNVKEIHQAADYLVKEBVVTKC KIKMEDFAFIANPSSTEISSITGNIELNQQTCLLTLRDYNNREK SEVSTDLIOANPKQALAKKSQTKKKKAFNSPKTGQNKTVQY PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN TFPAQDI VHTVTVKRKGKSPNCALKEHSMNSIASVKSPEAE NSGEELDQRYSAKPMCNTCGKVFSEASSLRHMRHKGVPKPYV CHLCGKRAFTQCNQLKTHVRTHTEKPYKCELCGKFAQKQCLVF HSRMHGEKPYKCDVNLQFATSSNLKI HARKHSGEKPYPVCDR CGQFAQASTLTTHVRRHTGEKPYVCDTCGKAFVSSSLITHSR KHTGEKPFICELGNSYTDIKNLKHKTKVHSGADKTLDSAE HTLSEQDSIQKSPSETMDVKPSDMTLPLALPLGTEDHMLLPV TDTQSPSTDTLLRSTVNGYSEPLIFLQQLY
6753	2	1305	VPSPYPYPQKVVATEFTTSSDSETANGIAKPDVPMGGEEKAS PPGIKLRRTNYSRLFNCDQQAQKQKKRHSSTGDSADAGPPAAG SARGEKEMEGVALKHGPSLPQERKQAPSTRDRSAEPSSSRSPV AHPGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSTPPAS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLSKLSRPYLVELLSRRAGRPDPPEPSEPSKEDQESSDRPPSPFP GPEERKGGQRDEEEETERKPASPPLPATQQEKPSQTPEAGRKE KPMQLSRHSLDGSKLTEKVETAQPLWITLALQKQGFREQQATR EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALP EEKRPETAVSRLEERQKKANTLPTSVTVEISYSSPAAPLVKE VSKRFSSPDDAPVSSPAWLALAKRKAKAWSDCPLIIK
6754	2	413	FVRRRRRLGGPEVNTMSSLHKSRIADFQDVLKEPSIALEKLRB LSFSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKQRELYAQ FLREMIQPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD NEVLL
6755	298	1343	PGQLQVALEADWFLDMPGRRGSPSRQQLSRALPSLQTLVGGG CGNGTGLRNRNGSAIGLPVPPITALITPGFVRHCQIPDLVDGS LLFEFLFFIYLLVALFIQYINIIYKTVMWYPYNHPASCTSLNFHL IDYHLAAFTVLMARRLVWALISEATKAGAASMIHYMVLSARL VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYFPFVGVVPLCCFHQ DSRAHLLLTIDYNYVQHEAVESASTVGGAKSKDFLSLLES KEQFNNTATPIPTHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS LFSAYYVAFPLCFVKVSGYLTFCFLDLCVNYINWVFLV
6756	180	754	IERALGSLPLSIPVSWGSLRTLKYQQQLRPKVLCCQTRVQCHD LRSLOPQPGLKQSFCLRVLGLQTGATTGRLDLCCKELIILTE REARQKRKKRKEKESGMALTQGLTPFRDVAIEFSQEEWKSLDPVQ KALYWDVMLENYRNLVFLGKDNFALEVKICPRVFLYFLCCLSW PFHYLTETEALLTHK
6757	2	459	NSRVEAPEAHSRESQSDAMRKHLSWWLATVCMLLFSLHSAVQ TRGIKHRIKWNKALPSTAQITEAQVAENRPGAFIKQGRKLDID FGAEGNRYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ AANQGEFQKPDNKLHQVWLW
6758	1	1008	ASGFELPGRFRDRAFWLPARLLRGVLAVVWSLSALGPGSFCRR RVPSLAQLGHSEAPSPDDVRWSRVPDRCPEDRDRAWPPPPPS LPPSFRNMANNSPALTGNSQPQHQAASAAAAQQQQCGGGGATK PAVSGKQGNVPLWGNKTMNLNPMILTNILSSPYFKVQLYELK TYHEVVDEIYFKVTHVEPWEKGSRTAGQTGCMCGVRGVGTGGI VSTAFCLLYKLFKLTRKQVMGLITHDTPYIRALGFMYIRYT QPPTDLWDNFESFLDDEEDLDVKAGGGCVMTIGEMLRSLFTKLE WFSTLFPRIIPVPVQKNIDQIKTRPRKI
6759	1	513	RKHNHSLDGTSTRAFPQTGLPLLSPVPQRKTQSGCFDLDSS LLHLKSFSSRSRPRCLNIEDDPDIHEKPLSSAPPITSLSLLG NFEESVLNYRFDPLGIVDGFTAEGVAGSACFPHLTLPEVVSFY SVSDDNAPSPYMGVITLES LGKRGYRVPPSGTIQVVCVL
6760	239	606	VLSKKKGLSAEEKRTRMMEIFSETKDVFLKDLKIAPKERGIT AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKL VLESQSLSEGSQKHSALQKSIKAKIGRCETEERT
6761	29	1733	ERTLRGLREVAAPSDVADAASRRGRCCCLHCTQTQVAQDCPS SSSSVQRCESLFLQSLHTMTSKKLNVSVAGCADDALAGLVACNP NLQLLQGHVLRSDLSLKGRLVALLSGGGSGHEPAHAGFIGKG MLTGVLAGAVFTSPAVGSILAAIRAVAQAGTVGTLIVKNYTG RLNFGALAREQARAEIPVEMVIGDDSAFTVLKAGRRGLGTV LIHKVAGALAEAGVGLEEIAKQVNVVKAMGTLGVSLSSCSVPG SKPTFELSADVELGLGIHGEAGVRRIKMATDEIVKLMMLDHMT NTTNASHVPVQPGSSVVMVNNLGGSLFLELGIADATVRSLEG RGVKIARALVGTFSALEMPGISLTLVDEPLKLLIDAETTA AWPNVAASVITGRKRSRVAPAEAPDSTAAGGSASKRMALVL BRVCSTLLGLEEHLNLDRAAGDGDGCTTHSRAARAIQEWLKEG PPPASPAQLLSKLSVLLLEKMGSSGALYGLFLTAAQPLKAKT SLPAWSAAMDAGLEAMQKYGKAAPGDRTMLDLSLWAAGQEL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \>possible nucleotide insertion)
6762	3	613	ASTISWRLCVAGAEARRPVPVAGERAGGGAMWFMVLLSWLSLFI QVAFITLAVAAGLYLAELIEBYTVATSRIIKYMIWFSTAVLIG LVYFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG LVVVNHYLAFQFFABEYYPFSEVLAYFTFCLWIIFFAFVVSLSA GENVLPSTMQPGDDVVSNYFTKGKRGK
6763	2	760	SGPDFPGRRRFRGCCVRRPPAGAGMELGGHWMNSAPRLVSETAE RKQEQTGTAEAAADSGAVGARRFLLCLYLGGFLDLFGVSMVVP LLSLHVKS LGASPTVAGIVGSSYGILQLFSSTLVGCWSDVVGRR SLLACILLSALGYLLGAATNVFLFVLARVPAGIFKHTLSISR ALLSDVVPEKERPLVIGHFNTASGVGFIILGPVVGGLTELEDGF YLTAFICFLVFIINAGLVWFFPRREAKPGSTE
6764	80	438	LKKMDTMMLSVRNLFQVLVRRVEILSEGNEVQFIQLAKDFEDFR KKWQRTDHELKGYKDLLMKAETERSALDVKLKHARNQVDVEIKR QRRAEADCEKLERQQLIREMLMCDTSGSIQ
6765	3	550	ARYSRVDHFCRRRCRAVARAPRFLLOFPSPGRHFLAACVARWL RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDLLSGSVLSSPNS NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLPGEVTTETE VIALGLPFGKVTNIMLMKGKNQAFLELATEEAAITNGNYYSAVT PHLRNQ
6766	1	1287	EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGV RAVLSLCQQTSTSRQPPVRAFLLISTLKDCKRGTRYELRENIEQFFT KPFDEGKATVRLKEPPVDICLSKANSSSLKGLFSAMRLAHRGN VDTVPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHL QTSYCGLVVRDMRLCLKSLRKLDSLHNHKKLPATIGDLIHLQ ELNLDNHLBSFSVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ LQBLKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF RNLSEYLDLFGNTFEQPKVLPVIKLQAPLTLESSARTILHNR IPYGSIIIPPHLCQDLDTAKICVCGRFCLNSFIQGTTIMNLHSV AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI
6767	336	919	APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPKMKHFLNV GRLOQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY RQPLPQPTCDPEQLGLRHAQKAHQLOSDVKYKSDNLNLRGVGWT PPGSYKVMARRAAELANARGLGLOQAYRGAEAVEAGDHQSGEV NPDATEILHVKKKKALLL
6768	2	363	PGSTISCYLLSEGLPLCMQVACGEEKHRAPTMTKLRLARFKKTE LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL
6769	284	396	MSTPDFSTAENNQELANEVSCLKAMLTMLQAMGQAD
6770	1	397	QRNYQVIWSSTMAKLHDYKDEVVKLWTEFNYSVMQVPRVEK ITLNMVGGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDPRGLSAKS
6771	3	378	APAGTLAMTGRSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM QEMGNKANRLYEAYLPETFRFPQIDPYLFWNSLEG
6772	1	1400	AAAFLOQMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA CLCLTFVSYPFGSG\HKPRWLWGR\VLMTGSLVFALPHFTAG P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMGLQFL HGVGATPLYTLGVTYLDENVKSSCSPYIYIAIFYTAAILGPAAGY LIGGALLNIYTEMGRTELTTESPLWVGAWVWVFLGSGAAFFT AVPIILGYPRQLPGSQRYAVMRAAEMHQLKDSRGEASNPDGKT IRDLPLSIWLLKNPTFILLCLAGATEATLITGMTSTFSKPFLES QFSLASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSVAVIK FCLFCTVVSLLGILVFLHCPSPVMAGVTASYGGSLLPEGHLNL TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG QKYVRDCSIPQNLSSGFGHATAGKCTST

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6773	1	630	PWEAPKEHKYKAEHTVVLTVTGEPCHFFQYHRQLYHKCTHKG RPGPQPCWATTNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT CVNMPSPGPHCLCPQHLTGNNHCQKEKCFEPQLLRFFHKNEIWYRT EQAAVARCQCKGPDHACQRLASQACRTNPLHGGRCLEVEGHRLL CHCPVGVTGPPCDVGE*GSGASRRPAPRWDLAR
6774	146	389	LTELSDQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIIS GLRIGFLTGPPLIERVILHIQVSTLHPSTFNQLMISQ
6775	104	614	TCPSQLRVLTARGGRAPSPQLWTLVLALIEEKWRSHRILRMNS GRPETMENLPALYTIFFQGEVAMVTDYGAFIGPQCRKQGLVHRT HMSSCRVDKPEIIVDVGDKVWVKLIGREMKNDRIVSLSMKVVN QGTGKDLDPNNV\SLSKKRGGGDPSPRITLGRSPRLRS
6776	3	1108	HERHERHEGALSQDALLRISIFLDSNMRPEKCRRFVHPQWQLLH LNGTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDQSLS TSVAKFVFMAGMMVGGILGGHLSDFRGRFVLRWCYLQVAIVGT CAALAPTFLIYCSLRFSLGIAAMSLITNTIMLTAEWATHRFQAM GITLGMCPSGIAFMTLAGLAFARDWHILQLVVSVPYFVIFLTS SWLESARWLIINNKPPEGLKELRKAHRSGMKNARDTLTLEIL KSTMKELEAAQKKKPFLEGRHMPNICKRISLLPFTKFANFMA YFGLNLHG/LKHLGNNVFLQLTLPFQAV/TPPGQLVLHLGHWSG RVSSRGVNCGLGLFVLQVW
6777	779	63	CFHGPAPWRDCEVRATFAKKQGGSGIISCIASFPAQPLYACGSY GRSLGLYAWDDGSPALALLGGHQQGITHLCFHPDGNRFFSGARKD AELLCDLRLQSGYPLWSLGRVTTNQRIFYDLDPQTGQFLVSGST SGAVSVWDTDGPNDGKPEPVLSFLPQKDTNGVSLHPSLPLLG HCLPVSVCLSPTESGGRRRGAGPSLGSPPRHVHLECRLLQLWWC GGGARLQHP**SPRARKGR
6778	311	805	IQSITDESRSIRKKNPANTRLRLNVP/EETAGDSE/ERSPEER VQADPRIASAPKCPSTSPFPKGRSPEGEGET/DPEKVHHPGP KDKSVAEK\KGP\SPVSEGIKDFSMKPEWENLQSNVRRMH T\AVRLNEVIVKSRDAKLVLNMPGPPRNRNGDENV
6779	2	535	RALRRQPRLLAANGIEPESMAISEPIKGRKPCVNKEBLAKKP MAKCAWKGPPEPPQDARAEAESPGGASESDQDGGHESPPKKKAV AWVSANPAPMRKKKVSIGPVSYVLVDSGDRKKPVMPPKKGP SRREASDQKAPRGQQPAEATASTSRGPKAKPEGSPRRATNESRK V
6780	3	403	HEVNDNKPBININLMSPGKEEISYIFEGDFIDTFVALVRVQDKD SGLNGEIVCKLHGHHFKLQKTYENNYLILTNATLDREKRSEYS LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQSRSEYEFVISE K
6781	1	1269	AETRPVFPFTLQDLSSSKEPSNSINLPHSNELCSSLVHPFELSEVS SNVAPSIIPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT SAALPTHLQSALMSTVVTMPNAGSKVMVSEGGQSAQAQSNARQFI TPVFINSSSI IQVMKGSQPSTIPAAPLTNTSGLMPPSVAVVGLP HIPQNIKFSAPVPPNALSSSPAPNIQTGRPLVLSRATPVQLP SPPCTSSPVVPSHPPVQVQKELNPDEASQVNTSADQNTLPSSQ STTMVSPLLTNSPGSSGNRRSPVSSSKGKGVKIGQILLTKAC KKVTGSLEKGEEQYADGETEGQGLDTPAPGLMGTEQLSTELDS KTPTPPAPTLLKMTSSPVPGTASAGPSLPGGALPTSVRSIVTT LVPSELISAVPTTKSNHGGIASESLAG
6782	3	1327	RKPTVIRIPAKPGKCLHEDPQSPPLPAEKPIGNTFTSVSGKLS NVERTNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTQQPPTK VPPERPPPKLSATRRSNKKLPFNRSSDMDLQKKQSNLATGLS KAKSQVFKNQDPVLPKPKPGHPLYSKYMLSVPHGIANEDIVSQ NPGELSCKRGDVLVMLKQTENNYLCQKGEDTGRVHLSOMKLIIT PLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI PEGNGKRECVSSHCVKGSRCVARFEYIGEQLDELFSFEGEIII LKEVYNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV PLKTKKEDSGSNSQVNSLPAEWCEALHSPTAETSDDLFSFKRGDR I
6783	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA TMPASVVGQRPTIAMVTAINSQAVALSTDVQNTFPVNLQTSSKVT GPGAEAVQIVAKNTVTLOVQATPPQPIKVPQFIPPPRLTPRPNF LPQVRPKPVQNNIPIAPAPPPMLAAPQLIQRVMLTKFTPTTL PTSQNSIHPVRVVGQTATIAKTFPMAQLTSIVIATPGTRLAGP QTVQLSKPSLEKQTVKSHETDEKQTESRTITPPAAPKPKREEN PQKLAFMVSLGLVTHDLEEIQSKRQERKRRTTANPVYSGAVFE PERKKS AVTYLNMHPGTRKGRPPKYNVAVLGFGALTPTSPQS SHPDSENEKTETTTFTFPAPVQVSLPSPSTSDGDIHEDFCSCV RKSGQLLMCDTCSR VYHLDCLDPPLKTI PKGMWICPRCQDMLK KEEAIWPVPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ LEQKVQKLSNSISKMEMKNTILARQKEMHSSLEKVKQLIRLIH GIDLSKPVDSSEATVGAI SNGPDCTPPANAATSTPAPSPSSQSCT ANCNQGEETK
6784	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA TMPASVVGQRPTIAMVTAINSQAVALSTDVQNTFPVNLQTSSKVT GPGAEAVQIVAKNTVTLOVQATPPQPIKVPQFIPPPRLTPRPNF LPQVRPKPVQNNIPIAPAPPPMLAAPQLIQRVMLTKFTPTTL PTSQNSIHPVRVVGQTATIAKTFPMAQLTSIVIATPGTRLAGP QTVQLSKPSLEKQTVKSHETDEKQTESRTITPPAAPKPKREEN PQKLAFMVSLGLVTHDLEEIQSKRQERKRRTTANPVYSGAVFE PERKKS AVTYLNMHPGTRKGRPPKYNVAVLGFGALTPTSPQS SHPDSENEKTETTTFTFPAPVQVSLPSPSTSDGDIHEDFCSCV RKSGQLLMCDTCSR VYHLDCLDPPLKTI PKGMWICPRCQDMLK KEEAIWPVPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ LEQKVQKLSNSISKMEMKNTILARQKEMHSSLEKVKQLIRLIH GIDLSKPVDSSEATVGAI SNGPDCTPPANAATSTPAPSPSSQSCT ANCNQGEETK
6785	1	528	LGNTVLHYCSMYSKPECLKLLRSKPTVDIVNQAGETALDIAKR LKAQCEDDLSSQAKSGKFNPHVHVEYEWNLQEEIDESDDDLDD KPSVPKKERSPRPQS FCHSSSISPQDKLALPGFSTPRDKQRLSY GAFTNQIFVSTSDSPTSPTTEAPPLPPRNAGKGTGPPITPHR
6786	1820	1397	RSPKVLVLAPTR ELANHVSRDFKDI\TRKLTVARFVGGTSYQSQ INHNRNGIDILVGTGRIKDHLSQGRDLKLRHVVLDEVDQML DLGF AEQVEDI I HESYKTDSEDNPTLLFSATCPQWYTTVA\KK YMKSRYEQVDLDGKMTQKAATTVEHLAIQCHWSQRPVIGDVLQ VYSGSEGRAIIFCETKKNVT EMAMNPHIKQNAQCLHGDIAQSQR EITLKG FREGSPKVLVATNVAARGLDIPVDLVIQSSPPQDVES YIHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAQLRIEKGAV DALAAALAHISGASSFEPRSLITSDKGFTMTLESLEEIQDVSC ANKELNRKLSSNAVSI TRMCLLKGNGVCFDVPTTESERLQAE WHDSDWILSVPAKLPEIEEYDGN TSSNSRQRSGWSSGRSGRSG RSGGRSGRSGRSGRSGRSGRSGRSGRSGRSGRSGRSGRSGRSG FD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS SVWN
6787	2646	2270	PSSFKNVPLEELEEPK*KRSGLSLTPKSIQNGP*PQTFFF FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI LVFLVEMGFHHVQAGLKLTL\VIHPPWPPKVLGLQT
6788	16	936	GGTVDLR\DM LAVSVLAAVRGGR\ATVRRVRESNVLHEKSKGKT REGAEDKMTSGDVL SNRMFYLLKTAFFSVQINTEEHVD\ELDQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=-possible nucleotide deletion, \=possible nucleotide insertion)
			EVILWGS*DS*GYPKKG*LLPKEVPSR/RVLLSGLTPLDATQE\FTEDLSK\YVTTMVCVAVNGKPMGLVVIHKPFSEYTAWAMVDGGS NVKARSSYNEKTPRIVVSRSHSGMVKQVALQTFGNQTTIIPAGG AGYKVLALLDVPDKSQEKADLYIHVYTIKKWDICAGNAILKALG GHMTTSLSGEEISYTGSDGIEGGLLASIRMNHQLVRKLPDLEKT GHK
6789	2	678	GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA GSLAGAIQAQSSIIYPMEVLKTRMALRKTGQYSGMLDCARRILARE GVAIFYKGYVPNMLGIIPIYAGIDLAVYETLKNALQHYAVNSAD PGVFPVLLACGTMSSTCGQLASYPPLALVTRMQAASIEGAPEVT MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVYENLKI TLGVQSR
6790	2	4068	APPAGRRRRQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD EPLVSGPLPHVAFSSSSSSISGSYSPGYAKINKRGAGGWSPSDS HYQWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSIDTGRNW KPYHQDGNIIWAFPGNINSDGVVRHELQHPHIIARYVRIVPLDWN EGRIGLRIEYVGCYSWADVINFDGHVVLPRFRNKKMKTLDKDI ALNFKTSESEGVILHGEQQQDYITLKLKAKLVLSNLGSLNQL GPIYGHSTVMTGSLDDHHVHSVIERQGRSINLTDRSMQHFR TNGEFDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNG VNITDLARRKKLEPSNVGNLSFSCVEPYTVPVFFNATSYLEVPG RLNQDLFSVSFQFRTWNPGLLVFSPHADNLGNVEIDLTESKVG VHINITQTKMSQIDISSGSLNDGQWHEVRFLAKENFAILTIDG DEASAVRTNSPLQVKTGEKYFFGGFLNQMNSSSHSVLQPSFQGC MQLIQVDDQLVNLVEVAQRKPGSFANVSIDMCAIDRCVPNHCE HGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQT SNYYWIDPDGSGPLGPKVYCNMTEDKVTIVSHDLQMOTPVVGY YNPEKYSVTQLVYSASMDQISAITDSABYCEQYVSFYCKMSRL NTPDGSPTTWVWGKANEKHYYWGSGGPGIQKACGIERNCTDPK YYCNCADADYKQWRKQDAGFLSYKDHLVPSQVVGDTDRQGEAKL SVGPLRCQGDNRNYNAASFNPSSYLHFSTFQGETSADISFYFK TLTPWGVFLENMGKEDFIKLELKSATEVSFSDVGNPGPEIIVR SPTPLNDDQWHRVTAERNVKQASLQVDRLPQKIRKAPTEGHTRL ELYSQLFVGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFI SGCSGHCTS YGTNCENGGKCLERYHGYSCDCSNTAYDGTFCNKD VGAFEBEGMWLRNFPQAPATNARDSSSRVDNAPDQNSHPDLAQ EEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLG GTREPYNIDVDHRNMANGQPHSVNITRHEKTIIFLKLHDHYSVSY HLPSSSDTLFNSPKSLFLGKVIETGKIDQBIHKYNTPGFTGCLS RVQFNQIAPLKAALRQTNASAHVHIQGELVESNCGASPLTLSPM SSATDPWHLDLHDSASADFPYNGGQQAIRNGVNRNSAIIGGVI A\VVIFTPLSLCTP\VLP*SR*HVS PHKGTLP IPNEAKGAGSRQK KPGRRPSMNNDPPTSQRPIDESKKEWPHLRGGYLANG
6791	1801	1193	TGHEGAKGEKGDGDLGPRGERGQHGPKEGYPGIPPEL/PGW SAVV*SWLTAATKVKQAILLPQPLE*LGLQIAFMASLATHFSNQ NSGIIFSSVETNIGNFFDVMTRFGAPVSGVYFFTFSMMKHEDV EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVALKLAKGDEVW LRMNGALHGDHQRFTFAGFLLFETK
6792	33	1073	VRHTNWGDMYFLSLGSES PKGAIGHIVSTEKTI LAVERNKVLL PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAGRCLCAV CPSPTTIIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHQAV TCLAAVTFSLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDEVCSWTASRRG APGSASKPKRPQVGEEPLESRAGR*HCFDREAQQNQF\ PVTAL AVSRNHTKLLVGDERGRIFCWSADG*EEGRSGSGTIVPG

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6793	2340	805	GRKEANY\YGS LTQAGTVSLGLDAEGQEVFVPFSAVLPMVAFND LVFDGWDISSLNLAEMRRRAKVLWDWGLQEQWLPHMEALRPRPSV YIPEFIAANQSARADNLIPGSRAQQLQEQIRRDIDFRSSAGLDK VIVLWTANTERFCEVIPGLNDTAENLLRTIELGLEVSPSTLFAV ASILEGCAFLNGSPQNTLVPGALELAWQHRVFGGDDFKSGQTK VKSVLVDFLIGSGLKTSIVSYNHLGNNDGENSEAPLQFRSKEV SKSNVDDMVQSNPVLYTPGEEPDHCVVYKYVPYVGSKRALDE YTSELMGLGTNTLVLHNTCEDSLLAAPIMLDLALLTELCQVRSF CTMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI ENILRACVGLPPQNHMLLEHKMERPGPSLKRVPVAAATYPMLNK KGPVPAATNGCTGDANGHLQEPPMPTT*GPGHTVSRFLPAAP HDPTLKAPTNGKGRCHFSPPTWGSWGL
6794	169	1349	DDVKRKPEASAH*EKPGPPSRPGVRGGRERAGRGSGHARSCR\ EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGKTYTQRCRLFVG NLPTDITEEDFKRLFERYGEPSEVF INDRGFGFIRLESRTLAE IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELEQA FSQFGPVEKAVVVDDRRGRATGKGFVEFAAKPPARKALERCQDG AFLLTTPRPVIVEPMEQFDDDEGLPEKLMQKTQQYHKEREQPP RFAQPGTFEFEYASRWKALDEMEKQOREQVDRNIREAKEKLEAE MEAARHEHQLMLMRQDLMRQEEELRLLEELRNQELQKRKQIQLR HEEHRRREEMIRHREQEELRRQEGFKPNYMENYVCHFLR
6795	1740	1010	GPRRQTQVRDHELDSE*DWAAQETDCAQNSGERL*KGVL/LENFS TMSKSAVKISLDLNSNPLCEQDQDLNMMVTALDTAMKRMDAFNQ EKVNIQKTVEIPLKKFGSVFPSLNMVAKRREQUALQDYRLQAK VEKYEKEKTGPVLAKLHQAREELRPVREDFEAKNRQLEEMPR FYGSRLDYFQPSFESLIRAQVVVYSEMCHKIFGDLSHQLDQPGHS DEQREERENEAKLSELRLSIVADD
6796	48	683	GKEIQPTIKLAWLLFGL*PVGALGKGVVSF**SHVALGQLGW LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSPVGCPSLNPPET SVQBGDRDCWQ*LPRLFSALVGQPGCWPGAPPERCV*PGRCKW HLQSQVLR*ERRRCCRLPRFA*GWRRRHQLGLGHPAPLGST SPHPPEGNSQQCR*GWAAELRLPSSVVL*GKLG*
6797	1620	211	TERMTPSQPTRGSSCTRFSSMLWTSTWRCLTCHWAGMRMSVVG V TLGPMAGLLSASGTTTTEATWTRPTHTLIRWLLTASRVDP ERPPPPSDDLTLLESSSYKNL/DAQIPQ/DWSMSPSTSG*RP LTSRASSIMRSRTAIPAS*SRLTTKHTVGGSPSAWRPRPTSRS VSTFVSSSTETTASGSCLTWWSSSPAPCPSSSAPAHSEASCK TSLWGS CGSGDGSACGSGWNLSMAGTSCSSPAMCSPSRAPS* RSASRPRTWRATTSAASSWAPRRCWGWA*SAT*PSSTTTISS PHCGWPCPASCASAAWLSSTWATASVAGSCWGPIM*SSAHS PW CLSACSRSSMGTTC*RSPP\SGASRAAAWCGSSPSSTFTPS ASSSTWCSASSRSPPATTPSSI PAAQAQRASCRPTSHSART APPPASSAAGAARPAAFSAAEGTPRRSIRCW
6798	3894	1696	STISWESLESWLNKATNPNSNRQEDWEYIIGFCQINKLE*VS ALWQGLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ/PQIA VRLLAHKIQSPQEWELQALTYLGDVSEKVKTKVIELLYSWT ALPEEAKIKDAYHMLKRQGIQSDPPIPVDRTLIPSPPPRPKNP VFDDEEKSKLLAKLLKSNPDDLQEBANKLIKSMVREDEARIQKV TKRLHTLEEYNNVRLLEMLLHYSQEDSSDGDRELMKELPDQC ENKRRTLFKLASETEDNDNSLQDILQASDNLSRVINSYKTIIEG QVINGEVATLTPDSEGNSSQCSNQGTLDLAELEDTTNSLSSVLA PAPTTPSSGPIPLPPPPQASGPPRSRSSQAEATLGPSSSTSNAL SWLDEBLLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPPAPVVPASVP APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL DQLEEAQVTSGLVKPTTSPLIPTTTTPARLLPFSTGPGSPFLQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLSFQSQGSPFKGPELSIASIHVPLESIKPSSALPVTAYDKNGF RILFHFAKECPPGRPDVLLVVVSMNLNTAPLVKSIVLQAAPVKS MKVKLQPPSGTELSPPFSPIQPPAAITQVMLLANPLKEKVRRLRYK LTFALGEQLSTEVEVDQFPFVEQWGNL
6799	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS ALWQQLRGSGLRGRTTMAKEGQPGSPRLSALECVLLVPQ\POIA VRLLAHKIQSPQEWELQALTYLGRVSEKVKTKVIELLYSWTM ALPEEAKIKDAYHMLKROGIVQSDPPIPVDRTLIPSPPRPKNP VFDDEEKSKLLAKLLKSNPDDLQEAANKLIKSMVREDEARIQKV TKRLHTLEEVMNNVRLLEMLLHYSQEDSSDGDRELMKELFDQC ENKRRTLFKLASETEDNDNSLDILQASDNLRSVINSYKTIIEG QVINGEVATLTLPDSEGSQCSNQGTLIDLAEELDTNSLSSVLA PAPTPPSSGIPILPPPQASGPPSRSSSQAEATLGPSSSTSNAL SWLDEELLCLGLADPAPNVPPKESAGNSQWHLQREQSDLDFFS PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPFPAPVVPASVP APSAGSSSLFTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL DQLEERAKVTSGLVKPTTSPLIPTTTPARLLPFSTGPGSPFLQ PLSFQSQGSPFKGPELSIASIHVPLESIKPSSALPVTAYDKNGF RILFHFAKECPPGRPDVLLVVVSMNLNTAPLVKSIVLQAAPVKS MKVKLQPPSGTELSPPFSPIQPPAAITQVMLLANPLKEKVRRLRYK LTFALGEQLSTEVEVDQFPFVEQWGNL
6800	404	1646	RRSPSTGLSPVPQSPSSPSLSDYSIPWSLLSGTIAWATPGK*AG *PQAW*LGLAPAIIFI/GLTRGRKQNKEMAEAGSGDVEDDAGDC SGARYNDWSDDDSDNESKSIWYPPWARIGTEAGTRARARARA RATRARRAVQKRASPNSDDTVLSPOELQKVLCLVEMSEKPYILE AALIALGNNAAYAFNRDIIRDGLGLPIVAKILNTRDPIVKEKAL IVLNNLSVNAENQRRLKVYMNQVCDTITSRNLSSVQLAGRLRL TNMTVTNEYQHMLANSISDFRFLFSAGNEETKLQVLKLLNLAE NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN FKWEENEPTQNGFEGGSLFFFLKEFQVCADKVLGIESHHDFLVK VKVGKFMAKLAEHMFPSQE
6801	2	1755	SAEEFESQQAQSVTMHVDVAESFEVLVDVYCTGRVSLSEANVERL YAASDMLQLEYVREACASFLARRDLNCTAILKFADAFGHRKL RSQAQSYIAQNFQQLSHMGSIREETLADLTLAQLLAVLRDLSD VESEQTVCHVAVQWLEAAPKERGPSAAEVFKCVRWMHFTBEDQD YLEGLLTKPIVKKYCLDVIEGALQMRYGDLKYSLVPVNSSSS /R*QQQLSCICSRKSTPETGYVCQGDGDLWTQPSLS\RYDPY SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDYILAAQPRKDLW VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPIITGVK LKEVECYSVQRNQWALVAPVEHSFYSFELIVVQNYLYAVNSKRM LCYDP SHNMWLN CASLKRSDFEACVFNDIYICIDI PMVKVYN PARGWRRISNIPLDSETHNYQIVNHDQKLLITSTTPQWKQNR VTVEYEDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLPEPG QSFINITEEDDARSESTEWDLGDFSELDSESGSSSSSFDDVEWVQ VAPQRNAQDQGS
6802	157	1341	ETFPFLFFLLSKTPGKTASMAHFVQGTSMIAAESSTEHEKCAE PSTRKNLMNSLEQKIRCLEKQKRELLEVNQQWQQFRSMKELYE RKVAELKTKLDAERFLSTREKDPHQQRKDDRRQREDRQRDLT RDRLOREBKEKERLNEELHELKEENKLLKGKNTLANKEKEHYEC EIKRLNKALQDALNICKSFSEDCLRKSRVBFCEEMRTEMEVLK QQVQIYEEDFKKERSDRERLNQEKEELQINETSQSQNLRLNSQ IKACQMEKEKLEKQLQMYCPCNCGLVFHLQDPWVPTGPGAVQ KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRE G
6803	1	2203	KLSGRPYRHMGLVGTSKLYDIRKTIFFTFPOFIDQQQFYLALDN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>KMIVEMLRITDLSYLCRWRMTGQPTITFPISHSMLEDEGTSINS SILAALRKMQDGYFGGARVQTGKLEFLTSCCTHLSFMDPGPE GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCDEVARVYLDHLL AHTAPHKPLAPTSQKGLDRFQAAVQTTCDLMSLVTKAKELHVQ NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD QSSEVDFKALVLQKETSLSLQEQADILYMLYTMKGPDWNTLYN ERSATVRELLTELYGKVGIRHGLIRYISGILRKKVEALDEAC TDLSSHQKHLTVGLPPEPREKTI SAPLPYEALTQLIDEASEGDM SISILTQEIIMVYLAMYMTQPGLFAEMFRLRIGLIQVMATELA HSLRCSAEAEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR PTDSNVSPAISIHEIGAVGATKTERGTGIMQLKSEIKQVEFRRLS ISAESQSPGTSMTSPSGSFPSAYDQSSKDSRQSQWQRRRLDG ALNRVPVGFYQKVKVLQKCHGLSVBGFVLPSSSTREMTPEIHK FSVHVES\VLNVLRLPEYRQLLVEAILVLTMLADIEIHSIGSII AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD SAPSGRFGTMTYLS\RAA\ATYVQEFPL\HSICAMQ</p>
6804	1	951	<p>GSFGKKEEKAKNKESLCMENSSNSSSDEDEETKAKMTPTKKYN GLEEKRSRLRTTGPYSGFSEVAEKRIKLNNSDERLQNSRAKDR KDVWSSIQQWPKKTLKELFSDSDTEAAASP PHPAPEEGVAEES LQTVAEESCSPPSVELEKPPPVNVDSKPIEKTVEVNDRAEFP SSGSNFS* IPLPYLHLNRLHQS* KQGSRRQSSVTVSEPLAPN QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF* CQCEL KQ**SARTRTS*KSLYRSEKSEKSGRRKFIKKAEEKP*SNSGK QQKEGKRHK</p>
6805	1539	206	<p>RQPDLYFGKSFQVSVSESSSLNSNDLPKPADGIKARNRNQNYL VPSVPLRILDHAFSTEKSADIVICDEECDSPEVSNQQTQEESE IEVHTAEDVPIAVEVHAISEDYDIETENSSSESLQDQDEEPPA KLCKILDKSQALNVTAQQKWPPLRANSSGLYKCELFENSKYFS DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSELY LHFQEHSCDEQYLQCFCEHETNDPEDLHSHVNEHACKLIELSD KYNGEHGQYSLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSGIIYLCQYW EYSTGQIEDLKIHLDFKHSADLPHKCSDCMLRFGNERELISHLP VHETT</p>
6806	272	3794	<p>VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV GFLGSGVFLALTTDACQKGLPKAQTGEVAAPKGWPPLSWLVI DGKHLAKPPKDWHLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA SLLAQCRALTQACGYSEATLTNVLDFKRDAGLWHGVLTSMVNR MHVSVVPYALMKANPLSWIQKVCIFYKARAALVKSMDHWSLLAQ RGQRDVSLSSRLMIVADGANPWSISSCDAPLNVFQSRGLRPEV ICPCASSPEALTVAIRPPDLGGPPPRKAVLSMNGLSYGVIRVD TBEKLSVLTVQDVGVMPGANVCVVKLEGTPYLCCTDEVGEICV SSATGTAYYGLGITKNVFEAVPVTGGAPIFDRPFTRTGLLG FIGPDHLVFI VGLDGLMVTGVRHNDVAVATLAVEPMKFVY RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLPCHN VLMCPHTCVTNLPKPRQKQPEVGPASMI VGNLVAGKRIAQASGR ELAHLEDSQARKFLFLADVLQWRAHTTDPHPLFLLNAGTGT STATCVQLHKRAERVAALMEKGRLSVGDHVALVYPPGVDLIAA FYGCLYCGCVPTVRPFPQNLGTTLPVKMIVEVSKSACVLT QAVTRLLRSKEAAAVIDRTWPTILDITDDIPKKKIASVFRPPSP DVLAYLDFSVSTTGILAGVKMSHAATSALCRS IKLQCELYPSRQ IAICLDPYCGIGFALWCLCSVYSGHQSVLPPELESNVSLWLS AVSQYKARVTFCCYSVMEMCTKGLGAQTGVLRMKGVNLSCVRTC MVVAERP\RIALTQSFSLFKDLGLPARAVSTTFGCRVNVIAIC</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>LQGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKIL PGVKVIIAHTETKGPLGDSHLGEIWWSSPHNATGYTVYVYGEAL HADHFSARLSFGDTQTIWARTGYLGFLRRELTDSAGGRHDALY VVGSLDETLELRGMRYHPIDIETSVIRAHRSIAECAVFTWTNLL VVVVELDGLEQDALDLVALVTNVVLEEHLVVGVVVIVDPGVIP INSRGEKQRMHLRDLADQLDPIYVAYNM</p>
6807	1444	606	<p>VGHDTVHAMFTCFPKCLGFSFPVNVTVSPRSESHTTTVSGGNG SVFQAGPQLQALANLEARRGSIGAAALSSRDVSGLPVYAQSGEPR RLTQAQVAAPFGENALEHSSDQDTWDSLRSPGFCSPLSSGGGAE SLPPGGPGHAEAGHLGKVCDFHLNHQQPSPTSVLPTEVAAPPLE KILSVDSVAVDCAYRTVPKPGPQPGPHGSLLTGECRLSLSGDLN RFPCEMEVHSGQRELESVVAVGEAMA\LKFPMGAMSYCLDRSR FLFRLPMGLSCPLQVQ</p>
6808	2063	737	<p>GVGGAASALARSRLASRLSSRRRTAPRSGAMQRLAMDRLML SRELSLYLEHQVRVGFPGSGVGLSLILGFSVAYAFYLLSSIAKK PQLVTGGESFSRFLQDHCPUVTETTYPTVWCWEGRGQTLRPF\ ITSKPPVQYRNELIKTADGGQISLDWFDNDNSTCYMDASTRPTI LLPLGLTGTSKESYILHMIHLEELGYRCVVFNNRGVAGENLLT PRTYCCANTEDLETVIHHVHSLYPSAPFLAAGVSMGMLLLNLYL GKIGSKTFLMAAATFSVGWNTFACSESLEKPLNWLFFNYLLTTC LQSSVNHKRMFVKQVMDHVMKAKSIREFDKRFTSVMFYQTI DDYYTADSPSRLKSVGIPVLCNSVDDVFSHPAIPDIETAKQN PNVALVLTSGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH ELS</p>
6809	939	65	<p>DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTKQPKRLHVSNI PFRFRDPLRQMF GQFGKILDVEIIFNERGSKGFGVTFETSSDADRAREKLNGLTIV EGRKIEVNNATARVMTNKTGNPYTNGWKLNPVVGAVYGPFFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHFRLLGP</p>
6810	939	65	<p>DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTKQPKRLHVSNI PFRFRDPLRQMF GQFGKILDVEIIFNERGSKGFGVTFETSSDADRAREKLNGLTIV EGRKIEVNNATARVMTNKTGNPYTNGWKLNPVVGAVYGPFFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHFRLLGP</p>
6811	1522	658	<p>DLVTVVSFVDCRVIASTHGH\KSWVSVAFDPTYTSVEEGDPME FSGSDEDFQDLLHFGDRADSTQCRLSRNSTDSPVSVTYRFG SVGQDTQLCLWDLTEDILFPHQPLSRARTHNVNMTSPAGSN GNSVTTPGNSVPPPLPRSNLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDKRKHHEKDKRHNHSMGHISKSSDKLNLVTKTK TDPAKTLGTPLCPMEDVPLLEPLICKIAHERLTVLIFLEDCCI VTACQEGFICTWGRPGKVVSFNP</p>
6812	4001	1682	<p>EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLLIHAVKHQDSGALVGFSCPGVQDSAAITIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHLILPEAKVQDSGEFECRTGVSFAFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQVEVE ESDFVLENEGPHRRLLVLPATQPSDGGEFQCVAGDECAFTVTI TDVSSWIVYPSGKVYVAARLERVVLTCELCRPAEVRWTKDGE EVVESPALLLQKEDTVRRLVLPVQLEDSEYLCIEDDESASFT VTVTBPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK DGLEVEESEALVLERDGPRLVLPAAQPEDGGEFVCDAGDDSA FFTVTVTPEPPVQFLAETTPSPLCVAPGEPVVLSCELSRAGAPV</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VWSHNGRPVQEGEGLELHAEGPRRVLCIQAGPAHAGLYTCQSG AAPGAPSLSTFTVQVAEPFVRVVAPEAAQTRVRSTPGGDLELVVH LSGPGGPVRWYKDGERLASQGRVQLEQAGARQVLRVQGARSGDA GEYLCDAPQDSRIFLVSVEEPLLVLKLVSDLTPLTVHEGDDATFR CEVSPPDADVTWLRNGAVVTPGPQRQSCCSYGGCRMCGQRKART CVSKWRQAEWVQRPACGCEVGSPPCTTLACPWFRMGSTSTASS MVSYWPTRAPTAARATTIAPWPGSA
6813	9	836	SSTQQRPGVPAGPRPLDGYLGVDHKLPMHCRDCALVTSSGHL LHSRQGSQIDQTECVIRMNDAPTRGYGRDVGNRSTSLRVIAHSSI QRILNRHDLNLSVQGTVFIFWGPSSYMRDRGKGQVYNLHLLS QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGWF TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYEYFPGPDEC TMYLSHERGRKGSHHRFITEKRVFKNWARTFNIHFFQPDWKPEPES LAINHPENKPVF
6814	3	737	KFRROEAN/ARERNRMHGLNDALDNLKRVVPCYSKTQKLSKIET LRLAKNYIWAELSEILRIGKRPDLTTFVQNLCKGLSQPTTNLVAG CLQLNARSFLMGQGGEEAAHTRSPYSTFYPPYHSPELTTPPGHG TLDNSKSMKPYNYCSAYESFYESTSPECASQFEGPLSPPPINY NGIFSLKQEBTLDYGNYNMGMYCAVPPRGLGQAMFRLPTD SHFPYDLHLSQSLTMQDELNAVPHN
6815	906	553	QGLDPASQTKVVELLKDGSGRRGDRSRDMAGGAGPRSESDLE DVGPATAEWNGDGSGLRRSGSGKLRDALRRSSEMLVKLQGGT PQEPNPRMKRASSLNFLNKSVEEPTQPGG
6816	1	803	NLLKTHKF\LLGQDEDSLHSVPVQMGNYQRYLKTASPLREID PDQPKRLHTFCNPFKQDKKGMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRRSMSLLLRKPQTPTVTNHHVGGKPPSASWFPSPYN LIKPTLVHTDATIIHDGHEEKMEHQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDFTSLSKDGLIQKPGSNAFVGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRF GRSK
6817	172	3457	LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGLGNFDSAKVPS DEYCPACKEKGLKALKTYRISFQESI\FLCEDLQCIYPLGSKSL NNLISPDL EECHTPHKPQKRKSLESSYKDSLLANSKKTNYIA IDGGKVLNSKHNGEVDYDTSNLPDSSGQNP IRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSQNEGCTSKLEMPLESKE TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYSQLSGVKDGDCCKLTSEIFAEIET CLNEVRDEIFISLQPLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSDWFECSQCGHQYQNRHMSLVTFNTVPEWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVGBLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFTWILDADGSWLECDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPKKTNDQHALSNE KPVSLTSCSVGDAASAEASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNLPPLTLEETIQKTASVSQLSNEAFL\LENKPV AENTGILKTNLLSQESLMASVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKETTADSQTTSKSLQNO SLKENQKKPFVGSWVKGLISRGASFMPCLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKASKPPPI SKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSYNGGISSANH EDLVEGQIHKRLKRLKRLKAEKKLAALMSSPQSRTVRSNLE QVPQDGS PNDCEI EDLLNELPYPIDIANESACTTVPGVSLYSS QTHEIILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNVCSPTKKNPCVQPDLSLTNNACVRTLN ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY
6818	2	240	RGFDKVLWT/LSGAVK\CVQFSRISPDGEEGYPGELKVWVTTYTL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPQI
6819	1	961	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAY GEEKKKKCNPYVKTYLLPDRSSQGRKKTGVQRNTVDPTFQETLK YQVAPQQLVTRQLQSVVHLGLTARRVFLGEVVIPLATWDFEDS TTQSFRRWHLRAKADKYEDSVQSNGLTVRAKLVLPSPRPRKIQ EAQEGTDQPSLHGQLCLVVLGAKNLPVRPDGTLNSFVKGLCTL DQQLRLKSPVLRKQACQWKHSFVFSGVTFAQLRQSSLELTVM DQALFGMNDRLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS PNLWTDMTLVH
6820	1014	340	GDMVYIVGHVPPGFFFEKTQNKAWFREGFNEKYLKVRKHHRVIA GQFFGHHTDSFRMLYDDAGVPIAMFITPGVTPWKTTLPGVVN GANNPAIRVFEYDRATLSLKDMVTYFMNLSQANAQGTPRWELEY QLTEAYGVPDASAHSMHTVLDRIAGDQSTLQRYVYVNSVSYSAG VCDEACSMQHVCMARQVDIDAYTTCLYASGTTFPVQPLPLLMAL LGLCT
6821	1088	518	EFDIYR/EVGGEFVFPVTRDDSSNGFPRTQHGFSPTVHPIQSPQN RFCVLTLDPELPAIATTLIDVLFYSHSTPKEAASSSPPESSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFHDHALVPEDGI GSVIEVLQRRQEGLAS
6822	1088	518	EFDIYR/EVGGEFVFPVTRDDSSNGFPRTQHGFSPTVHPIQSPQN RFCVLTLDPELPAIATTLIDVLFYSHSTPKEAASSSPPESSIT FFAFSLIEGYI\SIVMDAETQKKFPSDLLTSSSGELWRMVRIG GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFHDHALVPEDGI GSVIEVLQRRQEGLAS
6823	654	221	PPKLLSRWARMGHGBIV\LSDLNFPGLLHLPVVGWRSVQTAC GIPQLEAVLKLLPLDTYVESPAVMELVPSDKERGLQTPVWTE YESILRRAGCVRALAKIERFEFYERAKKAFVAVTGETALYGNL ILRKGVLALNPLL
6824	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLFPAGLLFLLLTQFGFRG ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV NWRFLPEALFLHRAFLALTLAHLTLLLFALCRWHRTGESILS LLRDPKRRKVPQPLTPNQIVSTLFTSNFIGICFPRSRLHYQFV WYFHTLPYLLWAMPARWLTHLLRLVLGLIELSWNTYPSTSCSS AALHICHAVILLQLWLGPQPPKSTQHSKKAH
6825	3	1173	SSGEFGLQASDIMWTISDTGNILILCSLMEPWALGACTFVHLL PKFDPVLVILKTLSSYPKSMGAPIVYRMLLQDLSSYKFPHLQ NCLAGGESILLPETLENWRAQTGLDIREFYGTETGLTCMVSKTM KIKPGYMGTAASCYDVQIIDDKNVLPPEGTEGDIRVKPIRPI GIFSGYVDNPKTAANIRGDFWLLGDRGKDEBGYPQFMGRADD IINSSGYRIGPSEVENALMEHPAVVETAVISSPDVPRGEVVKAF VILALQFLSHDPEQLTKELQHVKSVTAPYKYPKRIEFVLNLPK TVTGKIQRA\KLDRKWKMSGKAPCAVRHLRDIHLDSPLLSLSF PFGPLALPMDGYGDSLWEEHEYKFCIALVISTKLYHVRC
6826	2304	954	LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPREYDTP LYFEEDEVRLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA NKLPLKDSPTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPW DMCNHTNGLITTGYNLEDDRCEVALQDFRAGEQIYIFYGTRSN AEFVIHSGFFFDNNSHDRVKIKLGVS KSDRLYAMKA EVLARAGI PTSSVFALHFTPEPISAQLLAFLRVFCMTEEBELKEHLGDSAD RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIERDKS VLKNHDSVRAKMAIKLRLGEKEILEKAVKSAVNREYRQOME EKAPLPKYEESNLGLESSVGD SRLPLVLRNLEEEAGVQDALNI REAIKAKATENGLVNGENSI PNGTRSENE SLNQBSKRAVEDAK GSSSDSTAGVKE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6827	1	779	SSVVEFGLSVLGGFLFLFVLENNMLGGLLRHRLRPRCCRRKRRL ETRNLDPENGSGMALQPLQAAPEPGAQGGREKNSQHPALAPPG HQGHSHGHQGGTDITWVLLGDGLHNLTDGLAIGAAFSDGFSSG LSTTLAVFCHLPHLPGDFAMLLQSGLSFRRLLLSLVSGALGL GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALVMDLPAFPSS GAPAYA\HVLLQGLGLLGGCLMLAITLEERLLPVTTTEG
6828	3	1654	KSQHG/WILQLMHSCKEGYVKDLKGNPGLHRAMLDLDNGTRPSE LQHLSTASLKRGSFQSGRDDTWRYKTPHRVAFVEKLTKLVL S QLPNFWKLWISYVNGSLFSETAEKSGQIERSKNVRQRQNDPKKM IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEVKCELSGQWLA HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLRVCVMATLQH TAEIIRLAEKEDWIDNEGLTSLPCQPEQCIVCSLQSLKGVLE CKPGEASVFQPKTQEEVCQLSINIMQVPIYCLEQLSTKPDADI DTHLSVDVSSPDLFGSIHEDFSLTSEQRLLIVLSNCCYLERHT FLNIAEHFEKHNFQGIKTIQVSMASLKBELDQRLFENYIELKAD PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKEALVNI IAVHAEV FTISKELVPRVLSKVIEAVSEELSRLMQCVSSFSKNGALQARLE ICALRDTAVVYLTPEKSSSFQKQALEALPQLSSGADKKLLEELLN KFKSSMHLQLTCTFQAASSTMMKT
6829	1	782	MRMEAGEAAPAGAGGAGGAGGKWRVRLNVGGTVFLTRQTLCR EQKSLFSLRCQGEELQSDRDETGAYLIDRDPYTFGPILNFRHRG KLVLDKDMAEGVLEAEFYNIGPLIRIKDRMEEKDYTVTQVP PKHVYRVLQCCQEELTQMVTMSDGRFEQLVNISSYNYGSED QAEFLCVSKELHSTPNGLSSSESRKTKSTEEQLEEQQQEEVEV EEVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLQGLGVPI
6830	1	939	MRPGSVENLSIVYRSRDFLVVNKHWDVRIKAWRETLTLQKQL RYRFPPELADPDTCYGFRFCHQLDFSTGALCVALNKAAGSAYR CFKERRVTKAYLALLRGIHQESRVTISHAIGRNSTEGRAHTMCI EGSQGCENPKPSLTDLVLEHGLYAGDPVSKVLLKPLTGRTHQI RV\HCSALGHPVVGDLTYGEVSGREDRPFMRMLHAFYLRIPDTT ECEVECTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE DRGPRPGSPSALLPGPGRPPPTKPPETEAQRGPCLQWLSEWT LEPDS
6831	3	1087	SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF NVAEKPADHSLSEVLKLTADPRGTLVKSGDQGNVKEKSMILSN VEDLQPKFISEVSRDYGKKEISGDSEEMNINSVVTADGENL EIQSYSLIGBKLVMEEAKTIVPPHVTDSKRVQKPAIAPPKSWNI SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE SEKPEIILPVEESKGLIDFSEDRLKKEMQNPTSLKISEEETK LRSVSPTEKKDNLENR\SYTL\AEKKVLAEKQNSV\APLELRDS NEIGKTQITLGSRTSELKESKADAMPQHfyQNE DYNERPKIIVG SEKEKDEKKKK
6832	1809	412	MGSGLISGFPQDNGEALKEPERAQEHSLEPNFAGGQHFPBYLLV VSLKKKRSEDDYEPIITYQFPKRENLLRGQEEEEERLLKAIPLF CFPDGNWASLLEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG PRLPKVYCIISICIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL REAFAFPAGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFFSL LHCLSFQILQIFASAVLERKIIFLAEGSLTSLQCIHAAAALLY PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRQQEVMDSPEM EVLLVNLCEGTFILMSVGEKIDILPPLQDDILDLSLGGQGINELKT AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK ALTSKTNRRFVKFKVTQLFSLFIQEAESKNPPAGYFQOKILE YEEQKKQ/TETGKNCEIRAVVNKND
6833	1	1129	PLMTLSQCGGIPGHGSHGGHGHGHLPGKPRVKSTRPGSSDIN VAPGEGPDQEEENTLVANTSNNGCLKLDPADPENPRSGDTVEV QVNGNLVREPDMHELEDRAQLNMRGVFLHVLGDALGSVIVVV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NALVFYFSWKGCSEGDFCVNPFCFDPCKAFVEIINSTHASVVEA GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALILLQTVPKQID IRNLIKELRNVEGVVEVHELHVWQLAGSRIIATAHIKCEDPTSY MEVAKTIKDVFNHGHGIIATTIQPEFASVGSKSSVVPCELCARTQ CALKQCCGTLPOAPSGKDAEKTPAVVISCLLSNNLEKKPRRTK AENIPA\VVIEIKN\IPNK\QPESSL
6834	78	1151	AGQERPAPIWRLLWLTPSPSRKAEPAHIPINR*GA*E*RGGLP LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGP CSKVLVSGARGIVGTTVQVLVEAQPLLLFTGVWGLNLRAGEE SRAL*LIBEVTQVRDAHLGNNAVVGCAQLSQGVGSALAKALLE AAAAVRDCKEVLTVSGDKQQAEBVSRL*VRDVCVEAGCVFEGQ AHGRPGLALAKGRGGTNEVEEQVQVDGVQKLVLSAHECHELVAG QQDGEDQAARTRLQAGAHSVAHGRRQGGAPCRPHQEAGVSCHE LQQVVGDAI*ARE*APQIVLLLEDVAQLRTGKKA*DLVVDVE QLLRQL
6835	1	834	GIPAAADR\EASLELIKLDISRTFPNLCIFQGGPYHDMHSILG AYTCYRPDVGYYVQGMFIAAVLILNLDADAFIAPSNLLNKPCQ MAFFRVHDGLMLTYFAAEVFFFEENLPKLFHAFKKNLTPDIYL IDWIFTLYSKSLPLDLACRIWDVFCRDGEBFLFRTALGILKLF DILTMDFIHMAQFLTRLPELPAEELFASIIATIQMSRNKKWA QVLTALQKDSREMRGKSVPPTLRLQREFALGTNQSPMPRLCC FRLTPGQPRRTDAL
6836	1	850	MSCGRPPFDVDMITLKV\DNLTyrTSPDLSRRVFEKYGRVGDV YIPREHTKAPRGFAFVRFHDRRDAQDAEAMDGAEALDGRELRV QVARYGRDLPRSRQGRRHAGPEAA/RYGRRSRSYGRRSRSP RRHRSRSGPSCSRSRSRRYRGSRYSRSPYSRSPYSRYSRS PYSRYSRYRSGSGSHYSSSGYSNRYSRYSRSHSRSHSKSGSTS SRASSTSKSSSARRSKSSSVSRSRSRSSSMTRSPPRVSKRKS KSRSRSKRPKSPPEEGQMS
6837	1	1369	TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSSGSKASGP PNPQAQGDGTSLSPNYTLSTSGNDGKPVSGGGGRGRGRKRDS GHVSPGTFFDKYSAAPDSGGAPGVSPGQQASGAAGVSSAGET RGAPTPEKALTSPSWKGAEALLGDQPDIGSLDGGAKSDSSS PNVGEFASDEVSTSYANEDEVSSSDNPQALVKASRSLVVTGSP KLPPRGVAGEHGPKAPPALGLGIMSNSTSTPDSYGGGGGPGH PGTPGLEQVVRTPTSSSGAPPDEIHPLLEILQAQIQLRQQFSIS EDQPLGLKGGKKGECAGVAGSQAQNGDSELGSCCEAVKSAMSTI DLDSLMAEHSAAWMPADKALVDSADDDKTLAPWEKAKPQNPNS KEAHDLPANKASASQPGSHLQCLSVHCTDDVDGAKARASVPTWR SLHSDISNRFGTFVAALT
6838	16	499	LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMETITLTWQDEE DQTRDMELVETRPAGDGTQKWAADVVPSSGEE/Q/RYMCHVQHE GLPEPLTLRWEQSSQPTIPVIGIVAGLVLLGAVVTGAVVSAMC RKKNSDRVSYSEAASSDHAQGSVDVSLTACKV
6839	1	1195	AAPAGGGPDPEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIHG RGNFPTLSVQPRQIRAGGPPHGGAG\IHVHRVRLHGSAAASHVL HPESGLGYKDLDLVFRMDLRSEASFQTKAVVLACLLDFLPAGV SRAKITPLTLKEAYVQKLVKCTDSRWSLISLNSKSGKNVELK FVDSVRRQFEFSIDSFQIILDSLLLFQGCSTPMSEAFHPTVTG ESLYGDFTEALEHLRHRVIATRSPEIRGGGLLYCHLLVRGFR PRPSTDVRLQRYMCSRFFIDFPDLVEQRTTLERYLEAHFGGAD AARRYACLVTLHRVNVNESTVCLMNHERRQTLDLAALALQALAE QGPATAALAWRPPGTGVPATVNYVTPVQPLLAHAYPTWLP CN
6840	4254	2061	ELQGDFSVPDVPKSMWCENSICVGFKRDIYILRVDGKGSIKEL FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TDIPVAMEHQPPYIIAVLPYVEIRTFEPRLLVQSIQLQRPFI TSGGSNIIVASNHFWRLIPVPMATQIQQLQDKQFELALQLA EMKDDSDSEKQQQIHIIKNLYAFNLCQKRFEDESMQVFAKLGTD PTHVMGLYPDLLPTDYRKQLQYPNPLEVLSGALEKAHLALIDY LTQKRSQVLVKLNDSDHQSSSTSPMBGTPTIKSKKKLLQIIDTT LLKCYLHTNVALVAPLLRLNNHCHIEESEHVLLKAHKYSELI LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN FKGLAIPYLEHIIHVWEETGSRFHNCILQYCEKVQGLMKEYLL SFPAGKTPVPAGEEEGELGEYRQKLLMFLISSYDPRGLICDF PFDGLLEERALLGRMGKHEQALFIYVHILKOTRMABEYCHKHY DRNKDGNKDYLSLLRMYLSPPSIHCLGPIKLELLEPKANLQAA LQVLELHHSKLDTTKALNLLPANTQINDIRIFLEKVLLENAQKK RFNQVLKLLHAEFLRV\QEERILHQQVKCIITEKVMCMVCKKK IGNSAFARYPNGVVVHVFCS\KEVNPADT
6841	1	3206	TPSTTGKSNTPSSVPSAAVTPLNESLQPLGDYGVGSKNSKRA REKRDSDRNMEVQVTQEMRNVSIGMGSSDEWSDVDIIDSTPELD MCPETRLDRTGSSPTQGI VNKAFGINDTSLYHELSTAGSEVIGD VDEGADLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIA KVDQLSGEQEVLGELEAAKQAKVKLENRIKELEELKRVKSEA IIARREPKEEAEDVSSYLCTESDKIPMAQRRRFRVEMARVLM RNQYKERLMELQEA VRWTE MIRASREHPSVQEKKSTIWQFFSR LFSSSSSPPPAKRPYPSPGNIHYKSPPTAGFSQRRNHAMCPI SAG SRPLEFFPDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD QFTVCNAHVLCISSIPAAASDSDYPPGEMFLDSVDNPEDPGADGV LAGITLVGCATRCNVRSNCSRGDTPVLDKGQGEVATIANGKV NPSQSTEEATEATEVEPDGPSEPETATLRPGPLTEHVFTDPAPT PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMTWL AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRLVALAD GTLAI FHRGEDGQWDLNHYHMDLGHPHHSIRCMVVDYDRVWG YKNKVHVIQPKTMQIEKSFDAHPRESQVRQLAWIGDGVVVSIR LDSTLRLYHAHTQHLLQDVDI EPYVS KMLGTGKLGFSFVRITL LVAGSRLWVGTVNGVVISIPLTETVVLHRRGQ\LLG\LRANKTSP TSGE\ARPGG\IIHVY\DDSSDRAARSFI PYCSMAQAQLCFH GHRDAVKFFVSVPGNVATLNGSVLDSPAEGPGPAAPASEVEGQ KLRNVVLVSGGEGYIDFRIGDGEDDETEGAGDMSQVKPVL SKA ERSHIIWQVSYTPE
6842	3	926	RCQQLSATILTDHQLERTPLCAILKQKAPQYIRAKLRSYKP RRLFQSVKLHCPKCHLLQEVPHGEDLDIIFQDQATKTPDVKLQN TSLYDSKIWTTKNQKGRKVAHVFKVNGILPLSNECLLLIEGGT LSEICKLSNKFNSVI PVRSGHEDLELLDLSAPFLIQGTVHHYGC KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFMFTT LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFC PPGIKIDAYPWLECFIKSYNVNTNGTDNQICYQIFDTTVAEDVI
6843	2	851	NHRKVLGAKRYECNECGKSFAYTSSLIKHRRHTGERPYECSE CGRSPAENSSLIKHLRVHTGERPYECVECGKSPRRSSSLQHQH VHTRERPYECSECGKSFSLRNLIIHQVRHTGERHECGCGKGSF SRKSSLIHLRVHTGERPYECSDCGKSFENSSLIKHLRVHTGE RPYECIDCGKSFHSSSFRRHQVRHTGMRPYK*SKFWKFCPGF LLLQGRVHTGSRCECDKWGIFFS*NASFFT*KSAPTEEVFFE CNECEKAFSPLSLVTITFT
6844	244	642	EHQLAGFELRKTQTSMSLGTTRKTRDRVKSTAYLSPQLEDVFF QYDVKSEIYSFGIVLWEIATGDI PFQGCNSEKIRKLVAVKQOE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PLGEDCPSELREITDECRAHDPSVRPSVDEILKKLSTFSK*CIK I
6845	3	1519	VAVRDECYWRHVFDQDLWMLLFILMCHPETAARLEYRIRTLG GALENAQNLYGYQGAFAWESADSGLEVCPEDIYGVQEVHVNGAV GLAFELYHTTQDLQLFREAGGWDVVRVAEFWCSRVEWSPREE KYHLRGVMSPDEYHSGVNNVSYTNVLVQNSLRFAAALQDGLGP IPSQWLAVADKIKVPFDVEQNHFPEFDGYEPGEVVKQADVLLG YPVPFSLSPDVRKNLEIYEAVTSPQGPAMTWSMFVAGWMLKD AVRARGLLDRSFANMAEPFKVVTENADGSGAVNFLTGMGGFLQA VVFSGCTGFRVTRAGVTFDPVCLSGISRVSVSGIFYQGNKLNFSF SEDSVTVEVTARAGFWAPHLEAELWPSQSRLSLPGHKVSPFRS AGRIQMSPPKLPSSSSSEFPGRTFSDVRDPLQSPWLTGSSSP TESLTVDPASE*SGTGASETSLQPSLWFRLLHPPLLGTLACHPS PAARLSGKVHAAPFEKAFCL
6846	213	1258	LYFLKTIK*LNRLAHP*YENEKLTCLRNTIMEQYTRTEESARG IIFTKTRQSAYALSQWITENEKFAEVGVKAHLLIGAGHSSEFKP MTQNEQKEVISKFRGTGKINLLIATTVAEEGLDIKECNIVIRYGL VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDPREKM MYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTNRNIAKHK NNPSLITFLCKNCVLAACSGEDIHVIEKMHVNMTPFEKELYIV RENKTLQKKCADYQINGEIIICKGQAWGTMMVHKGDLPLCKIR NFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCFLSDED
6847	1450	348	SMCWNSDRLEMLDIDLALILYPPSYVPTGHLSDDSLRSKYCLT WFEDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQC PFAYGTLTVRSLDTRHCLNEFNFPDPYKVKQRENGVALRCF PGVVRSLDALGWEERQALALVKGLLAGNVFDWGAKAVSAVLESDF YFGFEEAKRKLQERPLVDSYSEWLQRLKGPCHKALIFADNSG IDIILGVFPFVRELLLRGTEVILACNSGPAALNDVTHSESLIVAE RIAGMDPVVHSALREERILLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE
6848	19	16	AMWNSLDGIRNTVLSNPKKRNLTSLAMLKSLQSDTLHDADSND LKVIIISAEGPVFSSGHDLEKLTTEEGRDYHAEVQTCVKMMH IRNHPVPVIAVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVS LGKATFFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH
6849	70	821	SLGVDGSCLEQGSFAPRPQTDTSF*PVGNNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNNINHEGLECLRLLNEIIADFDLLSK PKFGSVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGFPVAVGVIQAQKPQ YDIWGNTVNVASRMESTGVLGKIQTVEETAWALQSLGYTCYSRG VIKVGKQQLCTYFLNTDLTRTGPPSATLG
6850	2	1235	ARGLNHEWTFEKLQHISRNAQDKQELHFLMLSGVDPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCCHPAKVEQTAFSFL RDHLRCLHVKFTDVAETPAWVYLLKNLRELYLIGNLSENKMI GLESRLRELRLKILHVKSNTLKVPSNITDVAPHLTCLVIHNDGT KLLVLNSLKKMMNVAELELQNCLELRI PHAIFSLSNLQELDLKS NNIRTIEEIIISFQHLKRLTCLKLVHNKIYVTPPSITHVKNLES YFSNNKLESPLPAVFSLQKLRLCDVSYNNISMIPIEIGLQNLQ HLHITGNKVDILPKQLFKCIKLRTNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHFLDFTLPLEVK EALNQDINIPFANGI
6851	1765	660	VSAQVSAREGENCLGWNADSSQESYKSLLEEABDCYPPSLLTLD LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGMMAAGLMIGAGA CYCVYKLTIGRDDSEKLEBEGEEWDDQELDREEDPIWDFET

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MARPWTEDGDWTEPGAPGGTEDRPSGGGKANRAHPIKQRPFPYE HKNTWSAQNCCKNGSCVLDLSKCLFIQGGKLLFAEPKADAGFPFSQD INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESGGQIKM YINEVCRKTVSRCCNSFLQQAGLNLISMTVINMMLAKSASDLK FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLFSPMSL FIRNGNRBILLETAP
6852	1	407	RTRGEETYANFIKHNDGKNIFYAARTPATLFAVMFAMYIISGLT GFIGLNSIAVLNCLVMGLALIFLCTWAYVKYSGEFREIGTVIDQ IAETLWEQVLKPLGDNLMENIRQSVTNSIKAGLTDQVSHHARL KTD
6853	3	469	GDSCAVCIELYKPNLVRILTCHNFIHFKTCVDPWLEHRTCPMC KCDILKALGIEVDVEDGVSLSQVPVSNEIPNSASSHEEDNRSSET ASSGYASVQGTVEPPELHHVQSTNESLQLVNHEANSVAVDVIPH VDNPTFEEDETPNQETAVEREIKS
6854	1148	585	HESYIGTFDPGELCVCAAIQWLQDNSASYFLNRKLIVYEPSTQAK PVKNTFLRMWYSHHIYQQDLRKKILDVGRKLDVTGFCMTGKPG IICVEGFKHECEFFWHTIRYPNWKHISCKHAESVETEGNGEDLR LFHSFEELLLEAHGDYGLRNDYHMLNGQFLBFLKKHSEHVFI LFGIESKSSDS
6855	1913	1148	GRVGGRVGRITCSPLSGANEYIASTDTLKTEEVLLFTDQTDLLAK EEPTSLFQDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNLILNDRGHI QLTYFSRWSEVEDSCSDAIERMYCAPEVGAITEETACDWWSL GAVLPELLTGKTLVECHPAGINTHTLNMPEWVSEEARSLIQQL LQFNPLERLGAGVAGVEDIKSHPPFTPDVAELMR
6856	1617	997	VTQLYVSVDASTKDSLKKIDRLFKDFWQQFLDSLKALAVKQQR TVYRLTLVKAWNVDLQAYQLVSLGNPDFIEVKGVTYCGESSA SSLTMAHVPHWEEVQFVRELVDLIPEYEIACEHEHNSCLLIAH RKFKIGGEWTTWINYRPFQELIQEYEDSGGSKTFSKDYMARTP HWALFGASERGFDPKDRHQRKNKS KAISGC
6857	1	617	KGPEATAMVVCVSHPCNRQNHKPSHSAQTCWGSPTPASAPNH KLMAEQGKTLPSATEDAKEGLEAQISRLAELIGRLESKALWF DLQQLSDEDDGTMHLQLVRQEMAVCEQLSEFLDSLRLQYLRT TGVNRCFHITAVRLSDGFTFVIYEFWETEAWKRLQSPCLKAF RHVKVDTLSQPEALSRLVPAANCTVGRD
6858	2	669	RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA LRCVQTAKLILEELKLEKKIKIRVBPGEFTWKWEAGKTTPTLM SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ IVNTCPQDTGVILIVSHGSTLDSCTRPLGLPPRECDFPAQLVR KIPSLGMCFCENKECKWELVNPPVKTLTHGANAAFNRNWNIS GN
6859	1	1150	GETMFKKAKTKAKKKPRKRSDDSGGYNLSDIIQSPSSGTLKSG KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGPHSDKIE AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQIPSNRIDTT SSASVWAGSPSPVSPVVDLRTIMEIEESRQKCGATPKSHLGKT VSHGVKLSQKQKMLALTTKENNSGMNSMETVLFTPSKAPKPVN AWASSLHSVSSKSPRDFLEKKSVTSHSSGDHVKVVSFKGIEN SQAPKIVRCSTHGTGPEGNHISDLPLDSPNPWLSSTVAPSM VAPVTFASIVEEELQOEALIRSREKPLALIQIEEHAIQDLLVF YEAFGNPEEFVIVERTPQGPLAVPMWNKHGC
6860	1889	1515	DKDKKRQKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP MGSPVLGQQHMGIRPAGPMGGMGMNMGMGQWHYM
6861	1889	1515	DKDKKRQKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MGSFVLDGQQHMGIRPAGPMSGMGMTMGMDGQWHYM
6862	2	471	EEIDREFHNKLLKEDKLEKQKPVNGEDKGDGSDVTQNSEGNA DEEDPLGPNCCYDKTSTFFDNISCDNRERRPTWABERRINAET FGIPLRPNRGRGGYRGRGGLGFRGGRGRGGGRGGTFTAPRGFRG GFRGGRGGREFADFEYRKTTAFGP
6863	2216	487	PQEPALKSEFSQVANSNTIPLPLPQNTCKDNGPCKQVCSTVGGSS AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSF YCVNHTVLCAAGYILNAHRKCDVINECVTDLHTCSRGEHCVNTL GSFHCYKALTCEPGYALKDGECEVDCEAMGHTTCQPGFLQONT KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI NTVGSYTCQRNPLICARGYHASDDGTCKVDVNECETGVHRCGEG QVCHNLPGSYRCDCKAGFQORDAFGRGCDVNECWASPGRLCQHT CENTLGSYRCSCASGFLLAADGKRCEDVNECEAQRCSQECANIY GSYQCYCRQGYQLAEDGHTCTDIDECAQAGILCTFRCLNVPGS YQACACPEQGYTMTANGRSCKDVDECALGTHNCSEAECHNIQGS FRCLRFECPPNYVQVSKTKCERTTCHDFLECONSPARITHYQLN FQTGLLVPAHIFRIGPAPAFGTDTIALNIKNGEEGYFGTRRLN AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFT TFAL
6864	2	2933	LADSSPSNLQITIKELLSMHQPDPAITKEFDYLPVDSRSSSG FVGLRNGGATCYMNAVQQLYMQPLPESLLSVDNDDTNPDSDV FYQVQSLFGLHMEKSLQYYVPENFWKIFKMWKELYVREQQDAY EFTSLIDQMDYLLKMGDRDQIFKNTFQGIYSQKICKDCPHRY EREEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYCEKCK EKRIITVKRTCIKSLPSVLVIHLMRFGFDWESGRSICYDEQIRFP WMLNMEPYTVSGMARQDSSSEVGENGRSDVQGGGSPRKKVALT ENYELVGVIVHSGQAHAGHYYSFIKDRRGCKGKWKYKFNDTVIE EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAIMLFY QRVSDQNSPVLPPKSRVSVVRQEAEDLSLAPSSPEISPSQSPR PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYQMVREDNLKF MKNRDVSDDYFSFVLASLASLNATKLKHPYPYCPMAKVSLLQALQ FLFQTYLRTKKLVRDTEEWIATIEALLSKSFDACQWLVEYFIS SEGRELKIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKS HQLLEVLALLDKDVPENCKNCAQYFFLNTFVQKQGIKAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPIISAPSSPLPLHEEVEALLFM SEGKPYLLEVMFALRELTSLLALIEVMVYCCPCNEHFSFTMLH FIKNQLETAAPPHELKNTFQLLHEILVIEDPIQVERVKFVFSTEN GLLALMHSHNVDSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSNAVQWLQKKMSEHYWTLQSNVSNETSTGKTFTORTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSSESPMMIGEL RSDLDVDP
6865	1820	1242	DPERWKHLSKVTPPGSSVSTTFVQVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWKYGVRSYLHLFYEGYAVPPKLEBIGEGEFLV LDQRAADYNQALGTCLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS
6866	1571	495	DCPRPYTLYGLRATCMRDLDWAWINAVSAFAKALEQDLVNIKF IEGMEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFFGILHEPMADLVALG SLVDSSGHIIVPGIYDEVVPLTEEEINTYKAIHLDLBEYRNSSR VEKFLFDTKEEILMHLWRYPSSLIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSNKMVVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF QEIVHKSVVLLIPLGAVDDGEHSQNEKINRWNYIEGTLFAAFPL EMAQLH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6867	2833	1704	GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQSP LQSAESSPTAGKKLEVPPEEEEEAEWVALLGRIFWDFLGEK YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILQAF KPYVDHQGLWIDLEMSYNGSFLMTLETMNLTKLGKEPLVEALK VGEIGKEGCRPRAFCLADSDEESSAGSSEEDDAPEPSGGDKQL LPGAEGVVGHRSTS KIMRFVDKITKS KYFQKATETEFIKKKIEE VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVMYGRKPPHVELK ARPKLGEREVLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM HSANDPRSTSCLLKDPPEAADQP
6868	1	346	RPTRPPTREPIKNLILPYISDMNFVQDLCEDFYELFKTDKGF KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQ GSQGRIVHLSNSFTQTVNCRKPPFSSW
6869	3	1619	MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES KEISVEKSLYKEIQCLVGNKGIEVFYKIQEDVYETLKDRYPS FIVSDLYEKLKIEEEKHASQMISNKDEMGRDEAGEEAVDDGT NQINEQASFAVNKLRELNEKLEYKRALNSIQNAPKPKKIVSK LKDEIILIEKERTDLQLMARTDWWCENLGMWKASITSGEVTEE NGEQLPCYFVMVSLQEVGVETKNWTVPKRLEFHNLRKLSEC VPSLKKDQLPSLSKLPKSIDHTFMKFNQNLNKLQNLSDER LCQSEALYAFSPSPDYLVKIDVQGGKNSFSLSSFLERLPRDF SHQEEETEEDSDLSYDGDVDRKDALAEPCFNLIGETFEELRG FKWVRRTLIALVQVTFGRITNKQIRDTVSWIFSEQMLVYYINIF RDAFWPNGKLAPPTTIRSKESQETKQRAQQKLENI PDMLQSL VGQQNARHGIKIFNALQETRANKHLLYALMBLLLIELCPELRV HLDQLKAGQV
6870	1	1566	MAAVVAATRWQLLLVLSAAGMGASGAPQPPNILLMLDDMGWG DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANPLCSPSRAALLT GRLPFRNGFYTTNAHARNAYTPQEI VGGIPDSEQLLPELLKKAG YVSKI V GKWHLGHRPQFHLKHGFDWFGSPNCHFGPYDNKARP NIPVYRDWEMVGRYYEEFFINLKTGEANLTOIYLQEAALDFIKRQ ARHHPFFLYWAVDATHAFVYASKPFLGTSQRGRYGDVAREIDDS IGKILELLQDLHVADNTFVFFTSNGAALISAPEQGGSGNGPFLC GKQTTTFEGGMREPALAWNPGHVTAGQVSHQLGSI MDLPTTSLAL AGLTPPSDRAIDGLNLLPTLLQGRMLMDRPIFYRGTLMATLGL QHKAHFWTWTNSWENFRQIDFCPGQNVSGVTTNLEDHTKLPL IFHLGRDPGERFPLSFASAEYQEALSRITSVVQQHQAELVPAQF QLNVCNWAVMNVAPPGECKLGKCLTPPESIPKKCLWSH
6871	209	1126	RMSLNPPIFLKRSEENSSKFVETKQSQTTSIASBDPLQNLCLAS QEVQLQAQSGRSKCLKCGGSRMFYCYTCVVPVENVP IEQIPLV KLPLKIDI I KHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPYB EKDHEVALIFPGPQSIKIDISFHLQKRIQNNVRGKNDDPKPS FKRKRTEEQEFCDLNSCKCKGTTLKIIIFIDSTWNQTNKIFTDE RLQGLLQVELKTRKTCFWRHQKGPDTFLSTIEAIYYFLVDYHT DILKEKYRGQYDNLFFYSFMYQLIKNAKCSGDKRTGKLTH
6872	880	459	FGLLMVVLSLIFMKGNCVREDLIFNLFKLGLDVRETNGLFNGT KKLITEVFRQKYLEYRRIPYTEPAEYEFWNGPRAFLETSKMLV LRFLAKLHKDPQSWPFHYLEALAECEWEDTEDEPDTGDSAHG PTSRPPPR
6873	1929	955	DEQAVLCSKDKTYDLKIADTSNMLLFI PGCKTPDQLKKEDSHCN I IHTEIFGFSNNYWE LRRRRPKLKKLLMENPYEGPDSQKEK DSNSSKYTTEDLLDQIQASEEIMTQLQVLNACKIGGYWRILEF DYEMKLLNHVTQLVDSSESWSFGKVP LNTCLQELGLEPEEMIEH CLKCYGKKYVDEGEVYFELDADKICRAAARMLLQNAVKNLAEF QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDLPE DNQERFNSLFSLEKWTED IAPYIQDLCEGKQTIGALLTKYSH SSMQNGVKYNSRRPIS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6874	1	307	DSIAHDVNSAAVNVEEGTKNLGKAAKYKLAALPVAGALIGGMVG GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMMKELTS SCPDLPSTQDKKCS
6875	1688	349	VIGTGERGNSASEKWEIMFNEELGDPFIIHISISLLNAEHSIA TLLLRIEKBELDMKGSIFYVSLWVTISKKNQDNKKYBIIKRDI LRGKSVPHYAAIEPDGNLMIVSYKSLTFVQAGQDLEENMDEDI SEKIKEPLYWQOTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKNEGLTW PELVIGDKQGELIRDSAQCAIAERLMHLLTSEELNPNPDKEKPP CNAQELEECDIFFEESSSLCRFDGNTLKTTHVNLGSGNQYLFVS IVDPKEMPCFCLRHVDALLWOPHSSKQDDMWEHIATFNALGYV QASKRDKKFFACAPNYSYAALCECLRRVFIYRQAPAMSTVLNLR KEGRQVGQVAKQVASLETNDPILGFQATNERLFVLTTKNLFIL KVNTEN
6876	41	1285	VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS LHTKPRMPPCDFMPERYQVIFLVNSGSEANLAMLARAHNNI DIISFRGAYHGCSPTLGLTNVGIYKMLPGGTGCQPTMCPDVF RGPWGGSHCRDSPVQTRKCSAPDCCQAKDQYIEQFKDTLSTS VAKSIAGFFAEPIQGVNVVVQYPKGFLEAFELVRARGGVCIAN EVQTGFGRGLGSHFWGFQTHDVLDPDVTMAKIGINGFFMAAVIT PEIAKSLAKCLQHFNFTFGGNPMACAIGSAVLEVIKEENLQENSQ EVGTVMLLKFAKLRFDEFIIVGDVVRGKGLMIGIEMVQDKISCRPL PREEVNQIHEDCKHMGLLVGRGSIFSQTFRAPSMCITKPEVDF AVEVFRSALTQHMERRAK
6877	1	778	GTSPSPARAYAPPTERRKRYQNVSIQEGEGFEINLDRKLKTP QAKLFTVPSEALAIATAVEWDSQDDTIKYTYMHLTTLNLTSLDN PTQRNKDQLIRAAVKFLDITDIYRVEEPETLVELQRNEWDPII EWAERKYGVEISSSTSIMGPSIPAKTREVLVSHLASYNWALQG IEFVAAQLKSMVLTGLIDRLTVEQAVLLSRLEEEYQIQKWN IEWAHDYELQELRARTAGTLFIHLCESTTVKHKLKE
6878	931	263	QTLQGDPKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN LEEDTVTLEVLVAPVPSCEVPSSALSGTVVELRCQKBNPAP EYTWFKDGIIRLENPRLSQSTNSSYTMNTKTGTQLQFNTVSKLD TGEYSCEARNSVGYYRRCRPGKRMQVDDLNISGIIAAVVVVALVIS VCGLGVCYAQRKGYFSKETSFKQSNSSSKATTMSENDFKHTKSF II
6879	3	845	IRVIGESDIMQEFLESSENYNGVSDVELRVALPDGTTVTVRVK KNSTTDQVYQAIKAVGMDSTTVNYFALFEVISHSFVRKLAPNE FPKLYIQNYTSAVPGTCLTIRKWLFTTEEEILLNDNDLAVTYF FHQAVDDVKGYIKAEKSYQLQKLYEQRKMVMYLNMLRTCEGY NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWKIFTYPFNYMHE CFERVFCELKWRKEEY
6880	2110	1437	RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS NRDQIKNCGFFYGHRFASVALIFVTAFOGLSVAFILKFLDNMFH VLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLISIFINAS KPQVPEYAPRQERIRDLGNLWERSSSGDGEELERLTKPKSDESD EDTF
6881	2638	2244	NDSKWEDIHVITGALKMFFRELPELFTFNHFNDFVNAIKQEP QRVAARKDLIRQLPKPNQDTMQILFRHLRRVIEENGEKNRMTYQS IAIVFGPTLLKPEKETGNIAVHTVYQNVQIVELILLELSSIFGR
6882	1	850	GTPEAQLWITYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN QEGNMVTAQEPRLVLISLTCDGDTLTLASAAYTKDLLPIKTPT TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSQPYRLVHFEPH MRPRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			KVKATNFRPNIVISGCDVYAESDWEDELLIGDVBLKRVMACSRCLTTVDPTDGVMSRKEPLETLKSYRQCDPSEKLYGKSPLEFGQYFVLENPGTIKVGDPVYLLGQ
6883	2794	2256	NSKLLKLNQNLKLFITLTQVLSLHGWGPGIHLQKEGAFPVTONRALQLLYDLRYLNLIVLTAKGDEVKSGRSKPDSEKVTDLHLEALIDPFLLDVFTPHLSNLHRLVQRTSVLFGLVGTENQLAPRSSFTNSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYDANC
6884	2	99	EFERVTAEAVKPRETSEPRAAAQRFCEKFPFL
6885	297	1554	STGQFHWHTDLHLDPTVYHITDDHTKVCASSKGANASNPGPFQDVLCDSPPYQLILSAFDFIKNSGQEAASPMIWTGDSPPHVPVPELSTDVINVITNMTTIIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKVYNANANLWKPWLDEEAISTLRKGGFYSSQKVTTPNPLRIISLNTNLYYGPNIIMTLNKTDPANQFEWLESTLNNQQNKEKVYIIAHVPVGYLPSSQNTAMREYYNEKLIDIPQKYSVDIAGQFYGHTRDSIMVLSDDKKGSPVNSLFAVAVTPVKSVLEKQTNNPGIRLFQYDPRDYKLLDMLQYYLNLTEANLKGESIKWLEYILTQTYDIEDLQPESLYGLAKQFTILDSKQFIKYNYFFVSVDSSVTCDKTCKAFQICAIMNLDNISYADCLKQLYIKHNY
6886	2	1341	QCGGIPGREGSSSRPLEEGTGSSSPACVRGAAPGSEDAFYPTRAKQARVSOELKKAARTVSISEGPDTLGDGMREERETLALAPEPEPLEKEACEKWKRPFRSASATSLTSLHCVDVVKGLLDFKKRGRHSIGGAPEQRYQIIIPVCVAARLPTRAQDVLDAHLSEVNNAVRFQPNSSLLATGGADRLIHLNWNVGSRLLEANQTLLEGAGGSITSVDFFDSGYQVLAATYNQAAQLWKVGEAQSKETLSGHKDKVTAAKFLTRHQA VTGSRDRTVKEWDLGRAYCSRTINVLVSYCNDVVCGDHIIISGHN DQKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDQLHLLSCSRDNT LKVIDLRVSNIRQVFRADGFKCGSDWTAKVSPDRSYALAGSCD GALYIWDVDTGKLESRLQGP HCAAVNAVAVWCYSGSHMVSVDQGR KVVWLQ
6887	1047	116	WTARPSQKPFWEAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHGQQRAAGPTLPRGERGGPQQSGPGLAAQTPPTSQVAVRAFLGTYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVYNASGSEHCYDIYRLYHSCADPTGCGTGPDAWADYQACTEINLT FASNNTVDMFPDLPFTDELQRQYCLDTWGVWPRPDWLLTSFWGGDLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQQGAHLLDLRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGPRLSL
6888	1	992	FVAYVKEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVINFIKGRAPNHRLPQAFPEEIGIEYSVLLPHTMRWLRSRQILTHIFEMYBEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNLSASMQRGTGMNTVSAREKLSAFVRKFPFWQKRIEKNFTNFPFL EEIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWILDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC AQFTAFFPNLAKTALEILMPFATTYLCELGFSITFTPNKNVPEAA LILSDDIRVAISKVPSFLGHH
6889	1	1534	LTLNQIKEEREQDNSESPNGRTSPLVSQNNQGGSTLRDLLTTT AGKLRVGSTDAFIAPVYSMGPSSKSGRTMPNILDIIASVV ENKIPPSKTSKINVKPELKEEPEESIIISAVDENNKLYSDIPHWS ICEKHILWLKDYKNSSNWKLFKECNKQGGQPAVVSQVHKKMNSL WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDFEEVSKRQ KNKSGETVVLKLDWPSGDEFKTMMPARYEDLLKSLPLPEYCNPEGKFNLAHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI EVSDVNVNIIIVYGIAGNGILSKAGILKKPEEEDLDDILRKRLK DSSEIPGALWHIYAGKDVKIRBFLQKISKQGLEVLPEHDPIDR DQSWYVNNKLRQRLLEEYGVRTWTLIQFLGDAIVLPAGALHQVQ

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			NFHSCIQVTEDFVSPHELVESFHLTQELRLLEEINYDDKLQVK NILYHAVKEMVRALKIHEDEVDDMEEN
6890	3	667	THACGMWIPLYLHRLVVKHTAETCNSPPCGAKDSLIFGAITCF TGFLGVDTGAGATRWCRLLKTQRADPLVCAVGLGSAIFICLIFV AAKSSIVGAYICIFVGETLLEFSNWAITADILMYVVIPTRRATAV ALQSFTHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA LMLCFVVVLGGMFFLATALFFVSDRARAQQVQVNLAMPASVK V
6891	1980	1262	LRHQELLSKELKLLRGITTESIIHIGLAAGKEQFMQDASNVMO LLKKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKFKPNCNVND EVLPHWLSWLP LHEDKEEAIQTLFCLDIESNHPVVGPNNSN LPKIIISIIAEGKINETINYEDPCA KRLANVVRQVQTSSEDLWLEC VSQLDDEQEQEALQELLNFA
6892	3	876	RSVAAASGPGAWGTDDHYCLELLRKRDRYEGYLCSLLPAESRSSV FALRAFNVBLAQKDSVSEKTI GLMRMQFWKKTVEDIYCDNPPH QPVAIELWKAVKRHNLT KRWLMKIVDEREKNLDDKAYRNKELE NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAQGI VTC LRA TPYHGSRRKVF LPM DICMLHGV SQEDFLRRNQDKNVRDVIYDIA SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIQRVDFD IFHPSLQQKNTLLPLYLIQSWRKTY
6893	1	842	DGERKMSVVERTFSEINKAEEOYSLCQELCSELAQDLQKERLKG RTVTIKLKNVNFVKTRASTVSSVVSTAEBIFAIAKELLKTEID ADFPHELRLRLMGVRISSFPNEEDRKHQQRSIIIGFLQAGNQALS ATECTLEKTDKDKFVKPLEMSHKKSFFDKRSEKWSHQDTFKC EAVNKQSQTSPFQVLKKMNENLEISENSDDCQILTCPCVCFR AQGCISLEALNKHVDECLDGPISSENFKMFSCSHVSATKVNKKE NVPASSLCEKQDYEAH
6894	1742	1463	TTLCCKPLVPREHQFYETLPAEMRKFTPOYKGKSQLEGLPHWRG DVRDRGHGRPWQPSLEPSLPPTLCFPLSSFSSSWPSAQHLTPS VFNPW
6895	2379	478	VTVVELCDLASPTALLIMRTVLDLIVEDLQSTSEDKQYTSQT TRLLALLYALASHACKLAILHLINGTIKGDERYAEIFQDLAL VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSEGSISEL EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL AEHDYGLFHLKSSLRKNSSALHSLKRVVSTFSKDTGELASSFL EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKQLL QSKEESPENLFLELEKLVLEHSKDDDNLDLSDSVVGLKQML SGDPLPLSDQDVEPVL SAPESLQNLFNRTAYVLADVMDDQLKS MWFTPFQAEI DTDLDLVKVDLIELSEKCCSDFDLHSELER SEPSSPGRKTKTKGFKLGKHKHETFITSSGKSEYIEPAKRAHV PPPRGRGRGGFGQIRPHDI FRQRKQNTSRPPSMHVDDFVAES KEVVPQDGI PPPKRLKVSQKISSRGFGSGNRGGRGAFHSQNR FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGSNPNRG PLPPLRPLSSTGYRPSPRDRASRGGLGPSWASANS GSGSGRG KFSVSGSGRGRHVSFTTR
6896	1	555	GNIVIQKKYKQHIIPLENVTIDSIRDEGDLRNGWLIKTPTKS FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD SEATVCMRCQAKFTPVNRRHCRKCGFVVCGPCSEKRFLLPSQ SSKPVRICDFCYDLSAGDMATCQPARSDSYSQLKSPLNDMSD DDDDDDSSD
6897	3	920	GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY AGYEQVTNEDLLTNCTLLCRRLSPMNLISLHTASGLRLFSVL SLAWGFIADVLESEKYRRLGEMRFTLTGFLRLAALRTYRGRLA YLPVGRVGSKTPASPVVQGPVD AHLVPLEEPVPSHWTVVPDE DFVLVLALLHSHLGSEMFAPMGRCAAGVMHLFYVRAGVSRAML

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LRLFLAMEKGRHMEYECPLYVVPVVAFRLEPKDGKGVFAVDGE LMVSEAVQGGQVHPNYFWMVSGCEPPPSWKQPMPPPEEPL
6898	919	346	OKTVTAVASLLKGRQGIYTENERRMGAIVIKIRFFKIMLVLIICW LSNIINESLLFYLEMQTDINGGSLKPVRTAAKTTFIMGILNPA QGFLLSLAFYGTGCSLGFQSPRKEIQWESLTSSAEGAHPSPL MPHENPASGKVSQVGGQTSDEALSMLSEGSASTIEHTASESC KNNEGDPALPTHGDL
6899	120	827	MKVRKNNDAYLLDKNKINMDCFISCFKKMLTTLMFSGIISL LEHGEEYTFSLPCAYARSILTVPWVELGGKVSVCNCAKTGYSASI TFHTKPFYGGKLHRVTAEVKHNITNTVVCVRVQGEWNSVLEFTYS NGETKYVDLTKLAVTKKRVPRLEKQDPFESRRLWKNVTDLSRES EIDKATEHKHTLEERQRTTEERHRTETGTPWKTIFYKEGDGWVY HKPLWKIIPPTQPAE
6900	3	451	TEVLGSKGIHELRSSTSLHHALESASLLTMFWRAALPSTHIP VLPKGVGESTERELLELRTKVSQQEQLLQSTTEHLKNANQKES MEQFIVSQLTRTHDVLKARTNLEVRKLLHQSEAPSLSPTHHP LADLVGDSWPALRFQEK
6901	1	201	DDNMVQRLETFKMTLQQOSTLEQWAAWLDNMVQALKPYEGRP SFPKAARQFLLKWSFYRYHLGFS
6902	2	267	GAPPPPPSPPPPPQQAAPSSHPHSDLTFFNSSALEGQAGAQGA SDMPEPSLDLLPELTNPDELLSYLDPPDLPSNSNDLLSLFENN
6903	1	149	RINQVYRQGTGIHILVIDQMVFQNFQDESCFLPSTVKAESSDGI HIILK
6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRRVQAIQKKSNGFDLLC VGNFFGSTQDAEWEEYKTKGKAPIQTYVLGANNQETVKYFQDA DGCELAENITYLGRKGITGSSGLQIVYLSGTESLNEPVPYGYSF SPKDVSSLRMMLCTTSQFKGVDILLTSPWPKCVGNFGNSSGEVD TKKCGSALVSSLATGLKPRYHFAALEKTYERLPYRNHIILOEN AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAELVKQPPD VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS TGRDSKSSPHKQPRKPPQPPGCPWFCLASPEVEKHLVNVNIGTH CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEVEKYKATL RRFFKSRGKWCVFERNYKSHHLQLQVIVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR IKKNFPLQFGREVLASEAILNVDPKSDWRQCQISKEDDETLARR FRKDFEYDFTLDD
6905	1	226	VSKTGEAETITSHYLFALGVYRTLYLFNWIWRVHFEGFFDLIAI VAGLVQTVLYCDFYLYITKVLKGGKLSLPA
6906	3	611	SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI ATTTATVSGLVALEMIKVTGGYFPEAYKNWFLNLAIPVVFETET TEVRKTKIRNGISFTIWRWTVHGKEDFTLLDFINAVKEKYGIE PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV SFAPDIDGDEDLPGPPVRYFSDHDD
6907	2	2228	LRGVVVAAGAFRFSSEESTSHLIMSRRSQRLTRYSSQDDDDGS SSSGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS DAHTSYYESLVHESWFPFRSSLEELHGDANWGEDLVRVRRROT GGSESSRASGLVGRKATEDFLGSSSGYSSDDYVGYSDVDQSS SSRLRSVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA SLLDVFLVTRRFSSSLKFLWFLPLLLLTCLTYGAWYFYPIGLQ TFHPALVSWWAAKDSRRADGEWEARDSSPHFAQEQRVMSRVHSL ERRLEALAAEFSSNWQKAMRLERLELRQGAPGGGGGLSHBD TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQDSE DLFKKIVRASQSEARIQQLKSEWQSMQTESFQESSVKELRRLLE DQLAGLQQELAAALAKQSSVABEVGLLPQQIQAVRDDVESQFFA WISQFLARGGGGRVGLLQREEMQAQLRELESKILTHVAEMQGS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AREAAASLSLTQLKEGVIGVTEEQVHHIVKQALQRYSEDRIGLA DYALES GGASVISTRSETYETKTALLSLFGIPLWYHSQSPRVI LQPDVHPGNCWAFQGPQGFVAVVRLSARIRPTAVTLEHVPKALSP NSTISSAPKDFAI FGFDELDQEGTLLGKFTYDQDGEPIQTTFHP QAPTMTATYQVVELRILTNWGHPEYTCIYRFRVHGEPAH
6908	3	780	QVPSAAWMAVCGLSRLGLGSLRLGQCFCGAARLLYPRFQSRG PQGVEDGDRPQPSKTPRI PKIYTKTGDKGFSSTFTGERRPKDD QVFBAVGTDELSSAIGFALELVTEKGHTFAEELQKIQCTLDQDV GSALATPCSSAREAHLYTTFKAGPILELEQWIDKYTSQLPPLT AFILPSGGKISSALHFCRAVCRAERRVPLVQMGETDANVAKF LNRLSDYLFTLARYAAMKEGNQEKIYKNDPSAESEGL
6909	3	409	GRLLAVGTDLYGQRSSAPEQELLVQDATPVSNLLPEKAFSDIP SPYLRGTIKMMQAVRQAFQDQDDRTWDGRPLTMAATFDDCLYA LCVVDTIKRSSQTGEWQNIAMTEPELSPAYLISEAMRRSRMS LYC
6910	1	1068	LVPVVVIDSYYYGKLVIAPLNIVLYNIPTPHGPDLYGTEFWYFY LINGFLNPNVAFALALLVPLTSLMEYLLQRPHVQNLGHPYWL LAPMYIWFIIFFIQPHKEERFLFPVYPLICLGAVALSALQHSF LYPQKCYHFVFQYRLEHYTVTSNWLALGTVFLGLLSFSRSVA LFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYR PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY RPFLDASRSSKLLRAFYVFFLSDQYTVVNYTILKPRKAKQIRK KSGG
6911	1184	966	GEDAEEMETGNVANLISTFGSSFGLLRKSPGGGREGEEEGESG PEAAEPGQICCDKPVLRDMNPWSTAIVAF
6912	1	844	AMKPVETHSFQMLFTILSTGSALKAQSYEDAYRCIKSSILLGSI SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAVW GESGELVCTKPIPCQPTHFWDENGKRYKAYFSKFPGIWAHGD YCRINPKTGGIVMLGRSDGTLPNGVRFSGSEIYNIVESFEEVE DSLCPVQYNKYREERVILFLKMASGHAFQPDLVKIRDAIRMGL SARHVPSLILETKGIPYTLNGKKVEAVKQIIAGKAVEQGGAFS NPBTLDLYRDIPELQGF
6913	1643	1558	KKSHEESHKEELSYGAQASLPLPCSDFR
6914	1251	615	ELAAECKSAGYPGTLPYRCDLNNEEDILSMFSAIRSQHSQVDI CINNAGLARPDTLGSGSTSGWKDMFNVNVLALSICTREAYQSMK ERNVDDGHIININMSGHRVPLPSVTHFY SATKYAVTALTEGLR QELREAQTHIRATCISPGVVTQFAFKLHDKDPEKAAATYEQMK CLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT
6915	254	652	GRSLSFKTFLIWLISYQGGILMYGALVLFSEFVHVVAISFT ALILTELLMVALTVRTHWLMVVAEFLSLGCVVSSLAFLNEYFD VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6916	254	652	GRSLSFKTFLIWLISYQGGILMYGALVLFSEFVHVVAISFT ALILTELLMVALTVRTHWLMVVAEFLSLGCVVSSLAFLNEYFD VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6917	254	652	GRSLSFKTFLIWLISYQGGILMYGALVLFSEFVHVVAISFT ALILTELLMVALTVRTHWLMVVAEFLSLGCVVSSLAFLNEYFD VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6918	28	921	PEAGTRSWREPDPELRRFLLSAACRSFPQWLPGGGGGQVSSCS DTDVPYLLAVKSEPGRFAERQAVRETWGPAPGIRLLFLGSP VGEAGPDLDSLVAWESRRYDILLWDFLDVFPNQTLDLLLLAW LGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSYLGE VFTQAMPPLRKPGGPFYVPESFFEGGYPAYASGGGYIAGRLAPW LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRT ADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC

WO 01/53312

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *-Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6919	850	41	QGRRELSGSVFCFFIQOEPKEMLTSEYHERVRSQGGQLOQLQA ELDKLHKEVSTVRAANSERVAKLVFQRLNEDFVRKPDYALSSVG ASIDLQKTSHDYADRNTAYFWNRFSFWNYARPPTVILEPHVFP NCWAFEGDQGVVQLPGRVQLSDITLQHPPPSVEHTGGANSAP RDFAVFLLSFFTHQGLQVYDETVSLGKFTFDVEKSEIQTFHL QNDPPAAPPKVKIQLSNWGHPRFTCLYRVRAHGVRTSEGAEGS AQGPH
6920	1418	591	EAQGPSKVHLTLKKKK
6921	2	1711	MNATRSEEQFHVINHAEQTLRKMENYLKEKQLCDVLLIAGHLRI PAHRLVLSAVSDYFAAMFTNDVLEAKQEVMEGVDPNALNSLV QYAYTGLVQLKEDTIESLAAACLLQLTQVIDVCSNFLIKQLHP SNCLGIRSGDQAQCTELLNVAKHYTMEHFIEVIKNQEFLLLP NEISKLLCDDINVDEETIFHALMQWVGHDVQNRQGLGMLLS YIRLPLLPQLADLETSSMFTGDLECCQKLMAMKYHLLPERR SMMQSPRTKPRKSTVGALYAVGGMDAMKGTITIEKYDLRTNSWL HIGTMNGRRQLQFQVAVIDNKLIVVGGRDGLKTLNTVECFNPVGK IWTVMPPMSTHRLGLGVATLEGPMYAVGGHDGWSYLTNTVERWDP EGRQWNYVASMSTPRSTVGVALNNKLYAIGGRDSSCLKSMEX FDPHTNKWLSLCPMSKRRGGVGVATYNGFLYVVGHDAPASNHC SRLSDCVERYPKGDWSSTVAPLSVPRDAVAVCPGLDKLYVVG YDGHYTLNTVESYDAQRNEWKEVVPVNIAGRAGCVVVVCLP LTPPAGIRHEVRDREREREREREREREFLLDSTGSELKQNIHSIT GLPPAMQKVMYKGLAPEDKTLREIKVTSKAKIMGGGSTINDVLA VNTPKDAQAQDAKAEENKKEPLCRQKQHRKVLDDKGPEDVMP KGAQERLPTVPLSGMYNKGKVRILTFLKQDQLWIGTKERTK LPMGSIKNVVSSEPIEGHEDYHMAFQLGPTBASYWVWVPTQY VDAIKDTVLGKWQYF
6922	1075	369	LGLFCILFIDTLCAVLEDRDLSIRESLFGAVVRNAEBCQRRQ LPVTFGNKOKVLGKALSIRFPLMTIEEFAAGPAQSGILSDREV VNLFLHFTVNPKEPRVEYIDRPRCLRGKECCINRFQVQVSRWGY SGTSDIRFTVNRRIIVGFLYSGIHGPTDYQVNIQIIIEYKK QTLGQNDTGFSCTGTANTFRVMFKEPIBILPNVCYTACATLKGP DSHYGTGLKKVHETPAASKTVFFFSFGNNNGTSIEDGGQIP EIIIFT
6923	2469	1660	FEERVICFVEYLLTAFHEGRKGLAKKPYNEIIGETFHCSWEVP KDRVKPKRTASRSPASCHEHPMADDPKSKYKLPVABQVSHHP ISCFYCECEKRLCVNTHVWTKSKFMGMSVGVSMIGEVRLLE HGEEYVFTLPSAYARSILTIIPWVELGGKVSINCAKTGYSATVIF HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNG ETKVIDTTLTPVYPKKIRPLEKQGPMSRNLWREVTRYLRIGDI DAATEQKRHLEEKQVBERKRENLRTPWPKPKYFIQEGDGSILQ SPLESTLMGLEVSFPV
6924	2210	1235	RGAAGAAMEPDSVIEDKTIELMCSVPRSLWLCANLVESMCAL SCLQSMPSVRCQLISNGTSVIVSRKRPSEGNQKEKDLCKIFY DOWSESDQVEFVHLISRMCHYQHGINSYLPMLQDFITALP EQGLDHAENILSYLDARSLCAELVCKEQRVISEGMLWKKLI ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPNSFYRSYLPKI IQDIETIESNWRGGRHNLQRIQCRSENSKGVYCLQYDERVITGSSDS LRDINSIKINDKTSLECLKVLTGHTGSVLCQYDERVITGSSDS TVRVWDVNTGEVNLTIHNEAVLVHLRFSNGLMVTCSKDRSIAV WDMASATDITLRRVLVCHRAAVNVVDFDKYIVSAGDRTIKVW STSTCFVRTLNHKGRIACQLYRDLVSGSSDNTIRLWDIEC GACLRVLEGEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP RAPASTLCRLTVEHSGRVFRLQDFBQIISSSHDDTILINDFL NVPPSAQNETRSPRTYTYISR
6925	2	1653	SGRVAMDGLGLQFPEOGFPAGPFLP SGRVAMDGLGLQFPEOGFPAGPFLP
6926	1	733	

WO 01/53312

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6927	2	1484	DGYPLPTDTSPLDGVDPDPFAAPMGDCPAAAGTYSVAQVSD YAGPPEPPAGPMHFRLGPEPAGPSIPGLLAPPSALHVVYGMGS PGAGGGRGFQMPPQHQQHQQHPPGPGQPTPPPEALPCRDGT DPSQPAELLLGEVDRTFEQYLHFVCKPEMGLPVQGHDSGVNLPD SHGAISSVVS DASSAVYYCNPYDV LTLGGDIQLMLAQNANNRAAHLEEFHYQTKEDQEILHSLHRESS CQGFANATDLSTDLSQLSVSCCKYEANEILQFRDLKSNPEH YVQVLKRMGNIRNEIGVFFYMNQAAALQSERLVSKSVSAEQQLW KKSFSCEFEGHNFESIEDATNAALLCNTGRIMRICAQAHCA GDELKREFSPEEGLYNKADIDYLLKALRSIGTRDIHPAVDSVN WELSTTYFTMATLQDDYAPLSRKAQEQIEKEVSAMKSLKYCD VDSVSARQPLCQYRAATIHRLASMYHSLRNQVQDEHLRKQHR VLADLHYSKAAKFLQLLKDAPCELLRVQLERVAFAEQMTSQNS NVGKLKTLGSGALDIMVTEHAFLQIKELIEFGQPKSGDAAA ADASPSSLNREEVMKLLSIFESRLSFLLLQSIKLLSSTKKKTSNN IEDDTILKINKHIYSQLLRATANKTATLLERINVIHLLGQLAA GSAASSNAVQ EATDLINLLQVKMRKRYSDKTLSPHNLQDYQTLWDLRELECK IGERYITHEDDLWEKYAGEQGLQYPTHLINPSASHSDTPETE ETEMKALGERVSIL RDQGRVDRDRSPAREPGDVSARTSGGGGGRSATTAMPPVPNG NLHQHDPQDLRHNGNVVAGRPSCSRGPRRAIQKPPAGRRSG RGPAAGGLCLQPPDGGTCVPEEPVPMDEALEKHLAGLQFRE QEVNRQGGARTNSTSAQKNERESIRQKLAGSFFDDGPGIYTSC SKSGKPSLSRLSQGMNLQICFVNDSSGSDKSDADDSTKTSLD TPLSPMSKQSSSYSDRTTEESSESLDDMDLFRQKQLQAEAKM ALAMAKPMKMQVEVEKQNRKKSPPVADLLPHMHPHISECLMKRSL KPTDLRDMTIGQLQVIVNDLHSQIESLNEELVQLLIRDELHTE QDAMLVDIEDLTRHAESQKHMAEKMPAK FKDTANVFSVLFQMRNNFRHYFIEPSQLKLFYDVTWITQVAI SYTVVPFVLSIKPSLTFYSSWYVCLHILGLVLLLPVKKTQR RKNTHEINQLSQSKKFDENSLGQNSFSTNNVCNQNEIASR HSSLKQ FVERLPNRPACLLVASGAAGVSAQSFLHCFTMASTAFNLQVAT PGGKAMEFVDVTESNARWVQDFRLKAYAPAKLESIDGARYHAL LIPSCPGALITDLASSGSLARILQHFHSESKEICAVGHGVAALCC ATNEDRSWVFDYSYLTGFSVCELVRAFGFARLPLVVEDFVKDSG ACFSASEPDVAVHVVLDRLHVTGQNASSTVPAVQNLFLCGSRK FVDSFGQGEQAEIEEGGTQMNRMRAHSPAGASVESSSPGPKK SDMCBGCRLAAGHPGYISHDKETSIKYVSHQHPSPHQLFSIVR QACVRSLSCEVCPGREGPIFFGDEQHGFFVSHFFIKDSLARGF QRWYSIITIMMDRIYILNSWFLGKVRGIIIDELQKALKVFEA EQFGCPQRAQRMTAFTPFLHQRNGNAARSLTSLTSDNLWACL HTSFAWLLKACGSRLEKLEGAFTEDTLVQMEKLDLEESES WDNSEAEEEEKAPVLPSTEGRELTCQPAESSLSGCGSWQPRK LPVFKSLRHMQRVGGRTAHHELRRRANHGLCLPTRLASGPSTL KTLQEVTDLSLGGWLMAGVGGII SLNLHCTLPPPPHGYAGYPSDKGKKPKGSKQPSGTTKRP SDDDCPSASKVYKASDSAEAEAFQLTPOQHLIREDQCNQKLW DEVLSHLVEGPNFLKLEQSFMCVCCQELVYQVTTCECFHNVCK DCLQRSFKAQVFSCPACRHLGQNYIMIPNEILQTLDDLDFPGY SKGR DRDHSQCGGIRVALARVSSVKLISKAKIRTVKMTPIIVLAFIV CWTPFFVQMWVMDANAPKASAFIIVMLLASLNSCCNPWIYM LFTGHLFHELVQRFLCCSASYLKGRRLGETSASKNSSSSVLS HRSSSQRSQSPSTA
6928	1086	777	
6929	1749	607	
6930	131	545	
6931	2	659	
6932	2	1131	
6933	1431	890	
6934	3030	2588	

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6935	886	543	NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMNIRRSTHDL VAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS VGVAVLELLNFPPSSPTLSVSSTSL
6936	1347	567	RSRRQFLSRALLEFFGKSHPPHRLFRKSLNVGLHYSHIPFLT TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS LPSPLPNLGPQGPALTPEQENILHTTQTDCCYNLAACLLQMEPV NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL AAVNRQPKDANVRRYLQLTQSELSSYHRKEKQLYLGMPG
6937	1	727	AVEFRCCPGRDPACFARGWRLDRVYGTCTCDQACRFTGDCCFDY DRACPARPCFVGESWPWGGCADQCKPTTRVRRRSVQQEPQNGGA PCPPLERAGCLEYSTPQGDGCHTVVPAFITTSFNFKERTRQA TSPHWSTHTEDAGYCMFKTESLTPHCALENRPLTRWMQYLRG YTVCVDCQPPAMNSVSLRCSGDGLSDGNQTLHWQAIGNPRCQG TWKKVRRVDQCSCPAVHSFIFI
6938	3	719	NSRKLELAERVDTDQMQLKRRQSSEKENDSGTLDTVGAVVDH EGNVAAVSSGGLALKHPGRVGAALYGCSCWAENTGAHNPYST AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMONKFIS PFLASEDGVGGVIVLRSCRCSEPDSSQNKQTLLEFLWSHTT ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVABEGGVCRLGEP SELTQAECEASQRHFT
6939	3	810	KVTAPRRPQRYSSGHGSDNSSLGELPPAMGRTALFHHSGSS GYESLRRDSEATGSASSAPDSMESGAASPGARTSLKSPKKRA TGLQRRRLIPAPLPDPTALGRKPSLPGQWDLPPPLAGSLKEPF EIKVYEIDDVERLQRPPTPREAPTQGLACVSTRRLAERRQQR LREVQAKHKHLCEELAETQGRMLLEPGRWLEQFEVDPELEPESA EYLAALERATAALEQCVNLCKAHVMVTCFDISVAASAAIPGPQ EVDV
6940	1188	496	GKMAAQPLRHRRCATPPRGDFCGGTERAIDQASFTTSMENDTQ VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFOCAQCHAV LADSVHLAWDLRSRLGAVVFSRVTNVLEAPFLVGIIEGSLKGS TYNLLFCGSCGIPVGFHYSTHAALALRGHFLCSSDKMVCYLL KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS EVTDPQSKPEN
6941	1	713	SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEARQAEALGYQA VVLSSAMQGDVKSMQFYGLLAHVARTRLTPSMAGASVEEDAQL HELAELQIPDLQLEEALETMAWGRGPVCLLAGGEPTVQLQSG RGGRNQELALRVGAELRRWPLGPIIDVFLSGGTGQDGPTEAAG AWVTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGAHLHTG MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDWTMGAPLSMPTNAVGGCLLDRLYADGGYDG QTYLNTMESYDPQTNWTQMASLNIAGRAGACVVVIKQP
6943	1	739	PMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWRLG HSPAGGSITETLVQGBKTEYLLTALEPKPTYIICMVTMETTNAY VADETPVCAKAETADSYGPTTLNQEQNAGPMASLPLAGIIGGA VALVFLFLVGAICWYVHQAGELLTRERAYNRGSRKKDDYMESG TKKDNSILEIRGPGLQMLPINPYRAKEEYVHTIFPNSGSSLCK ATHTIGYGTTRGYRDGGIPDIDYSY
6944	960	156	VANILLNGVKEYSELTGSSERAEQPLSVGRCLSTICNMPKALRT LCVNHFLGWLSEFGLLFYTFMGGEVVFQGDPAKPHTEAYOKY NSGVTMGCGMCIYAFSAFYSAILEKLEEFVSVRTLYFIAYLA FGLGTGLATLSRNLYVVLSCITYGILFSTLCTLPYSLLCDYQ SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVGLPLTSA VGSANGVMYFSSLVSLGCLYSSLFVIYEIPPSDAADEHRPLL LNV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6945	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAGGC HSPKGPAPVPVPLKKRGYDVTRNPHLNKGMAFTLEERLQGIHGL IPPCFLSQDVQLLRIMRYEROQSDLDKYIILMTLQDRNEKLFY RVLTSDEKFMPIVYTPTVGLACQHYGLTFRPRGLFITIHDKG HLATMLNSWPEDNIKAVVVDGERILGLGLGCGYGMGIPVKGKLA LYTACGGVNPQQCLEVLLDVGTTNNEELLRDPLYIGLKHQRVHGK AYDDLDEFMQAVTDKFGINCLIQFEDFANANAFRLNKNYRNKY CMFNDDIQGTASVAVAGILALRITKNKLSNVFGGQAGAGEAAM G\IAHLLVMALE\KEGVPKA\EATRKIW\WVDF\KGLIVQGRDH LNHEKEMFAQD\HPEVNSLEEVRVLPKPTAIIGVAAIAEA\FTE QILRDMASFHERP\IIFALSNPTSKECTA\EKCYRVTEGPRGF FAS\GSPF*GVLIWEMGKTIFPGRGNNA*RVPRGWQLGVHSPG GDPGHP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR NVFLRIAIVFD*GYKHNLV\SYYPEPKD\KEAFCKIPGSYTPD YDSFYT/VDSYIWAQKAMNVQTV
6946	133	2551	SCEYSGITVAPGDCPGVAHLLAPSMASDTPESLMALCTDFCLR NLDGTLGLYLLDKETLRHHPDIFLSEI\CDRLVNEYVELVNAAC NF\EPHE\SFFNPLFRDPRKQASRR\IHL\RED\LVQD\QD\LE AIRKQDL\VEL\YLTN\CEKLSAKSLQTLRSFSHTLGVP*AFFG C\TNILLRKENPGGL/CEDEYLFNPTCQVLVKDFTFEGPRLR F\KLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ WKDSL\VSLVL\YNMDLSDDHIR\VIQVQLHKLRLHLDISDRRLSS YYKFKLTREVLVSLFVQKLGNLMSLDISG\HMLENCISIKGR EAGQTSI\EPSK\SSIIIPRGFEGGPLQF\LGVF*GIFCGRLTH IPAYKVSGDKNEEQVNAIEAYTEHRPEITSRAINLLFDIARIE RCNQLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSEYRSE QSVKLRRQVIQVVLNGMESYQEVTVQRNCCLTLCNFSIPELEF QYRRVNEILLSILNPTRQDESIIQRIAVHLCNALVCQVNDNDHEA VGKMGFVVTMLKLTQKLLDKTCDQVMEPSW\SALWNIIDETPD NCEMFLNFMNGMKLFLDCLNEFPEKQELHRNMLGLLGNVAEVEL RPQLMTSQFISVFSNLLSKADGIEVSYNACGVLSHIMFDGPEA WGVCEPQREBEERMWAAIQSWDINSRRNINYSFEPILRLLPQ GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM ATARQETKEMARKVIEHCNSNFKEENMDTSR
6947	2	1682	TSVSTIPRGLASARPQSRSWRCCPVWRSPGRARGRGLKMLNVP SQSFPAPRSQQRVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG LKGRLEIETEEELKHNKDDCWCICIRGFVYNVSPYMEYHPGGE DELMRAAGSDGTETLFDQVHRWVNYESMLKECLVGRMAIKPAVLK DYREEKKVLNGMLPKSQVTDTLAKEGSPSYSDWFQDTSLVTI /EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLISYTYW/R*A MRFRKIFLCGL/CESVGKIEIVLQKKENTSWDFLGHLKHNHNSL IPRKDTGLYRKQQLISKEDVTHDTRLFCLMLPPSTHLQVPFG HVYLKLPITGTEIVKPYTPVSGSLLSEFFKEPVLNNKYIYFLIK IYPTGLFTPELDRLOIGDFVSVSSPBGNFKISKFQLEDLFLLA AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSQLE KLAPDKRLDVEFVLSAPISEWNGKQGHISPAALLSEFLKRNLDK SKVLVLCICGPVPFTEQGVRLHDLNFSKNEIHSFTA
6948	104	58	PDGAHSFPFDEYFTCSSLCLSCGVGCKKSMNHGKEGVPEAKSR CRYSHQYDNRVYTKACYERGEVSVVPKTSASTDSPNMGLAKY AWSGYVIECPNCGVYRSRQYWFNGQDPVDTVVRTETIWHVWPGT DGFLKDNNAQRLLDGMNFMAQSVSBLSLGPTKAVTSWLTQDI APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGBGFCDCSSSK TRPVPERGWGPAPVRVCDNCEYAR/TRPVSCYRGTSGR*RRRRT QETVE
6949	152	4656	GLRLCLSRPLTRPGDSDVCGSAMASGAGGVGGGGGGKIRTRRCH QGPIKPYQQGRQHQGILSRVTSVKNI VPGWLQRYFNKNEEDVC

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			<p>SCSTDTSEVPRWPNKEDHLVYADEESSNITDGRITPEPAVSNT EEPSTTTSTAST\YPDVLTRVSLYRSHLNFMSLESPALHCQPST SAFFIGSSGFLVKRIKDSTSQHDDDNISTSGFSSRASDKDIT VSKNTSLPPLWSPEAERSHLSQHTATSSKKPAFNLSAFGTLSP SLGNSSILKTSQLGDSPFYPGKTTYGAAAVRQSKLRNTFYQA PVRQMKAKQLSAQSYGVTSSTARRILQSLKMSPLADAKRIP SIVSSPLNSPLDRSGIDITDFQAKREKVDQYPPVQRLMTPKPV SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN REQRESGFSPNFSLPAANGLSSGVGGGGKMRERHAFVASKP LEEEEMEGPVLPKISLPITSSSLPTFNFSSPEITSSSPINSS QALTNKVQMTSPSSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF SVPVAKTAEALSGSSSTLEPIISSAHHVTTVNSTNCKKTPPEDC EGPFRPAEILKEGSLVDILKSPGFASPKIDSVAQAQPTATSPVVY TRPAISSFSSSGIGFESLKGAGSQWQCDTCLLQNKVTDNKCAC QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVI WDCDTCLVQNKPEAIKVCACETPKPGTCVKRALTLTVSESAET MTASSSSCTVTGTGFGDKFKRPIGSWECSVCCVSNNAEDNKC VSCMSEKPGSSVPTSSSSTVPVSLPSGSGSLGLEKFKKPEGIWDC ELCLVQNKADSTKCLACESAKPGTKSGFGFDTSSSSSSNAASS SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP MSEGF*FSKHIVGFKPGVSSSESKPEEVKDKSKNDNFKFGLS SNPVFLTPFGVSNLQGEKEEELLKSSCAGFRFGTGVINSTR VPANTIVTSENKSSFNLTGTIETKSVSVAPLKCQTSKAKKEEMPA TKGGFSFGNVEPASLPSASVFLGRTEEQEPVTSLSLVFGE KLTMKEPKC/QPVFSFGEFORQTKDENSSTFSFMTKPEKE SEQPAKATFAPGAQTNTTADQGAAPDLSYLNSSSSSSTPAT AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST SQSLFQSQSKLATTSTGTAVTPFVFGPAGSSNNTTSGFGFG ATTTSSAGSSFVFGTGPSAPSAPAFGANQTPTFGQSQGASQP NPPGFGSISSTALFPTGSQPAPPTFTVSSSSQPPVFGQPSQ SAFGSGTTPNSSSAFQFGSSTTNFTNNSPSGVFTFGANSSTP AASQPSGSGGFPFNQSPAFTVGSNGKIVFSSSGTSFSGRKIK TAVRRRK</p>
6950	2585	411	<p>PRPGSRSGLCRRAGERGAVRAGGLSRRTAE*IMDELHYQDTS DVPEQRDSKCKVKWTHEEDEQLRALVRQFGQDQWKLASHFPNR TDQQCYRWRVLRVLPDLVKGPTKEEDQKVIELVKYGTQKQWTL IAKHLKGRLGKQCRERWHNHLNPEVKKSCWTEEDRIICEAHKV LGNRWAEIAKMLPORTDNAKNHWNSTIKRKVDTGGLSESKDC KPPVYLLLELEDKDLQSAQPTGEGSLLTNWPSVPTTKEEN SEELAAATTSKEQEPIGTDLDAVRTPEPLEEFPKREDEQGSPP ETSLPYKWVVEANLLIPAVGSSSLSEALDIESDPDAWCDLSKF DLPEEPSAEDSINNSLVQLQASHQQQVLPFRQPSA\LVPSVTEY RLDGHITISDLRSRSGELIPISPSTEVGSGIGTPPSVLKRQRK RRVALSPVTENSTSLSFSDSCNSLTPKSTPVKTLFPSPSQFLNF WNKQDTLELESPLSTTPVCSQKVVTTPHHRDKTPLHQKHAAP VTPDQKYSMDNTPHTPTPFKNALEKYGLKPLPQTPHLEEDLKE VLRSEAGIELIEDDIRPEKQKRKPLRRSPIKKVRKSLALDIV DEDMKLMMSTLPKLSLPTTAPSNSSSLTSGIKEDNSLLNQGF LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTACCGTRDQLFMQE KARQLLGRLLKPSHTSRTLILS</p>
6951	1940	239	<p>AGPDDTMKRSLOALYQQLSFLILALTEALAFATQEPSPRESL QVLPSGTTPGTMVTAHPSSTRHTSVVMLTNPNDGPPSQAAAPMA TPTPRAEGHPT\TPSPPSLRQ*PPPIKAP/SSTGPAPAAAMAT TSSKPEGRPRGQAAPTILLTKPPGATSRPTTAPRTTTRPPRP PGSSRKAGNSSRPVPPAPGGHSRSKEGQRGRNPSSTPLGQKRP LGKIPQIYKGNFTGSVEPEPSTLTPRTPLWGYSSSPQQTVAAT</p>

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			TVPSNTSWAPTITSLGPAKDKPGLRRAAQGGSTFTSQGGTPDA TAASGAPVSP/PSCPSAFSAFPPR*PTGWQP**LLAYCYP\CT SRPLSTSSGVFTAAATGPTPAADTSVSAPSQGI PQGASTTPQAP THPSRVSESTISGAKEETVA\PS*PTGCPVLSQWYPPQQAIS STAWSPPGPGSLGQQGTS PMWFRGTNRSTEPPSA*ARWISPG*S WPSACPSPP\LCPADGVLHEEEEEEDRQPGEQPEAYGNNTHTHPT TFQQAC\RGAAPEIPVPLKPLRLQLSEPRSPANGDYRDTGMVPC
6952	658	304	PESEGESGEMTDRTYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE PTPRLVLLHGLRPSQLLRHCGE*EQSASPLQLDGKDSALWT ASRQARGELRLCLTTAVRGTSPPSVSPVCQSS
6953	1512	349	NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES FSPHFRGKMGV\KLEKELENTEQPVGNEG*EHEVTGNLNSD PLLELCQCPLCQLDCGSREQLIAHVYQHTAAVVSASYM\CPVC GRALSSPGSLGRHLIHSQDQRSCAVCGARFTSHATFNSEKLP EVLNMESEPTVHNEGPSSAEGKDIAFSPVYPAGILLVCNNCAA YRKLLAEQTPSVRKWALRRQNEPLEVRLQRLEERTAKKSRDN ETPEEREVRMRDREAKRLQRMQETDEQARRLQDRDREARLKR AIETPEKRQARLIREREAKRLKRRLEKMDMLRAQFGQDPSAMA ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH
6954	819	1	PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAQN *PQR*RWTEGNSPQASAVATPGOGASPAAPRCTP*PSRRHRLP PGARPPAG*AAPAPT KPWLAGPASAPQGAAPLSPPAPPLIRTR *CAGAAARGRPRDRSPRPTPGGCSWSEPTPPAVSASAQTPS DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSRRREGTIPGNPHR AS*RAGWQR*PGP/REWGL*EPQGBEMSGPGGPGAPPNQVGSS VMQAMSTGI
6955	1568	782	PPGRRQVRAQVAGAPVGHWGTRARQVKTGRRRRARRIMPFLLQD WRSPGWSWIKTEDGWKRCESCSQKLERENNHCHNISHSIIILNSD GEIFNNEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKESTK ERHGYCTLGEAFNRDLDFSSAIQDIRFNVVVKLLQLIAKSQLS LSGVAQKNYFNILDKIVQKVLDDHNPRLIKDLLQDLSSTLCIL /N*RSREVCISGKHQYLDLPIRNYSLRATTATGSSDD*ASE\NG LTLSDLPLHMLNLIYRPSDGDNDIITLGQVTPPLYMLSEDRQLW KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPKEQY GDTLHFCRHCSILFWKDSGHPCTAADPDSCTFVSPQHFIDLFK F
6956	8605	3839	QTSSTIFASPTSPVVLGESVLQDNSFDLNNGSDAEQEEMETQSS DFPPSLTQPAPDQSSSTIQLHPATSPAVSPPTSPAVSLVSPAAS PEISPEVCPAASTVVS PAVFSVVS PASSAVLPVSLVPLTASV TSPKASPVTSPAAFP TASPANKDVSSFLETTADVVEITGEGLT ASGSGDVMRRRIATPEEVRLPLQHGWRREVR IKKGSRRWQGETW YYPGCGKRMKQFPEVIKYLNRNVHVSRRHFSFSPRMPVGDFF EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKEV PKVKRGRGRPPKVKITELLNKTDNRLPKKLEAQETLNEEDKAKI AKSKKKMRQKVQRGECQTTIQGQARNKRQETKSLKQKEAKKKS KAEKEKGTKQEKLEKVKREKKEKVKMKEKEEVTAKAPACKAD KTLATQRRLEERQRMILEEMKKPTEDMCLTDHQPLPDFSRVP GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEGE LCQGDLSLGEVQDLLVRLKALHDPGFFSYCQSLKILGEKVSEI PLTRDNVSEILRCFLMAYGVEPALCDRLRTQFPQAQPPQKAAV LAFLVHELNGSTLIINEIDKTLESMSYRKNKWIVEGRLRLRLKT VLAKRTGRSEVEMEGPEECIGRRRSSRIMEVTSMEEEEEES I AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRLFFRKLLH SSQMLRAVSLGQDRYRRYVWLPYLAGIFVETGEGNLVPEEVIK KETDSLKVAHASLNPALFSMKMELAGSNTTASSPARAGRPRK

577

578

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPOLASSAGH STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEKPHQCSI CWRFSFLKDYLIK\HMTHTGVRAVQCSICNKRFTQKSSLNVMH RLHRGEKSYBCYICKKKFSKHTLLERHVALHSASNGTPPAGTTP GARAGPPGVVACTEGTIVVCSVCPAKFDQIEQFNDHMRMHVSDG SGRFFFFFSNTDVYFIKKVTNRWTAGSSYKMRMKSIGKILL QIFIG\NCSMFVLVI
6964	1	178	NVFIEPRIQGFMTSAHPGQKHPDFSMGLLPFLAALVCSGGS SGSLGYNLPQNH\GLGRNTLVLLGQMRRISPFLCLKDRSDFRF PQEKVEVSLQKA\QAMFLYDVLQVFNFSHKALL\CCMEHDL PGPTPHFTSSAAGTPGDLLGAGDGRRRSWGQVIEGSTLALRRY PQESISTLE
6965	757	208	IITALGVRCMPGCPFCPCGCMAGPRLLFLTALALELLGRAGGSQP ALRSRGATACRLDNKESSESWGALLSGERLDTWICSLGLSMVG LSGVFPLLVIPLEMTLMRSEAGAWRLKQLLSFALGGLIGNVFL HLLPEAWAYTCSASPGGEGQSLQQQQQLGLWVLAGILTFLEALEK /HVPQQQGGDQPGPQQRPHCCRRARWRPLSGPAGCRARPRCR GP\DIKVSGLNLLANTIDNFTHGLAVAASFLVSKIGLLTTMA ILLHEIPHEVGDFAILLRAGFDRWSAAKLQLSTALGGLLGAGFA ICTQSPKGVETAAVVLFTSGGFLYIALVNVLPDLLEEDPW
6967	162	633	GFDPFKYIWLDSASSRMETDCNPMELSSMSGFESENGFEG TDMKMRLEAEAVNDVLFVANNMFVSKSLRCADDVAYINVETK ERNRYCLELTEAGLKVVGYAFDQVDDHLQTPYHETVYSLDLTL\ SPAYREAFGR\LLQRLALKRDGQS
6968	1	2265	RGGGGGRGCGPAGRERERPEPERTMEAAAGRGCFQPHPGLOKT LEQFHLSSMSLGGPAAFSARWAQEAYKKEAKEAGAAVPAVP PAATEPPVHLPAIQPPPPVLPGPFFMPDRSTERCETVLEGE TISCFVVGGEKRLCLPQILNSVLRDFSLLQINAVCDELHIYCSR CTADQLEILKVMGILPFSAPSCGLITKTDARLCNALLYGGAYP PPCKKELAAASLALGLELSERSVRVYHE\CFGKCKGL\LVPELYS SPSAACIQCLD\CRMLYPPHKFVVHSHKALENRTCHWGF\DSA\ NWRAYILLSQDYTGKEEQARLGR\CLDDVKEKFDYGNKYKRRVP RVSEPPASIRPKDDTSSQSPAPSEKDKPSSWLRTLAGSSNKS LGCVHPQRQLSAFRPWSPAVSASEKELSPHLPALIRDSFYYSKS FETAVAPNVALAPPQKQVSSPPCAAASVRAPEPLATCTQPRK RKLTVDTPGAPETLAPVAPEEDKDSAEVEVESREEFTSSLS LSSPSFTSSSSAKDLGSPGARALPSAVPDAAPADAPSGLEAEL EHLRQALEGGDLTKEAKEFLHEVVKMRVQKEKLSAALQAKRS LHQELEFLRVAKKEKLREATEAKRNLKEIERLRAENEKMKKEA NESRLRLKRELEQARQARVCDKGCEAGRLRAKYSAQIEDLQVKL QHAADREQLRADLLREAREHLEK\VVK\ELQEQWLWPRARPE AAGSEG\AAELEP
6969	1855	118	AGTMHGRLLKVKTSSEEAQAEAKRLEREQKLLYQSATQAVFQKRQA GELDESVLELTSQILGANPDFATLWNCREVLQQLTQKSPEEL AALVKAELGFLESLRVNPKSYGTWHHRCWLLGRLEPNWTRREL ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFDLSLITR NFSNYSWHYRSCLLPQLHPQDPSGPQGRLPEDVLLKELELVQN AFPTDPNDQSAWFYHRWLLGRADPDALRCLHVSDEACTVVSF SRPLLVGSRMEILLMVDDSLIVWRTPDGRNRP SHVWLCDL AASLNDQLPQHTFRVIWTAGDVOKECVLLKGRQEGWCRDSTTDE QLFRCELSVEKSTVLQSELESCKELQELEPENKWL\LTIIILM RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDLRSKFLLENS VLKMEYAEVRVLHLAKDLTVLCHLEQLLVTHLDLSHNRRLTL PPALAAALRCLEDPPT\VLQASDNATIESLDGVTNLPRLELL CNNRLQPAVLQPLASCPRLVLLNLQGNPLCAVGIQLELAELL PSVSSVLT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=-possible nucleotide deletion, \=possible nucleotide insertion)
6970	3	1528	SFPPLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIQLRPLNE GFLSRISGLLLCRWTCRHCCQKCYESSCCQSSSEDEVEILGPFPA QTPPWLMASRSSDKDGSVHTASEVPLTPRTNSPDGRRSSSDTS KSTYSLTRRISSLESRRPSSPLIDIKPIBFVLSAKKEPIQPSV LRRTYNPDDYFRKFEPHLYSLDSNDDVDLSLTDEEILSKYQLGM LHFSTQYDLLHNLTVRVIEARDLPPPISHDGRQDMAHSPYV KICLLPDQKNSKQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLL LTVVDFDKFSRHCVIGKVSVPVCEVDLVKGGHWWKALIPSSQNE VELGELLNLYLPSAGRLNVDVIRAKQLLQTDVVSQGSDFPVKI QLVHGLKLKTKTSFLRGITIDPFYNESFSFKVPQEELENASLV FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRMLNTHRT AVEQWHSLSRAECDRVSPASLEVT
6971	37	3702	ACFYVPGSRSEFKLIPRHGLVNMGRSGKLFSGVSAKLKRWKKGHS SDSNPAICRHRQAARSFRFSRPSGRSDLTVDVAVKLHNELOSGSL RLGKSEAPETPMEEAEVLVTEKSSGTFLLSGLSDCTNVTFSKVQ RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEYFAALIRKA AQHGVCVSLKGSSEFMFEKAPAHHPAAISTAKFCIQEIEKSGGSK EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA CAMQAFHSLFHARPGSLTSLAELNAQIITALYDYVPSENDLQPL LAWLKVMEKAHINLVRLQWDLGLHLPRFFGTAVTCLLSPHSQV LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV EEGLTYKFHAAWSSVLQLLCVFEACGRQAHFVMRKCLQSLCDL RLSPHFPHTAALDQAVGAAVTSMGPEVVLQAVPLEIDGSEETLD FFRSWLLPVIDHVQETRLGFFTTYFLPLANTLKSAMDLAQAG STVESKIYDTLQWQMTLLPGFCTRPTDVAISFKGLARTLGMAI SERPDLRVTVQALRTLITKGCQAEADRAEVSRFAKNFLPILEN LYGQPVAAADTPAPRRAVLETIRTYLTITDTQLVNSLLEKASEK VLDPASSDFTRLSVLDLVVALAPCADEAAISKLYSTIRPYLESK AHGVQKKAYRVLEEVCAAPQGGALFVQSHLEDLKKTLDSLSRS TSSPAKRPRLLKCLLHIVRKLSAEHKEFITALIPEVILCTKEVSV GARKNAFALLVEMGHAFRLFGSNQEEALQCYLVLIYPGLVGAVT MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLASRTRDVV KSAIGFIKVAVTVMVAHLAKHVQLVMEAGKLSDDMRHFRMK LRNLT\KFIPK\FGILTWGKKAVGPKEYHRVLVNIKAEARAK RHRALSQAABEEEEEEEEEPAGGKGSIEEILADSEDEEDNE EEERSRGKEQRLARQRSRAWLKEGGGDEPLNFDLPKVAQRVLA TQPGPGRGRKKDHSFKVSADGRLIIREADGNKMEEEGAKGED EEMADPMEDVIIRNKKHQKLLKHQKEAEEEELEIPPQYQAGSGGI HRPVAKKAMPGAEYKAKKAGDVKKGRPDYAYIPLNRSKLNLR RKKMKLQGFKGLVKAQGRGSQVGHKNRRKDRRP
6972	2179	973	PGGAILLPLWRRTRPREATVPRGAAQRGRARSAGRI PSSQSPS PAEAGGATRSPPPRPPRPPGSAAPLLRS DAGPGATVSA AAATERARRGATMGAQLSTLGHMVLPPVNFYSLLMKLFQRSTP AITLESPIKYPLRLIDREIISHDTRFRFALPSPQHILGLPVG QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK FPAGGKMSQYLESQIGDTIEFRGPGSLVYQGGKFAIRPDKK SNPIIRTVKSVMIAAGGTGITPMLQVIRAIMKDPDDHTVCHLLF ANQTEKDILLRPELEELRNKHSARFKLWYTLDRAPAEADYQGG\ FVNEEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPLN\DHVGH PTERCVFV
6973	1	1964	LQPRCAHRLRAQKGRPA PGVDAMVLCVPVIGKLLHKRVVLASA SPRRQEILSNAGLRFVVPSPKFKEKLDKASFATPYGYAMETAKQ KALEVANRLYQKDLRAPDVVIGADTIVTVGGLILEKPVQKQDAY RMLSRFE/SGREHSVFTGVAVHCSKDHQLDTRVSEFYEETKV KFSSELSEELLWEYVHSGEPMKAGGYGIQALGMLVESVHGDFL NVVGFPNLHFCKQLVKLYPPRPEDLRRSVKHDSIPAADTFEDL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=-possible nucleotide deletion, \=possible nucleotide insertion)
			SDVEGGGSEPTQRDAGSRDEKAEAGEAGQATAEABCHRTRETLP PFPTRLLELIEGFMLS KGLLTACKLKVFDLLKDEAPQKAADIAS KVDSACAGMERLLDICAAMGLLEKTEQGYSENTETANVYLASDGE YSLHGFIMHNNDLTNLFTYLEFAIREGNTQHHRALGKKAEDLF QDAYYQSPETRLRFMRAMHGMKLTACQVATAFNLSRFSSACDV GGCTGALARELAREYPRMQVTVFDLPDIIELAHFQPPGPQAVQ IHFAAGDFFRDPLPSAELYVLCRILHDWDDKVKHLLSRVAESC KPGAGLLLVETLLDEEKRAVQALMQSLNMLVQTEGKERSLGEY QCLLELHGFHQVQVVHLGGVLDAIL\PPKWPPEQAACSL
6974	3082	2172	RSCAAFASFASRPLELFAPPGSHRSPPGGRVATSAQCALSVRK LLAARPLGLTKYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV SLPTNIIVPTTIWTSPPQNTDADTASPSNGTHNNSVLPTASAP TSLLPKNISIESREEEITSPGSNWEGTNTDPSPGFSSTSGGVH LTTTLEEHLGTPEAGVAATLSQSAEPPTLISQAPASSPSSL STSPPEVFSASVITNHSSTVTSTQPTGAPTAPESPTIESSSDHT PTSHATAEPVPQEKTPPTTVSGKVMCELI DMET\PPPPFG
6975	2	500	RPRPTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKEL KELLQTELSGGLFDVKELML*ATEALKTFEEA*KSPIIQCSSRS SLPPAPQPPPYL*LSAVPFPPIHLPLPLPPQAQKQDVAVDKVMK BLDENGDEVDQFQBYVVLVAALTVCACNNFFWENS
6976	1216	970	GCQL*VAYGTTENSFVTFAHFPEDTVEQKAESVGRIMPHTEAR NMMEAGTLAKLNTPEGLCIRGYCVMLGYWGEPOKTEEAVDQDKW YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFHTH PKVQEVQVVGKDDRMGEEICACIRLKDGBETTVEEIKAFCKGK ISHFKIPKIYIVFVTNYPLTISGKIQFKLREQMERHLNL*IKQQ ACPGRLA
6977	1298	588	SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLTPTDFA*R ANKKSKHHVNGNRTVEPPEGTOMAVFGMCGFNGAERKFWVLKG VYSTQVGFAGGYTNSNPTYKEVCSSEKTHAEVVRVYQPEHMSFE ELLKVFWEHNDPTQGMROGNDHGTQYRSAIYPTSAKQMEALSS KENYQKVLSEHGFGPITTDIREGQTFYAYEDYHQYLSKNPNGY CGLGGTGVS CPVGIKK
6978	3	242	SFFPRDSRRCCGCKGSSLRHTAVAMVKLSKEAQRLQQLFKGSQ FAIRNGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
6979	3917	1146	DEARVRGEAVAAALSRCRHWSGPPPPPPSPDRKGLRGTEPWE AGPGSGATPGARAMDVRLKVNLEELQRRGLDTRGLKTELAE RLQAALAEAEPPDERELDADDEPRPGHINEEVETEGSELEGT AQPPPPGLQPHAEPPGGYSGPDGHYAMDNI TRONQFYDTQVIKQE NESGYERRPLEMEQQAYRPEMKTEMKQGAFTSLPPEASQLKP DRQQFQSRKRPIYENNRGRGYFEHREDRRGRSPQPAEDEDDED DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDS CSTQL GEEPFSYGGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN DVELSFTKNGKMMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF GQRAEPPYCSVLPGFTFIQHLPLSERIRGTVGPKSACEELMMV GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR NYAGRWDLVLIQQATQCLNRLIQIAARKKRNILQDNTNVSQAQR RKMRFPEFGQRKAIVICPTDEDLKDRTIKRTDEBGKDVDPHVL EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP PPEKRFDNRGGGGFRGRGGGGGFQRYENRGP PGGNRGGFQNRGG GSGGGGNYRGGFNRSGGGGYSQNRWGNMNRDNNSNNRGSYNRA PQQPPPPQPPPPPPPPPPPPPSYSPARNPPGASTYNKNSNI PGSSANTSTPTVSSYSPPQSGFFPSTFQPSYSQPPYNQGGYSQ GYTAPPPPPPPPAAYNQSGWGYNPAPYTPPPPTAQTPYQPSY NQYQCYAQQWNQYQNGQWPPYYGNPYDGSYSGNTQGGTSTQ
6980	1	420	GTRGRKTGRVAAPSTRRTGNMQKLQTRSPAMLSDPGLGYHPT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			CWTLRWFPPLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCSCEA GGSCACAGSCCKCKCKCTSCCKSCCSCCPLGCAKCAQGCICKGA SEKSCCA
6981	10	1054	PGRGFRRLRPAFAARGVFQGGGLGQAKQARTRACAALPTPHPS APRLLEPQGVFSLFPFPPGPWPNMILTAKQYDEIAQCIVSVPT RQSLRLKQRFPSQSQTALLSIFSQYQKHKRTHAKHHTSEAI ESYYQRYLNGVVKNGAAPVLLDLANEVDYAPSLMARLILERFLQ EHEETPPSKSIINSMRLDPSQIPDGVLANQVYQCIVNDCCYGFL VDCIKHAIGHEHEVLLRDLLLEKNLSFLDEDLRAKGYDKTPDF ILQVPVAVEGHIHWIESKASFGDECSHHAYLHDQFWSYWNRF PGLVIYWGFIQELDCNRERGILLKACFPPTNIVTLCHSIA
6982	153	1285	FFQDDCSAPAAPGLAGSEPRRLRAYRRRRQRARGLKRVAVLAPP PSLLQGLQGWAPVDGTLGPDERSASSPMIQNSRPSLLQPDQV GDTVETLMLHPVIKAFLCGSI SGTCTLLFQPLDLLKTRQLTLQ PSDHGSRVRGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI YFGTLYSLKQYFLRGHPPTALESVMLGVGSRVAGVCMSPITVI KTRYESGKYGESIYAALRSIYHSEHGRGLFSGLTATLLRDAPP SGIYLMFYNTKNI VPHDQVDATLIPITNFCGIPAGILASLVT QPADVIKTHMQLYPLKFQWIGQAVTLIFKDYGLRGFFQGGIPRA LRRTLMAAMAWTVYEEMAKMGLKS
6983	82	773	EMSFLLQDPSFPTMGWSTIGAGALGAALALLANTDVLSPKPKQ AALEYLEDIDLKTLKEKEPRTFKAKELWEKNGAVIMAVRRPGCF CREEAADLSLKSMLDQLGVPLYAVVKEHIRTVEVKDFQPYFKGE IFLDEKKKFFYGPQRKMMFMGFIRLGVWYNFFRAWNGGFSGNLE GBGFILGGVPVVGSGKGILHEHREKEFGDKVNLLSVLEAAKMI KPQTLASEKR
6984	1845	1282	GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVR KCSTPEEIKRRKKAVIFCLSDKKCIIVEEGKEILVGDVGVTTIT DPFKHFVGMLEPKDCRYALYDASFETKESRKEIMFFLWAPELA PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNACIAEKL GSLIVAFEGCPV
6985	1887	1324	RRTAGIYPCFPKGRTRHALCSVVLILLTGQLAFDDFQESCAMM WQKYAGSRRSMPGARI LFGVGYAGGFAIVYYLIQKFSRALY YKLAVEQLQSHPEAQEALGPPLNIHVLKLDRENFVDIVDAKLL IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDQGIIPVFK LSGENGDEVKKE
6986	642	1350	YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQDFKMYIAF VFKEKKKKSALFEVSEVIPVMTNNEYENILKGVDRDSSYSLESSL ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC LLFSRWKESDEPPRPVQAKFEFHGDYEQQLHVLRSRKDKTGIV VNNPNQSVFLFIDRQHLQTPKNKATIFKLCSICLYLPQEQLTHW AVGTIEDHLRPYME
6987	1623	341	LEAAEKASRAFKESQRQTD SKNYETENWSPQKSQRRYDMYNTAC FLGEIEVGLYTIQILQLTPFFHKENELSKGHMVQFLSGKWTIPP DPRNECYLALS KFTSHLKNLQSDLRKCFDFFIDYMLVKMRYTQ KEIABIIMLSKKVSRFCFRKYTELFCCLDPLQLQSKESQLQBE RKKLEALRADRFAGLLEVLNPNYKDATTMESIVNEYAFLQONS KKPMTNEKQNSILANIILSCLKPNKLIQPLTLKKQLREVLFQ VGLSHQYPGPYFLACLLFWPENQELDQDSKLEKYVSSLNRSFR GQYKRMCRSKQASTLFYLGKRKGLNSIVHKAKIEQYFDKAQNTN SLWHSQDVNKKNEVKDLRLRLTGQAEGKLISVEYGTEEKIKIPV ISVYSGPLRSGRNIERSVYLGFSIEGPPGL
6988	3	689	TQLLRPAVFGSAASGIRSLWSASSGHWCAAGRAHAPVPR LVRLGLAATAAPQDAQTPQPMPRADCMRHLPHYFCRGQVVRG FGRGSKQLGIPTANFPQVVDNLPADISTGIYGWASVSGSDVH KMVVSIGWNPYYKNTKKSMETHIMTFKEDFYGEILNVAIVGYL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
			RPEKNFDSLESLSIAIQGDIBEAKKRLPEHLKIKEDNFFQVS KSKIMNGH
6989	2	1118	LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPFGSKSNMATL KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADEL ALVDVIEDKLKGEEMMDLQHGSLFLRTPKIVSGKDYNTVANSKLV IITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIV SNPVDILTIVAWKISGFPPKNRVIGSGCNLDSARFYLMDGERLGV HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDK EQWKEVHKQVVESAYEVIKLGYYTSAIGLSVADLAESIMKNLR RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE EARLKKSADTLWGIQKELQF
6990	719	258	THASGMASVVLALRTRTAVTSLSPPTALAVRYASKKSGGSS KNLGKSSGRRQGIKKMEGHYVHAGNIATQRHFRWHPGAHVGV GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY KTFVHVVPAPKEGTFKLVLAM
6991	169	451	RRSSDFHNPGLSRPVSLRENIHQVICSTKNRRNPKKIAYLL SLLMTNLNPNESTENQPVDAWAFDLDQEFLLTYACVEGTGCLF CGRHVH
6992	944	510	RQAPGCSSLALRQVRQVYCGLVRAVQVQTRPLSSRFVVERRGALY RSPMNQENPPYPGPGPTAPYPPYPQPMGPGMGPPYPPQGY PYQGYPYQGWQGGPQEPKTTVVVVEDQRRDELGPSTCLTACWT ALCCCCLDWMLT
6993	1	374	QWCVTCPQHNRQGPVAPPGIQAYGAAPPEDLQVDFTEMSKCRG DRVWIKNWNVASLCPWLKGPQTVVLSPPATAVKVEGIPAWIHSH VKPAARETWEARSPDNPFRTVLKKTSPAPVTPGS
6994	346	1100	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAQR RDPFAPPGQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES SSQVLWAISSAISVAFFALSGIAAQLNLALGLAGDYLALQGLKLS PGQVQTFLLWGAGALVVYWLSSLLGLVLALLGRILWGLKLVI F LAGFVALMRVDPSTRALLLLALLILYALLSRLTGSRASGAQL EAKVRGLERQVEELRWRQRRRAAGARSVEEE
6995	144	1346	GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL LLEQFFLPHSRGSSHGQSRIRKAYLEDFTYRMHECYQIWAQL EHEAGTQLHRQTGLLLGMKENQELKTIQANLSRQRVEHQCLSS EELKQRFNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG GIVRDGEKVVEINPGLLVTKTTSRSYQAKSLVITAGPWTNQLL RPLGIEMPLQTLRINVCYWRMVPGSYGVSAFFCFLWLGLCPH HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL SSFVRDHLPLDKPEPAVIESCMYTNTPDQFILDHHPKYDNIVI GAGFSGHGFKLAPVVGKILYELSMKLTSPSYDLAPFRISRFP SLG KAH
6996	543	1942	ETANAEEAAARKSAMDWKEVLRRLATPNTCPNKKKSEQELKDEE MDLFTKYSEWKGRKNTNEFYKTI PRFYRLPAENEVLQLKL R EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTTPMIGEAMIN YENFLKVGKAGAKCKQFFTAQVFAKLLHTDSYGRISIMQFFNY VMRKVWLHQTRIGLSLYDVAGQGYLRESOLENYILELIPTLPQL DGLEKSFYSFYVCTAVRKFFFLDPLRTGKIKIQDILACSFLDD LLELRDEELSKESQETNWFSAFSAFVYGYLNLDKDHNGMSK EELSRYGATATMTNVFLDRVFQECITYDGEDYKTYLDFVLALEN RKEPAALQYIFKLLDIENKGYLVNVSFNYFFRAIQELMKIHGQD PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTITLIDL NGFWTYENREALVANDSENSADLDDT
6997	370	1104	AMELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFYFLVRF TVIYNEQMAKKRELFSNLQEFAGPSGKLSLLEVCGGTGANFKF YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QVADGSVDVVVCTLVLCVSKQERILREVCRVLRPGGAFYFMEH VAAECSTWNYFWQVLDPAHLLFDGCNLTRESWKALERASF LKLOHIQAPLSWELVRPHIYGAVK
6998	2	616	FVSRALLRVSRRHFAERAAAPGRFEDAPIECPGATNCPEPLWC SHLPVPYAPPTMESRGKSASSPKPDTKVPQVTEAKVPPAADGK APLTKPSKKEAPAEKQPPAAPTAPAKKTSKADPALLNNHNSN LKPAPTVPSSPDATPEPKPGDGAEEDEAASGGPGGRGPWSCN FNPLLAVAGVAVAAIALILGVAFLVRKK
6999	14	1591	GRAGACSRRTAMSTIESSDVIRLIMQYKENS LHRALATLQE ETTVSLNTVDSIESFVADINSCHWDTVLQAIQSLKLPDKTLIDL YEQVLELIELRELGAARSLLRQDPMIMLKQTQPERYIHLENL LARSYFDPREAYPDGSSKEKRAAIAQALAGEVSVVPPSRMLAL LQQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFTQLSRH IKFGQKSHVECARFSPDQYLVGTSGVDGFIEVWNTTGKIRKDL KYQAQDNFMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKISG QCLRRFERAHSKGVTCLSFSKDSQILSASFQDQIRIHGLKSGK TLKEFRGHSSFVNEATPTQDGHYIISASSDGTVKIWNMKTECS NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVIMNMQ GQIVRSFSSGKREGGDFVCCALSPRGEWIVCVGEDFVLYCFSTV TGKLERLTVEKDVIGIAHHPQNLATYSBDGLLKLWKP
7000	2	827	GPGVVFLMESEGPPESESEFFSQRENEEEEAQEPETGP KNPLLQPALTGDEGLQKIFEDPENPHHEQAMQLLEEDIVGRN LLYAACMAGQSDVIRALAKYGVNLNEKTRGYTLHCAAAGRL ETLKALVELDVDI EALNFEERARDVAARYSQTECVFELDWADA RLTLKKYIAKVS LAVTDTEKSGSKLLKEDKNTILSACRAKNEW ETHTEASINELFEQRQQLDIVTPIFTKMTTPCQVKSASVTSH DQKRSQDDTSN
7001	2056	844	RRCLIIAFLKGCFFIYFIFIFETEFSLCCPGWSAVAQSRLIAN FASQVQAI FILPKDSQVGPDKSEAPKRALYESVFGSGEICGP TSPKRLCIRPSEPVDVAVVSVKHDPLPLPEANGHRSTNSPTI VSPAIVSPTQDSRPNMSRPLITRSPASPLNNQGIPTPAQLTKSN APVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDLSLQ HYFIDRDGQMFYIILNFLRTSKLLIPDDFKDYTLLEYEAKYFQL QPMLEMERWKQDRETGRFSRPECCLVVRVAPDLGERITLSGDK SLIEEVFPFEGDVMCSNVAGWNHDS THVIRFPLNGYCHLNSVQ VLERLQQRGFIEVSGCGGVDSQFSEYVLRRELRTTPRVPSVI RIKQEPDL
7002	1043	498	PMPSSSTRWITS*TYTDTSSAWACRPTTGCT*TAAPGPTVRWWP TPCSRHQSRRLTCWCSTSRPCGR*GGLCVRTAPTPTTSASSS SWTSAGTSWPAGRRGTATSGTATTSVWPGCGTRMWSTQWSSV PRSRCCSRPATTPPSKPGAPHAPCASSRHLAHLAPSSPGLPA RGAEVC
7003	818	61	QGRFRAFQWQDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRPVVVEPISEDDWYLFCDTVEILBGKDA GKQGVVQVIRQRNVVVGGLNTHYRYIGKTM DYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLTQLQEEVMEAM GIKETR\NTRRSIGIEPGAEQLLPNFCPSLEG
7004	121	2285	FLLPVLTSRSLRQPAVPHARLGGVEPAAAMKSARAKTPRKPTVKK G\PKRTLKTLQGL/YICRVRLPGFPDQCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVGTSGKTHMTGSPGEGGLLPRCLDMI FNSIGSF QAKRYVFKSNDNRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQEFCKAEVEDEDSVYGVFVSYIEIYNNYIDLL EEVPPDPINPNLHNLNCFVKIKNHNMVYAGCTEVEVKSTEBAFE VFWRGQKKRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
			QEKEQITISQLSLVDLAGSERTNRTAEGNRLREAGNINQSLMT LRTCMDVLRENQMYGTNKMVPYRDSKLTFLFKNYFDGEGKVRMI VCVNPKAEDYEENLQVMRFAEVTQVEVEVARPVDKAIICGLTPGRR YRNQPRGP\IGNEPLVTDVVLQSFPLPSCEILDINDEQTLPLRL IEALEKRHNLRQMMIDEFNKQSNAFKALLQEFDAVLSKENHMQ GKLNEKEKMLISGQKLEIERLEKKNKTLEYKIEILEKTTIYEED KRNLOQEELETQNKQLQRQFSDKRRLEARLQGMVTETTMKWEKEC ERRVAAKOLEMONKLVKDEKQKQKAIIVTEPKTEKPERPSRER DREKVTQRSVSPSPVPVSYL
7005	63	876	RNMALVQRWRCLRLQGLQACRLHTAVVSTPPRWLABRLGLFEEL WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ ISSTLADTAAQAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV FWHSSTHVLGAAAEQFLGAVLCRGPSTBYGFYHDFLKGERTIR GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHL IEEKVTGPTATVYGCGLVDLQCGPHLRHTGQIGLKLSSNSS LWRSSG
7006	22	898	NAFGRHSTAVKMAAAWLQVLVILLLLGAHPSPLSPFSGAGPAT VAAADRSKWHIPISPGKNYFSFGKILFRNTTIFLKFDEGEPCLDS LNTITWYLSADCYNEIYNFKAEEVELYLEKLEKRGSLGKYQTS SKLPQNCSELFKTQTFSGDFMHRPLPLGKQEKENGNTNLTFIG DKTAMHEPLQTWDAPYIFIVHIGISSSESSKENSLSNLFMT VEVKGPPYEYLTLEDYPLMIFMVMCIIVYVLFVGLWLWASACYWR DLLRIQFWIGAVIFLGMLEKAVFYAGFQ
7007	2	1001	AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA YTQALGLDATPDQAVLHNRNRAACHLKLEDYDKAETEASKAIEK DGGDVKALYRRSQALEKLRDLQAVLDLQRCVSLPEPKNVFQEA LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKGTETKQKAS QNLVVLAREDAAGABKIFRSNGVQLLQRLDMGETDMLAALRTL VGICSEHQSRVATLSILGTRRVVSILGVESQAVSLAACHLLQ MFDALKEGVKKGFRGKEGAIIVGEWKQVWGLLDVTVMEGMGLSQ PGQFFGDQTCSCRLPGIRFGDIILL
7008	70	1478	CRSALGHERPPPAHLFAGGRRLQTCPRSCRWLGRPPSGLPFGPR SPPLAGPGQKMVQKPAELQCFHRSFKQNPFEALFSLDQDPDH GDSDFGLQCSARPDMPASQPIDIPDAKRGKKKRGRATDSFSG RFEDVYQLQEDVLGEGAHARVQTCINLITSQYAVKIEKQPGH IRSRVPREVEMLYQCQGHNRVLELIEFFEEEDRFYLVFEKMRGG SILSHIHKRRHFNELEASVVQDVASALDFLHNKGIAHRDLKPE NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS AEYMAPEVVEAFSEASIVDKRCDLWSLGVILYILLSGYPPFVG RCGSDCGWDRGEACPACQNMFLFESIQEGKYEPDKDWAHISCAA KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR WDSHFLPPPHCRIHVRPGGLVRTVTVNE
7009	1	626	ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA LRLVACAQSGHEVTLSNLSMPPPKFHDTSPLMVTPPSAEAH WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMSKLPDLVL GRVWDLSDIDKDGHVLRDEFAMHLVYRALE
7010	79	571	SHTRRVVPETLLSPLCPLGGGTAMSGGEQKPERVYVGVVDVGT GSVRAALVDQSGVLLAFADQFIKNWEPQFNHHEQSSEDIWAACC VVTKKVVGIDLNQIRGLGFDTCSLVVLDKQFHPLPVNQEGBDS HRNVIMWLDHRAVSQVNRINETHKSVLQYVGG
7011	3	994	RIQTLPNQNSQTOPLKTPFAVLQPIABQTTFGVQTQPPQPSL LQAQISAASITPLLQTPQLLQPPQKAGLLQPPVRIVSQPPQ ARRLDPPSRFSGRNDRGDQVFNRRKDRSRERERERRRSRERSPO RKRSRERSPRRERERSRPRVRRVFRYTVQFSKFSLCDPCSCDM ELRRRYQNLVIPSDFDAQFTWVDAFPLSRPFQLGNYCNFYVMH

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			REVESLEKNMILDPDADHLYSAKVMLMASPMSMEDLYHKSCAL AEDPQBLRDGFQHPARLVKFLVGMKGKDEAMAIGHWSPLDGP DPEKDPVLIKT\AIRCKALTG
7012	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKA AAAAAAATGTEAGPGTAGGSENGSEVAAQAGLSGPAEVGPGA VGERTPRKKEPPRASPPGGLAEPGSGAGPQAGPTVVPGSATPME TGIAETPEG\RRTSRRKRAKVEYREMDSELANLSEDEYYSEER NAKAEKEKKLPPPPQAPPEEENESEPEEPGVEGAFAQSRLPH DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQWLNDNPKIQL TFEATLQQLLEAPYNSDTVLVHRVHVSYLERHGLINFGIYKRIKPL PTKKTGKVIIGSGVSGLAARQLQSFQMDVTLLEARDRVGGRV ATFRKGNVADLGAMVVTGLGPNMAVVSQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATS YLSHQLDFNVLNKMP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELEKLLNKMV NLKEKIKELHQYKEASEVKPPRDTAEFLVKS KHRDLTALCKE YDELAETQGLKEELQLEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFBTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNRSTSTQTFIYKCDAVLCTL PLGVLKQPPAVQFVPPLEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGS TTASRGELFLFVNLKAPILLALVAGEAAG IMENISDDVIVGRCLA ILKGIFGSSAVPQPKETVVSRRWADPWA RGSYSYVAAGSSGNDYDLMAQPIITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPQATPGVP AQQSPSM
7013	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKA AAAAAAATGTEAGPGTAGGSENGSEVAAQAGLSGPAEVGPGA VGERTPRKKEPPRASPPGGLAEPGSGAGPQAGPTVVPGSATPME TGIAETPEG\RRTSRRKRAKVEYREMDSELANLSEDEYYSEER NAKAEKEKKLPPPPQAPPEEENESEPEEPGVEGAFAQSRLPH DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQWLNDNPKIQL TFEATLQQLLEAPYNSDTVLVHRVHVSYLERHGLINFGIYKRIKPL PTKKTGKVIIGSGVSGLAARQLQSFQMDVTLLEARDRVGGRV ATFRKGNVADLGAMVVTGLGPNMAVVSQVNMELAKIKQKCP LYEANGQAVPKEKDEMVEQEFNRLLEATS YLSHQLDFNVLNKMP VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELEKLLNKMV NLKEKIKELHQYKEASEVKPPRDTAEFLVKS KHRDLTALCKE YDELAETQGLKEELQLEANPPSDVYLSSRDRQILDWHFANLE FANATPLSTLSLKHWDQDDDFBTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVNRSTSTQTFIYKCDAVLCTL PLGVLKQPPAVQFVPPLEWKTSAVQRMGFGNLNKVVLCFDRV FWDPSVNLFGHVGS TTASRGELFLFVNLKAPILLALVAGEAAG IMENISDDVIVGRCLA ILKGIFGSSAVPQPKETVVSRRWADPWA RGSYSYVAAGSSGNDYDLMAQPIITPGPSIPGAPQPIPRLFFAGE HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPQATPGVP AQQSPSM
7014	3	3950	DFEVGDKIRILATLEDGWLEGLKGRGTGIFPYRFVKLCPDTRVE ETMALPQEGSLARI PETS LDCLNTLGVEEQRHETS DHEASEPD CIISEAPTSPLGHLTSEYDTRNSYQDEDTAGGPPRSPGVWEM PLATDSPTSDPTEVVNGISSQPVFPFHPNLQKSQYYS TVGGSHP HSEQYPDLLPLEARTRDYASLPKRMYSQLKTLQKPVLPYRGS SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG PQAQGLVMEAAHSGQDGSTDLDSKLTQQLIEFEKSLAGPGTEP DKILRHFSIMDFNSEKDIVRGSSKLTITEQELPERRKALRPPPPR PCTFVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPSPAQQRTNAV SPKLLSRHPTCETLEKEGPGHMGSRSLDQTS PCPLVLVRIEME RDLDMYSRAQEELNLMLEEKQDESSRAETLEDLKFCESNIESLN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			MELQQLRBMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIE ELLQTERDYIRDLEMCIERIMVPMQQAQVFNIDFEGFLFGNMQMV IKVSKQLLALEISDAVGVPVFLGHRDELBGTYYKIYCNHDEAIA LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFLIKP VQRVMRYPLLMELLNSTPESHDPKVPILTNAVLAKEINVNINE YKRRKDLVLKYRKGDDESLMEKISKLNHISIIKKNRVSSHLKH LTGFAPQIKDEVFEETKFNFRMQLERLIKSFIRDLSLYLQHIRE ACVKVVAVSMWDVCMERGHRLDQFERVHRYISDQLFTNFKER TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAELK DKKTEELQSARNNYEALNAQLLDELPHKQYQAQGLFTNCVHG AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEHSRLVQ QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYMLQSE ELRASLLARYYPEKLFQAERNFNAQQLDVSLEGLDVGVIKKK DPMGQNRWLIDNGVTGKGFVYSSFLKPYNPRRSHSDASVGS TESEHGSSSPRFRQNSGSTLTFTNPN\S\MAVSFTSGSCQKQPO DASPPPKWDQGTLSASLNPSNSESPPSRCPSPDPSTSQPRSGD SADVARDVKQPTATPRSYRNFHPEIVGYSVPGRNGSQDVLVK CARTAQAPEDRSTPDGSEAEGNQVYFAVYTFKARNPNELSVSA NQKLKILEFKDVTGNTTEWLLAEVNGKKGYVPSNYIRKTEYT
7015	1842	513	RQAWHE\VAAPSWRGARLVQSVLRVWQVGHVAREVIFFSLL GFORRCVSCVAGSAFSGPRLASASRNGQSALDHFLGFSQDPS SVTPCVPVAVSMNRDEQDVLVHHPDMPENSRVLRVVLGAPNAG KSTLSNQLLGRKVFPVSRKVHTTRCQALGVI TEKETQVILLDTP GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTNR QLSPQLLRCLTKYSQIFSVLVNMKVDCLKQKSVLLELTAALTEG VVNGKKLKMRAQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIWPH FKEIFMLSALSQEDVTKLQVLLTQAQPGFWEYHSAVLTSTQTP ETCANIREKLEHLPEBVPYVQVQKTAVWEBGPGGELVIOQKL LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRLSV KLLK
7016	167	2513	ILNAPKPPPPRDSVEAVAARKTGGGSGWTGMDVSGQETDWRST AFRQKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYLS LVARLIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAAGIGM PPRGPGQSLGGMGSLGAMGQPMSSGQPPPGTSGMAPHSMVVS TATPQTQLQLQVAAAAAATARSSSSSSSRRYSSSSSSSSNSKQ FQAQSSAMQQ\QFQA\VVQQQQQL\QQQQQQQHLIKLHHQNNQ QIQQQQQQLQRIAQQLQQQQQQQQQQQQQQALQAQPPPIQPP PMQPPQPPPSQALPQQLQOMHTQHHPQPPQPPQPPVAQNQPSQ LPPQSQTQPLVSAQALPGOMLYTQPLKFRVAPMVVQPPVQPP QVQQQQTAVQTAQAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP QSMPPPPQPPSPQPGQPSQPNNSVSSGPAPSPSSFLPSPPQPF \QSPVTARTPQNFVSPSPGLNTPVNPSSVMSFAGSSQAEEQQY LDKQLKLSKYIEPLRRMINKIDKNEDRKKDLKMKSLLDILTDP SKRCPLKTLQKCEIALEKLNDAVPTPPPPVPPTKQQYLCQP LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR RLEDDERQSIPSVLQGEVARLDPKFLVNLDPHSCSNNGTVHLIC KLDDKDLPSVPPLELSVPADYPAQSPLWIDRWQYDANPFLQSV HRCMTRLLQLPDKHSVTALLNTWAQSVHQAACLSAA
7017	1	1785	INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL FAFLAHTQREAYAPRIFFEASRPWFPTPRSQDCEYLRFLDDR LHEEEKILKVQASHKPSLEILECSETSLQEVASKAAVLTETPTS DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEFTDLSLAFWPS YSLEYMSCPDCSQSPSIQDGLMQASVPGPSEEPVYNPTTAAF ICDSLNEKTIIGSPNEFYCSENTSVPNESNKILVNKDVQPKPG GETTPSVTDLLNYFLAPEILTGNQYYCENCASLQNAEKTMTIT EEPEYLILTLRFSYDQKXHVRRKILDNVSLPLVLELPVKRITS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			FSSLSESWSDVDFTDLSENLAKKLKPSGTDEASCTKLVPYLLS SVVVHSGISSESGHYYSYARNITSTDSSYQMYHQSEALALASSQ SHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSRVTFTSFQSVQK ITSRFPKDTAYVLLYKKQHSTNGLSGNNPTSGLWINGDEPLQKE LMDAITKDNKLYLQEQELNARARALQAASASCSPRPNFGDDNDP PGSCGPTGGGGGGGENTVGRLLVF
7018	464	1066	SLVFRGNTWSGEAGHHCALFNLAAYHQLFVGTERIRAPEIIFQ PSLIGEEQAGIAETLQYILDYRYPKDVQEMLVQNVLTGGNTMYP GMKARMEKELLEMRPFRSSFQVQLASNPVLDWYCARDWALNHL DDNEVWITRKEYEKGGEYLKEHCASNIYVPIRLFKQASRSSDA QASSKGSAAAGGGGAGEQA
7019	1048	335	APGGFLVTMVFPAPSPPPWMLGCCSHEVTAGPPTLCKDMSALVAA RMRHIPLAGSDWRDLPNIEVRLSDGTMARKLRYTHHDKNGRS SSGALRGVCSCEAGKACDPAARQFNTLIPWCLPHTGNRHNHWA GLYGRLEWDGFFSTTVTNPEPMGKQGRVLEHPEQHRVSVRECAR SQGFDPDYRLFGNILDKHRQVGNVPPPLAKAIGLEIKLCMLAK AREASAKIKEEEAAKD
7020	1	2154	FADSKRKSVDLTKIKNLQVALTSKQQSLETAMSFVARNTFKVR NGFLMRKVAVFFSNTPTRASQRLREAVLKLSDAGITPLFLTRQE DRQLINALQINNTAVGHALVLPAGRDLTDFLENVLTCHVCLDIC NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAEITTLFQF NEMKKYIAYLVRLQDMSDPKASQHFARVAVVQHAPSESVDNAS MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGSAIETI ENVFESAPNPRDLKIVVLMILTGEVPEQQLEAQRVILQAKCKGY FFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLMR FGRLLPSFVSSSENAFYLSPIRQCDWFQGDQPTKNLVKFGHKQ VNVPNVTSSPTSNEPVTITTKPVTITTKPVTITTKPVTITTKPVTI INQPSVKPAAAKPAPAKPVAAPKPVATKTATVRPPVAVKPATAAK PVAAPKPAVRPPAAAAAKPVATKPEVPRPQAAPKPAATKPAATKP MYKMSREVQVFEITENSARKLHWRPEPPGPYFYDLTVTSAHQDS LVLKQNLTVTDRIVIGLLAGQTYHVAUVVCLRSQVRATYHGSFS TKRSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG TCRDFILKWYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA PVLAKPGVISVMGT
7021	2	338	VNAVFFPNGYAFATGSDDATCRLFDLRADQELLYSHDNIICG ITSVAFSKSGRLLLAGYDDFN CNVWDTLKGDRAVLGHNDNRVS CLGVTDDGMAVATGSWDSFLRIWN
7022	2	856	VYIGSFWSHPLIPDNRLFEAEQDLFRDIQSLPRNAALRKLN DLIKRARLAKVHAYIISSLKEMPSVFGKDNKKKELVNLAETIY GRIEREHQISPGDFPNLKRMDQLQAQDFSKPQLKSKLLEVVD DMLAHDIAQLMVLVRQEESSORPIQMVKGGAFFGLHGFPGHGYG EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH ELPNELPAHLPPSKRKVAE
7023	2	748	AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF WFGRRFESPLLWQSAIMILTMLMLKLTCEVVRVANELNARRRSF TAADSKDEEVKAPRRSFLDFDPHFWQWSSFSYVQCVLAFQT VAGYITLSDISALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMTSGDAFKTAYFLKGAFLQFSVCGLLQVLVDLA ILGOYAFARHPQKPAPHAVHTGTAL
7024	1207	190	RTGVTGVVAQVWMFGGGVLSSGEQLQMPVKPERGLGPSDGLV SSRRGSPGTVLGLPFWLLTPVLVSRISIRSMLLLTRSPTAHRRLS QLKPPVLPPTLGGQALHLRSWLLSRQQPAETGGGQGPQGPGLRT RLITGLFGAGLGGAWLALRAEKRLQQQKRTALRQAAVGQGD FHLLDHRGRARCKADFRGQVWLMYFGFTHCPDICPDELEKLVQV VRQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHERLLGL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7025	232	832	TGSTKQVAQASHSYRVYNNAGPKDEDDQDYIVDHSIATYLLNPDG LFTDYGRSRSAEQISDSVRRHMAAFRSVLS ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNQEECF KQVIRTCERPTFNQHTVFNLHQRNLNTGDKLNEFKELGKAFISG SDHTQHQLIHTSEKFCGDKCEGNTFLPDSEVIQYQTVHTVKKTY ECKECGKSFSLSRLTGHKRIHTGEKPFCKDCGKAFRHSQLS VHKRIHTGEKSYECKECGKAFSCG
7026	328	1146	NPNSIGDIDKIKKAASMLDPAHKSHFHPVTPSLVFLCFIDG LHQALLSVGVSKRSNTVVGNEENERGTPYASRFKMPNFIALEK SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS HGESADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE EKKNNG*KGIGEIF*VWGCTLPPHYWGAVTNVPKLSNSGKLLG QDEQPHIFG
7027	43	954	GRRLOQQRPEDAEDGAEGGGKRGEGAGWEGGYPEIVKENKLFEB YYQELKIVPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL KNKYFKELEDLEMDGQKVEVPQPLSWYPERLAWHTNLSRKILRK SPHLEKFHQFLVSETESGNISRQEAIVSMIPLLLNVRPHHKILD MCAAPGSKTTQLIEMHADMNVPFPEGFVIANDVDNKRCLLVH QAKRLSSPCIMVVDHASSIPRLQIDVDGRKEILFYDRILCDVP CSGDGTMRNIDVWKKWTTLSNLQLHGLQLRIATRGAEQL
7028	189	608	SRPPEPEPGTMEVKEGSDSSSEKGGVPGTPTSTQSLGSRNFIRNS KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQR EILLOGRLYLSENWICFYSNIPRWETTISIQLKEVTCLKKEKTA KLIPNAIQ
7029	1343	40	VLESNTEAKQATGTSSKLRHGTGQEKREGPRCPGSLAQLRLWG /PCPHAGRETGPASAPIPGS*GHGWHW*RKDGGERSEGPSAL SPHSPSLNNMQAPTHVPGMGSSQRPSSVVEQVGVGSQLSRE RWRA*RLPGAAASERTEMTKERSP/RPCQGYDSSNWPQPGKK TRKNSRRNTMVSRRGGCLLYPLQSIMPE*QLR*GAHASPTTG R*GKGGRSPLTKASGTTHIPTFFGSIIP/RPTRDSGPGTNDNS AAPGQKRGHREA*QGPEPV/WGRVTTHLQGEAG*TKPLGS\RNW VPGPAEGEQGEGAGLEGRP*PLKGCRLSTLTFSPQLSIPMVGKKP PEGTTASFFP\RSCHSE*RKPPSCPHAPALSLPHPLPLPLPL PLPLPGAGT*HSARSGRPGQSETGSLCHNCHCPCPKCSPGG T
7030	2	521	FVCFSPAGSGQGGKRRVNMELSAVGERVFAAEALLKRRIRKGRM EYLVKWKGSQKYSTWEPEENILDARLLAAFEEREREMELYGPK KRGPKPKTFLKQAQAKAKAKTYEFRRSDSARGIRIPYGRSPQDL ASTSRAREGLRN\RVCPRQRAAPAPAAP\PRRGPSGPGPRPG*G PGLHFPGGGPKKHGFVPASEQHQQHQLPRRGPSGPGPRPG
7031	960	59	HCSVPGAWEPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG /CKPS/RHCDLHEGFSRTAALPCGKPOPKHGVECG/PCPCLA PRRLTEPPALTVPVGRAPSGAL*PSGRACSACSHRLAPEAAL SAAAPRPSLGSQNASGLPAASLPPQDSSQPHKTVPSPARSVPP LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGPTPTST SGSTASHSRRC*SPR*TPAPPRRDHGRSAAFEVLTAASAQPC ASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCHPSL
7032	1393	2104	RRPGRTEPVEPPPPVPPPPRASNKSRRC*RNHLAPL*QSLRK SRQIGTSSLPFGRSAGERPRPAATFCLSRGSSPVFL*PSSSL EPWMKQFGRLLHSLFWKSWQKMNSFLLTPKLDTSLSMGWRYRQR LPRLHTFLKKSLSQASELAPPLTPAPLASSLPPPPGPPPLPV PLA*LSRSGILVPPNSGFSLSCLPLGDH*GSSGEVRGSCGSPPP HHCWVLPPPP*LLLPPR
7033	689	815	RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LMPSSCPWRTGALGPSAGSRALGRCTSSVGPGRWLRTSSP GCATRTWRTMRMEPRPLSRMGESAPGIPAEPLSAAPSGPSAPS AAAPSAPTTPAAAGPNTL*SRRTAENCWPPSCSCCWGWC*SWSA WDWRRPPLQVSPAPSSSCCRASCWCLESIT*SSSTARSRTGAS SSSTCPTSRSRGAATP\SPMGAPLLPCSVPPLISREELQDPR NPSP*GVCSGSSGHAGLALGKPPVACSVF
7034	92	1942	EDTSSMPFRLLIPLGLLCALLPQHGGAPGPDGSAPDPAHYRERV KAMFYHAYDSYLENAPFDELRLPTCDGHDWGSFSLTLIDALD TLL\TLFFYQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL TGDVPFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLWVQMYKGTVMMPVFQSLAYWPGQLSLIGDIDNAMRTFLNYY TVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDRNMFESF FLAETVKYL YLLFDPTNFIHNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFP KNTVSSGPWEPPARPPTLFSPEHNDQARERKPAKQKVPLLSGPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K
7035	92	1942	EDTSSMPFRLLIPLGLLCALLPQHGGAPGPDGSAPDPAHYRERV KAMFYHAYDSYLENAPFDELRLPTCDGHDWGSFSLTLIDALD TLL\TLFFYQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL TGDVPFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW YLWVQMYKGTVMMPVFQSLAYWPGQLSLIGDIDNAMRTFLNYY TVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRAT GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDRNMFESF FLAETVKYL YLLFDPTNFIHNGSTFDAVITPYGECILGAGGYI FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFP KNTVSSGPWEPPARPPTLFSPEHNDQARERKPAKQKVPLLSGPS QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK K
7036	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPDRDPHTTLRPLPP PPPPPPPPRRPPRRNRPG
7037	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPDRDPHTTLRPLPP PPPPPPPPRRPPRRNRPG
7038	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRAAFEEIIL QYNKLEKSDLHSLVAQKLQAEKHDVNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTIISDLETECLDLRTKCLDLERANQTLKDEYDA LQITFTALEGKLRTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAERACRSSKGTSTSRGT
7039	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRAAFEEIIL QYNKLEKSDLHSLVAQKLQAEKHDVNRHEISPGHDGTWNDNQ LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM QMNEAKIAECLQTIISDLETECLDLRTKCLDLERANQTLKDEYDA LQITFTALEGKLRTTEENQELVTRWMAEKAQEANRLNARE*KR LQEAASPAERACRSSKGTSTSRGT
7040	34	789	KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PGSQRRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRSSPRGLG EPFEIKVYEIDDVERLQRRRGASKEAMCFNAKLKILEHRQORI AEVRKAYEWLMKELEATKQYLM LDPNKLWSEFDLEQVWELDSLE YLEALECVTERLESRVNFCKAHLMMITCFDIT
7041	1	567	SGRVAMGRRRAPAGGSLGRALMRHQTRSRSHRHTDSWLHTSEL NDGYDWGRNLNLSVTEQSSLDLFLATAELAGTEFVAEKLNIKFV PAEARTGLLSFEBSQRIKKLHEENKQFLCIPRRPNWNQNTTPE LKQAEKDNFLEWRRQL\VRLEEQKLILTPERNLDFWRQLWRV IERSDIVVQIVDA
7042	7	345	PLHMAAALRAD\ISPLPFPHIQGYLLLSASHG\ATSLHTKGAL PLETVTMYTVIPKSKYVLVKPDTQYPYSENLEDFKRLAENSASN DDLMAEVAISDYGDKLTLELREKY
7043	2	2170	ARGMAARDSDSEEDLVSYGTGLEPLEBGERPKKPIPLQDQTVRD EKGRYKRFHGFAGSGGFSAGYFNTVGSKEGWTPSTFVSSRQNRAD KSVLGPEDFMDDEEDLSEFGIAPKAIVTDDFASKTKDRIREKAR QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMKGWKEGGVGP RVKRRPRRQKPDGPVKIYGCALPPGSEGESEGEDDYLDPNVT APKDVTPVDFTPKDNVHGLAYKGLDPHQALFGTSGEHFNLFSGG SERAGDLGEIGLNKGRKLGISGQAFGVGALEEDDDIYATETLS KYDTVLKDEEPGDGLYGTAPRQYKNQKESEKDLRYVGKILDF SLASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSENHLLQV LSESAGKATPDPGTHSKHQLNASKRAELLGETPIQGSATSVLEF LSQKDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQSPAAA AGHCSWNMALGGGTATLKASNFKPFKADPEKQKRYDEFLVHMKQ GQKDALERCIDPSMTEWERGRBRDEFARAALLYASSHSTLSSRF THAKEEDSDSQVEVPRDQENDVGDQKQSAVKMKMFGKLTDRDTEW HPDKLLFQ/RLVGLPRVKRDKYSVFNFLLTPETASLPTTQASSE KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPK QQSSPLVNKEEHAPELSAN
7044	276	734	EVYLTDEFAGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG EPTDEETGDISDSMDFVLLNFAEMNKLWVRMQHGHSRDREKR ERERQELRILVGTNLVRLSQV
7045	3	513	LGFKMEALS RAGQEMS LAALKQHDPIYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHHRHFGDAEQSQG
7046	3	513	LGFKMEALS RAGQEMS LAALKQHDPIYITSIADLTGQVALYTFCP KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK DLEFQLHEPFLLYRNASLSIYSIWFDKNDCHRIAKLMADVVEE ETRRSQQA/RSGQTESQPGQWLQRPQAHHRHFGDAEQSQG
7047	103	486	QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLNSKN IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY NEVKPSKSDS/IVPSYLAGVRSKKALDTAISLGPHSYER
7048	92	627	PFCLTLLSSWDYRHHATRRVSSPVFTMEDSGKTFSSSEEEANY WKDLAMTYKQRAENTQEELREFQEGSREYEALETQLQOIETRN RDLLSENNRLRMELETIKEKFEVQHSSEGYRQISALEDDLAQTKA IKDQLQKYIRELEQANDLERAKRATDHGLSKTFE\QRLN\QAI EKKW
7049	393	938	KRTGSASVGGPPPLGGPATXASVAGRCSSVGKIPARRCYEDEL VPVFEAVGRIYELRLMDFDGNRQYAFVMYCHKHEAKRAVREL NNYEIRPGRLLGVCCSDNCRFIGGIPKMKKREIELEIAKVT EGVLDVIVYASADKMKNRGLRLRGVREPPRGCHWLGRKLIAXW ASSLWG
7050	393	938	KRTGSASVGGPPPLGGPATXASVAGRCSSVGKIPARRCYEDEL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			VPVFEAVGRIYELRLMMDFDGKNRGYAFVVMYCHKHEAKRAVREL NNYEIRPGRLLGVCSSVDNCRLEFIGGIPKMKKREILEEIAKVT EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAX ASSLWG
7051	119	816	KKMNLAEICDNAKKGREYALLGNYDSSMVYYQGVMMQIQRHCS VRDPAIKGKQVVRQELLEEEYEQVKIVGTLESFKIDKPPDFPV SCQDEFFRDPAVWPPPPVPAEHRAPPQIRR/RQSRSKTSEERNR SRSPGTCRPS\PISKSEKPSRDKDYRARGRDDKGRKNMQDG ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDADIADLEEA KLLREAGVLPMMW
7052	467	715	SCPGRGKMSKLLNPEEMTSRDYFFDSYAHFGIHEEMLKDEVRTL TYRNSMYHNKHVPKDKVLDVSGGTGILSMFAARQGPRR
7053	467	715	SCPGRGKMSKLLNPEEMTSRDYFFDSYAHFGIHEEMLKDEVRTL TYRNSMYHNKHVPKDKVLDVSGGTGILSMFAARQGPRR
7054	1	1036	GTSQSRRETDARRRSAGAEPTARLPWPAALAEWPSCPCEPLGPG RRCRWDAMEYDEKLARFRQAHLPFNKQSGPRQHEQGPGEEVPD VTPEALPLPPGEPFRCPERVMDLGLSEDFSRPVGLFLASD VQQLRQAIBECKQVILELPEQSEKQKDAVRLIHLRLKQELKD PNEDEPNIRVLLSHRFYKEKSKSVKQTCDCNTI IWGLIQWTWT CTGCYYRCHSKCLNLISKPCVSSKVSQAEYELNICPETGLDSQ DYRCAECRAPI/CS/DGVVPSEARQCDYTGQYYCSHCHWNDAV IPARVVHNWDFEPRKVSRCMSRYLALMVSRPVLRLREIN
7055	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLFWKTFLLYNQGP EYHYLHQMLG/ALCLSRASASVLNLCNLILLPMCRITLLAYLRG SQKVPSSRRTRRLLDKSRTHITCGATICIFSGVHVAHLVNLALN FSVNYSEDFVELNAARYRDEDPKLLFTTVPGLTGVCMEVVLFL M
7056	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLFWKTFLLYNQGP EYHYLHQMLG/ALCLSRASASVLNLCNLILLPMCRITLLAYLRG SQKVPSSRRTRRLLDKSRTHITCGATICIFSGVHVAHLVNLALN FSVNYSEDFVELNAARYRDEDPKLLFTTVPGLTGVCMEVVLFL M
7057	1368	431	GIYLVNEKIPRPTCIGDRQENDKENLNLENHRDQELLHASCQA SGEVPQSASLRGFFTEDEPGCFGEENLPEALQNIQDEGTGQQL SPQERISEKQLGQHLPPNPHSGEMSTMWLEEKRETSQKQGPAPM AQKLPTCRECGKTFYRNSQLIFHQRTHGTETYPQCTICKKAPLR SSDFVKHQRTHTGKPKCKDCYCGKGFSDPSGLRHHEKIHTGEKP YKCPICEKSFQIRSNFNRHQRVHTGEKPKYKSCHCCKSFWSSSL DKHQRSHLGKKPFQ*PVTKLSFPISISQPSHKNTQLHQEELCLR GYPC
7058	1	469	FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRALCCKGPPPAR PEYDLVCIGLTGSGKTSLLSKLCESEPDNVVSTTGFSIKAVPFQ NAILNVKELGGADNIRKYWSRYQGSQGVIFVLDSASSEDDLEA ARN*SCTQLLQHPQLCTLPFLILA
7059	1	1178	WPAFPRQPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA APWARPSAWLECVVTFDLELGQALELVYPNDFRLTDKEKSSI CYLSFPDSHSGCLGDTQFSFRMRQCGGQSPWHADDRHYNSRAP VALOREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAAPAGQTLNLPVM GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF RCFRPVLTHMQTLWELMLLGEPLLVLAAPSDDVSEMVLALTSCL QPLRFCCDFRPYFTIHDSEFKBFTTRTQAPPNVVLGVNTPFFIK TLQHWPHILRVGEFKMSGDLPKQVKLKKPFKV*RPWDTKP
7060	90	1670	SVNLPPLSLWPWEEAMDSTKSEPLKGSPEAEDGNIYKKLVPNSQ YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEMRAS

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LKTLHRMAEKVGADITVLREREDVDSDMPRKITEVLVRKVPDN QQFLDLRVAVLGNVDSGKSTLLGVLTQGEIDNGRGRARLNLFRH LHEIQSGRTSSISFEILGFNSKGEVHGINTQWGGQTLRMGW*** RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNG VKIKRQGHGPNGLGPGNSEGVGRAGRRH*GPWALGQVVNYSDSR TAEIICBSSSKMITFIDLAGHHKYLHTTIFGLTSYCPDCALLIV SANTGIAGTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR QLERVLPKPGCHKVPMVLTSEDDAVTAAQQAQSPNVTPIFTLS SVSGESLDLLKVFNLPLPLTNSKEQEELMQQLTEFQVDEIYTV PEVGTVVGGTSLR*IDLLATLPTQPSPIYKSTSWPKGGDPGI
7061	364	710	ARMPSFLGPPCLFVMDPETTLEEPETARLRFPGFCYQEVAGPRE ALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPPEIQAWV RGQRPGSPPEAAALVEGLQHD*ARMPSPLGPPCLFVMDPETTL EEPETARLRFPGFCYQEVAGPREALARLRELCCQWLQPEAHSKE QMLEMLVLEQFLGTLPPPEIQAWVRGQRPGSPPEAAALVEGLQHD PGQLLG
7062	71	744	AKAGTNLERLHWLSYFFCIPKHKLKSSQKDKVRQFMACTQAGER TAIYCLTQNEWRLDEATDSFFQNPDSLHRESMRNAVDDKKLERL YGRYKDPQDENKIGVDGIQQFCDDLSLDPASISVLVIAWKFRRA TQCEFSRKEFLDGMTELGCDSEMKLKALLPRLEQELKDTAKPKD FYQFTFTFAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL MEHH
7063	2	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR LTBYIHCLQPATGRWRMLLIVSVCTATGAWNWLIDPETQKVSF FTSLWNHFFFTTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA EYNMSCDDTGKLLKPRPHVQ*QSSLIVMGLKIAFLRISDTAKS HKGFLRLRLDM
7064	300	884	RDTSDFPSSTRRLCTCCTGH*PAEPIASPHPSRGTCPPASSAS SRRTGCTWCPPESGHAQARRSRASASRWGARGAVRSABAARGC SSRAGRWLETGRRRRGPPACAAAAGRLRGAP*AAFPASVVPAR CRCPAARTGAPAAATWLRRLSGLRAPALGRRSPGPSPKSAAP PLLTPLGAGRAGGSRANS
7065	1	555	ATTTHSARRSCRGAAAEAAASAAGGRQKGFDRKAWEGRRTTPGG RSQSEPKAPPPQKRSEAAAFASMAHSFVAVQVPGMQNNIADPEEL FTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEARDEIEDI QQEITVLSQCDSSSYVTKYGSYLKGSKLWII MEYLGGSALDLL RAGPFDEFQ
7066	356	676	PGPQRGPWRAREGGHPLDPADHPRAPASLRNSVRAATMMQICDT YNQKHSLEFNAMNRFIGAVNNMDQTMVPSLLRDVPLADPGLDND VGVEVGSGGCGLEERTPP
7067	152	973	KENITMATEIGSPRRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ QLTFDGKMRKAVNRKTIIDYNPSVIKYLENRIWQRDQDRMRAIQ PDAGYYNDLVPPIGMLNPNMAVTTKFRVSTNKVKCPVFVVRW TPEGRLVTGASSGEFTLWNGLTNFETILQAHDSFVRAMTWSH NDMWMLTADHGGYVYKQSNMNNVVMFQAHKEAIREARFIHNIP FSVVPIMVVKLFKSCILGAEMHGLCQFLGNLHPINTIFFFVFT HSPFCWAPP
7068	222	816	DTMKEYVLLFLALCSAKFFSPSHIALKNMMLKDMEDTDDDDDD DDDDDDDDDDNSLFPTRPRSHFFPFDLFPMCFPGCQCSRV VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY GLILNNKLTIKHPKAFLTTKLRRLYLSHNQLSEIPLNLPKSL AELRIHENKVKKIQKDTFKKK
7069	1147	1765	FRDHRRYFYVNEQSGESQWFFPDGEEEEESQAQENRDETAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW TLQSNVPLQPLPLEMPPPPPPPPPPPPPPPPPPPPAPKMPPP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDEEDNSSSEEDRVSTAQKRIEHWKQQLVSGMAERNANFEA
7070	1	547	DGTMEDSEAVQRATALIEQRLAQEEENEKLRGDARQKLPMDLLVLEDEKHHGAQSAALQKVKQGERVVKTSLDLRREIIDVGGIQNLI ELRKKRKQKRDALAASHEPPPEPEEITGPDDEETFLKAAVEGK MKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG ATVDFO
7071	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY FQDPRTQIPFEVPPQYPTGYPPPPPTVPAGVAPCVPRFVRSNNV PESSLPASMPYADHYSTFSRDRMNSSPYQPPPPQPYGVPVPPV PSGMYAPVYDSRRIRWPPMYQRDDIIRSNSLPPMDVMHSSVYQT SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ IRRKPDQWAQYHTQKAPLVSSSTLPVATQSPPTPSTLNRGEGS
7072	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY FQDPRTQIPFEVPPQYPTGYPPPPPTVPAGVAPCVPRFVRSNNV PESSLPASMPYADHYSTFSRDRMNSSPYQPPPPQPYGVPVPPV PSGMYAPVYDSRRIRWPPMYQRDDIIRSNSLPPMDVMHSSVYQT SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ IRRKPDQWAQYHTQKAPLVSSSTLPVATQSPPTPSTLNRGEGS
7073	50	504	LAHGSFGVSDFFPAPAAAPAHLLTSFSGSLSPQFRKPLGRAPAMP LVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI VTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVSVTSL HSFQVIESLYQKLHEGHGK
7074	263	1003	VCPVLCSSTRQEPGHSSIVTYFGKPTRRKEFLGHGICIAAGKMNIS VDLETNYAELVLDVGRVTLGENSRKKMKDCKLRKKQNERVSRAM CALLNSGGGVIAEINENEDYSYTKDGIGLDLENSPSNILLFVPE YLDFMQNGNYFLIFVKSWSLNTSGLRITTLSSNLYKRDITS AKV MNATAALEFLKDMKKTGRGLYLRPELLAKRPRVDIQEENNMKAL AGVFFDRTELDREKELTFTESTHVEI
7075	598	1005	NYINFFFRKEYPPHVKVEINPVLRSRLQGVIRIMKKTSESESQ VEPEIKRKVQKQKHCSTYQPTPLSPASKKCLTHLEDLQRNCRQ ATTLNESTGPLLRTSIHQNSGGQKSQNTGLTTKKFYGNVNEKVP IDII
7076	279	1049	LQSESSNAEAGNEQRHEDEQRSKRGWSKGRKRKKPLRDSNAPK SPLTGYVRFMNERREQLRAKRPVFPPEITRMIGNWSKLPPEE KORYLDEADRDKERYMKELEQYQKTEAYKVFSRKTQDRQKQKSH RQDAARQATHDHEKETEVKERSVFDIPIFTEEFNLHNSKAREAE L RQLRKS NMFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV LQOHLTLRQVLTSSFASMFLEPXEGETPTVDTIDSYM
7077	3	1119	SSMGSNSEINGLALRKTDKYGLGGSQYSGSLKSSIPVDVARQR ELKWLDMFSNWDKLSRRFQKVKLCRCRKGIPSSLRKAWQYLSN SKELLEQNPRKFEELEAPGDPKWLVDVIEKDLHRQFPFHMFMAA RGGHGQQLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ AFWCLVQICDKYLPGYYSAGLEAQLDGEIFFALLRRASPLAHR HLRRQRIDPVLYMTWFMCI FARTLPWASVLVRVDMFFCEGVKI IFRVALVLLRHTLGSVEKLRSCQGMETMBQLRNLFPQCMQEDF LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLHGS RAIHEERRRQPPPLGPSSS
7078	483	767	FQQRMMAGEQKPSNNLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQELAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY
7079	2	376	SVVEFFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ MQARKKRRGII EKRRDRINSSLSLRLVPTAFKQGSCKLEK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			AEVLQMTVDHLKMLHATGGTGTALLFQASFIQIIF
7080	200	595	VQLPLEAPCLSLSCRDHSGGNRDLRRHRDCRVYGSPODGIPY LTHPLCHQDVVSVGRLQIRALATPGHTQGHVLYLLDGGSPYKGPS CLFSGDLLFLSGCGEFPKRKEELGEGETEVRATVPWRALKP
7081	213	506	AVTEEEMILNSLSLCYHNKLLILAPMVRVGTLPMLLLALDYGADI VYCEELIDLKMIQCKRVVNEVLSTVDFVAPDDRVRVFCEREQN RVVFQMGTS
7082	3	1137	APSRNTMLMAWCRGPVLLCLRQGLGTNSFLHGLGQEPFEGARSL CCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSISDGTGCL SSLENLRLPTLREESSPRELEDSGQGRGCPHTQGSSEDPMSLS QAQSATEVEERHVSFSCSTSRBRPFQAGELILAETGEGETKFKK LFRLLNNFCLLNSNWGAVPFGKIVGKFPQGIILRSSEFGKQYMLRRP ALEDYVVLKRGTAITFPKDINMILSMMDINPGDTVLEAGSGSG GMSLFSLKAVGSGQGRVISEFVRKDHDLAKNKYKHWRDSWKLSH VEEWPDNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLVPV YPHLKHGGVCPVYVNNITQVIELLD
7083	115	541	RSNAVQLTRMEYAMKSLSLLYPKSLSRHVSVRTSVVTQQLLSEP SPKAPRARPCRVSTADRSVRKGMAYSLEDLLKVRDTLMLADK PFFLVLEEDGTTVETEEYFQALAGDTVFMVLQKGQKQWPPSEQG TRHPLSLSHK
7084	3	522	NSVSVSSQSRFLASVPGTGVRSAADMAASTAGKQRIKPAK VKNKAPAEVQITAEQLLREAKELELLPPPQOKITDEEELND YKLRKRKT FEDNIRKNRTVISNWKYQWBSLKEIQARRSIYE RALDVDYRNITLWLKYAEMEMKNRQVNHARNIWDRAITL
7085	243	1499	RQLARLRRRRGWSRPFPGAPMAHITINQYLQVYEAIDSRDGASC AELVSFKHPHVANPRLQMASPEEKCCQVLEPPYDEMFAHLRCT YAVGNHDFIEAYKQCTVIVQSFLRAFQAHKEENWALPVMYAVAL DLRVFANNADQQLVKKGKSKVGMLEKAAELLMSCFRVCASDTR AGIEDSKKGMFLVLNQLFKIYFKINKLHLCKPLIRAIDSSNLK DDYSTAQRVTYKYVGRKAMFSDFKQAEYLSFAFEHCHRSSQ KNKRMILYLLPVKMLLGHMPTVELLKKYHLMQFAEVTRAVSEG NLLLLHEALAKHEAFFIRCIGIFLILEKLKIITYRNLFFKVYLLL KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGYYI SHQHQLVVSQKNPFPPLSTGC
7086	256	525	ILAARMGKQNSKLRPEVMQDLLESTDFTEHEIQEWYKGLRDCP SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRFTDANGDGTIDFR EF
7087	166	723	LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEASRGG NTRKSLEDNGSTRVTPSVQPHLQPIRNMVSVRTMEDSCBLDLVY VTERIIAVSFPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLS ERRPDITKLHAKVLEFGWPDLHTPALEKICSIKAMDITWLNHP HRCRVLHNKG
7088	104	759	GTSASPSSLLEMAEITETGELYSSYVGLVYMFNLIVGTGALT MPKAFATAGWLSVLVLLVFLGFMSPMTTTFVIEAMAAANAQLHW KRMLNKEEEDDDSSSTASDVLIRDNYERABKRPILSVQRRGS PNPPEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDLAIYA AAVFSLMQVTCATGNDSCGVEADTKYNDTDRCWGPLRRVD
7089	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFNLVARTYIPNTKVEC HYTLPPGTMPASDWIGIFKVEAACVRDYHTFVWSSVPESTDG SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGVQVCGQSPFPQFRE PRPMDELVTLEADGGSDILLVVPKATVLQNLDESQOERNLDM QKLQLEGVTELSRVQELERALARATARQEHTELMEQYKGISRS HGEITEERDILSRQGDHVARILELEDDIQTISEKVLTKVEELD RLRDTVKALTRQEKLLGQLKEVQADKEQSEAELOVAQOENHHL NLDLKEAKSWQEEQSAQAQRLLKDKVAQMKDTLQQAQRVALEP

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LKEQLRGAQELAASSQQKATLLGEEELASAAAARDRTIAELHRSR LEVAEVNGKLAELGLHLKKEKQWSKERAGLLQSVAEKDKILK LSAEILRLLEKAVQEERTQNQVFKTELAREKDSLVQLSESKREL TELRSALRVLQKEKEQLQEEKQELLEMYMRKLEARLEKVADEKWN EDATTEDEEAAGVGLSCPAALTDSEDESPEDMRLHMPAFVSVETQ ASLLGLLE
7090	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFVARTYIPNTKVEC HYTLPPGTMPASDWDIGIFKVEAACVRDYHTFVWSSVPESTTDG SPIHTSVQFOASYLFPKPAQLYQFRVYVNRQGVQCGSPFPQFRE PRPMDELVTLEEADGGSDILLVVPKATVLQNLDESQQERNLDM QLKLQLEGQVTELRSRVQELERALARQEHTELMEQYKGISRS HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKVELLD RLRDTVKALTREQEKLGLQKQVADKEQSEAEQVAAQENHHL NLDLKEAKSWQEEQSAQAQLKDKVAQMKDTLGGQQRVALELP LKEQLRGAQELAASSQQKATLLGEEELASAAAARDRTIAELHRSR LEVAEVNGKLAELGLHLKKEKQWSKERAGLLQSVAEKDKILK LSAEILRLLEKAVQEERTQNQVFKTELAREKDSLVQLSESKREL TELRSALRVLQKEKEQLQEEKQELLEMYMRKLEARLEKVADEKWN EDATTEDEEAAGVGLSCPAALTDSEDESPEDMRLHMPAFVSVETQ ASLLGLLE
7091	186	1076	EGMLTREHRCGRSEEQELEPWSPKKARSGRWLRNGFKRKMEEP EPPADSGQSLVPVYIYSPYVSMCDLAKIPKRASMVHSLIEAY ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDHDPD STIEYGLGYDCPATBGI FDYAAAIGGATITAAQCLIDGMCKVAIN WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY YSVNVPIQDGIQDEKYYQICERYEPPAPNFGI
7092	522	809	KQGINEDQEESSQKPRLEGCEPISKQRMKKLIKQKQWEEQRELR KQKRKEKRKRKKLERQCMENSDGHDRKRVRRDVVHSTLRLLII DCSFDXLM
7093	454	655	NFGVSGVELAQASMVMSFVIAACQLVLGLLMTSLTESSIONS ECPQLCVCEIRPWFTPTQSTYREA
7094	2	508	FVRSWHWGVGFASSRPPCVDLWNQSIISFFGWAGSEEPFSFYG DIIAFPLQDYGGIMAGLSDPWWKTLTYLTGGALLAAAYLLHE LLVIRKQQEI DSKDAIILHQFARPNNGVPSLSPFLCKMETYLRM ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGETEFTII
7095	1	411	IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR SLECVSHEVD SHYCPSCLNMPASAEAKLKKNRNCANCFDCPGCMH TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMD KSVGE
7096	224	2067	ETRS LAVQEKPSQAGRRSSRISFAGALFLTRFLQELLNNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDSIEKLFCTCDQTFQNHQ QREHYKLDWHRFNLKQRLKDKPLLSALDFEQSSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQQGF LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAGHFA GAI FQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGSPHSAGAN LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRLVHLKLTTLHVYE EDPREAVRLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ NEESPQKQSGSEGEDGFQVELELVELTVGTDLDCSEVLPKRRR RKRNKKEKSRDQEGAHRTLLQQTQEEEPSTQSSQAVAAPLGL LDEAKAPGQPELWNALLAACRAGDVGLKLQLAPSPADPRVLSL LSAPLGGSGFTLLHAAAAGRGSVVRLLEAGADPTVQCQDH
7097	256	1228	IRTKSAATWEAWPQCGREGSRIITEPCANAGSRQELQTERISS FLAAQGDQAFHSGLETNKNSNELPLRVGLKVAQGSPLMGGQVSA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSPGSHDTMTYC LNKKSPISHEESRLQLLNKALPCITRPVVLKWSVTQALDVTEQ LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTALVEDTLTEISE WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGDMLCPRG EVPTLRQLWSRGGQVIVSYEDESSLRRHHBLWPGVPYWGNNRVK TEALIRYLETMKSCGR
7098	82	956	SSFLKRCRKVLGCWGPSEQLFSTLEPRDKEIDNYCVMRIQT EARSQFWAPNRPVNICRMTAVDGRGGSSRETCHFPHPLEA LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLPSKPLLG LGSSVIYFLWNLNLLWPRVLAVALFSAFSPSYVALHFLGLWLVL LLWVWLQGTDFMPDPSSSEWLYRVTVATILYFSWFNVAEGRTGR AIIHFAFLSDSILLVATWVTHSSWLPSPGIPLQLWLPVGGCGCF LGLALRLVYHHLHPSCCCKPDPDQVD
7099	992	210	LFRLAPGFLRLSLARQGYHQIWAFFPLPSGATATWPAASRSLSLA ARSLPRSPARPGPNDAALGEHDFRGGQVRAQRFSEBPGPAD GAVLEVHPVQIGAGVSLPILAAKCGAEVILSDSSELPCHCLEVC RQSCQMNNLPHLQVGLTWGHISWDLALPQDIILASDVFFEP EDFEDILATIYFLMHKNPKVQLWSTYQVRSADWSLEALLYKWD KCVHIPLESFDADKEDIAESTLPGRHTVEMLVISPAKDSL
7100	205	671	ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPHLSVL FLFSPFPQLGDPLEAFPVFKKYDRNGLNVSIECKRVSGLEPATV DWAFLDTKTNNQMTYEQSEWGWKDKREEMTDDRAWYLIWEN SSVPVAFSHPRFDVERGDEVLYW
7101	2	503	WRGGPRRAKRLAGGAVGVLLVRGVHVSVRAGGGRPPRAADMKKD VRILLVGEPRVGKTSLIMSLVSEEFPEEVPRAEETIPADVTP ERVPTTHVDYSEAEQSDQLHQEISQANVICIVAVNNKHSIDK VTSRWIPLINERTDKDSRLPLILGGNKSDLVESR
7102	2	503	WRGGPRRAKRLAGGAVGVLLVRGVHVSVRAGGGRPPRAADMKKD VRILLVGEPRVGKTSLIMSLVSEEFPEEVPRAEETIPADVTP ERVPTTHVDYSEAEQSDQLHQEISQANVICIVAVNNKHSIDK VTSRWIPLINERTDKDSRLPLILGGNKSDLVESR
7103	119	438	GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEKSSSES LSDKGSELKKSFDVAVFDVLKVTPEYAGQITLMDVPVFKAIQF DELSSCGWNKKEYSSAP
7104	1670	795	RLWEHRSVSAGASGWLSSPGCLLLHPSLPPEEERVDILINAGV MRCPHWTTEDGFEMQFGVNHLEAWAGAAPVQAILPRRPPKVL GF*V*VKSDLFIILNPGHFLLTNLLLDKLKASAPSRILNLSLA HVAGHIDFDDLWQTRKYNTKAAYCQS\KLAIVLFTKELSRRLQ GSGVTVNALHPGVARTELGRHTGIGSTPLQHHN\WAHLLAANS KSPRSWPAPAQHNTLAVAEELA\VISGKYFDGLKQKAPAPEAD EEVARRLWAESARLVGLEAPSVREQLPR
7105	765	143	GQMCRRPSPKSTSCLSMTCDLR/RGLQDPQCLALFRVAVDKHQA LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWQLST SQIPVQQMHLFDVHNYPDYVSSGGGFGPADDHGYGVSYIFMGDG MITFHISKKSTKTDSHRLGQHIEDALLDVASLFQAGQHFKRR FRGSGKENSRRHRCGFLSRQTGASKASMTSTDF
7106	14	1064	GLQAGHPHPRSASRIPEADTH\YSKLQRAFDSIVNKDHKRMFGT YFRVGFSGSFGDLDEQEFVYKEPAITKLPEISHRLEAFYGCQF GAEFVEVIKDSPTVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV TYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTMTMAF PYIKTRISVIQKEEFVLTPIEVAIEDMKKTKLQLAVINQEPED AKMLQMVLCQSGVATVNGQPLEVAQVPLAEIPADPKLYRHKNL RLCFKEFIMRCGEAVEKNKRLITADQREYQQLKKNYNKLBKBL RPMIERKIPELYKPIFRVESQKRDSEHRSFRKCBTQLSQGS
7107	1145	591	*I*WLQTGKKK

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
7108	1	942	VKVALLLTNLEQPRTESEWENSFTLKMFLQFVNLNSSTFYIAF FLGRFTGHPGAYLRLINRWLEECPSGCLIDLQMGMIIIMVLK QWNNFMELGYPLIQNWWRTRKVRQEHGPERKISFPQWEKDYNL QPMNAYGLPDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEI RLDAYKFTVQWRRPLASRAKDIGIWIYGILEGIGILSVITNAFVI AITSDFIPRLVYAYKYGPCAGQGEAGQCMVGYVNASLSVFRIS DENRSEPESDGSEFSGTPLKYCRYRDYRDPHSLVPVGYTTLQF WHVLAW
7109	964	102	WDQRKRNLSVPGPAHGAQEEPEWKKESLGAQAELSILQPKPE TQPPFKSEQVYLHFLSVVTEDEGPEPKDKGSLPQPPITEVESQVF SEKLATDTSTFEATSEGTLELQQRNPKAERLRWSPAQESFRQM VVIHKEIPTGKKDHECSECGKTFIYNHSLVHVQRVHSGEKPYKC SDCGKTFKQSSNLGQHQRHTGEEKPFECNECGKAFRWGAHLVQH QRIHSGEKPPECNECGKAFSSQSYLSQHRRHISGEEKPFICECG KAYGWCSELIRHRRVHARKEPSH
7110	96	697	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKQMLTRASITPVLG SPSTKRRGQMLQPIIEGETAHFPEEIKKEEEDGVNLSSELGDM KTAVQVQSSLNKSESDVEENQEKALDLRLSSRAASMPLELQ LWKARAEKKLRKTLREFEEAFYQNGRQAQKEDRVPVLEEYRE YKKIKAKLRLEVLISKQDSSKSI
7111	2	414	GSGLYRGPTPGGQCIWKPNMPPDHERNFGFTQFALELNELTAE LKRSLPSTDTRLRPDQRYLEBGNIAAQAQKRRIEQLQDRRRKV MEENNIVHQAARFFRRQTDSGKEWVTNNTYWRRAEPGYGNMD GAVLW
7112	103	495	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW FKNDQDIQLEHFSVKVQAKYVSMITKGVTSSESGKYSINIKN KYGGEKIDTVSVYKHGEKIPDMAPPQQAQKPLIPASASAAGQ
7113	1	824	KCLRQAWHEAPSSLAFTRWCSREERAEGGNLHRSITRDPKPPG LRFSQRPMDDKKKRSPKPCLAQPAQAPGLRRVPVPTSHSGSL ALGLPHLPSPKQRAKFRVGEKCRPVLAGGGSGSAGTPLQHSF I.TEVTDVYEMEGGLNLNDFHSGRLQAQKECSFEQLEHVREM QEKLARLHFSLDVCGEEEDDEEEDGVTEGLPBEQKKTMDARNL DQLLSNLGSLGALVPGMGRGEGTYSQSHSWALGEKGVVHSGK SSGPLNLPRR
7114	3	1492	VWEVDEQIDHYKESQDKFLWQAAFIGKETLWDESGQECCKICRKI IYLNDFVSVKQRLPKYYSWERCSKHLNLFQGNRSYVRKKDDG CKAYWKVCLHYNLHKAQPAERFFDPNQRGKALHQKQALRKSQRS QTGEKLYKCTECGVFIQKANLVVHQRTHTGEEKPYECCECAKAF SQKSTLIAHQRTHTGEEKPYECSECGKTFIQKSTLIKHQRTHTG KPFVCDKCPKAPKSSYHLIRHEKTHIRQAPYKGIKCTTSLLIYQ RIHTSEKPCSEHGKASDEKPSPTKHWRTHTKENIYECSCGKS FRGKSHLSVHQRIHTGEEKPYECICGKTFSGKSHLSVHHRTHTG EKPPECRRCGKAFGEKSTLIVHQRMTGEEKPYKNECGKAFSEK SPLIKHQRIHTGERPYECTDCKAFSRKSTLIKHQRIHTGEEKPY KCSECGKAFSVKSTLIVHHRTHTGEEKPYECRCGKAFSGKSTLI KHORSHTGDKNL
7115	1	947	NAAHGYNWGLWCMIYIPPDWLDRGDESAPIRTPAMIGCSFVVD REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA HIERTKPYNNIDYAKRNALRAAEVWMDDFKSHVYMAWNIIPM SNPGVDFGDVSERLALRQLKCRSFKWYLENVYPENRYNNLT YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSDGL LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD FTQSGPIVSRATGRCLVEMSKDANFGLRLVVQRCGSGQKWMIRN WIKHARH
7116	866	95	RVRMRNNAEVIEEKLMSKSWAKFRPGEPWKGYPNIDPETDPYVT PGSVINNLISINTVREVDHLDRNSGSSSSSLNTTLPSTSAWSSIR

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ASNYNVPLSSTAQSTARSNSDKLTWSPGSVTNTSLAHELWKVP LPPKNITAPSRPPGLTGKPPPLSTWDNSPLRIGGGWNSDARY TPGSSWGESSSGRITNWLVLKNLTPQIDGSTLRTLCMQHGPLIT PHLNLPHGNALVRYSSKEEVVKAQKSLHISDLFLLTL
7117	695	1261	LLISTPGGCHPPPSSTIEFTYTGAWGKALPAPHMPCAPGALPQGA FVSQAARAIPLLQPSQAQAEGLSQPARACGALCSLPWPLRNWG SPILRLPGGLRTPPTNDRKTRRSAMACWARAQWDTLGPLKLSHR GKVCLRHPRPTGVRGGPGAAGRQGGMGTRRRGTFTSGARDPDDL RVKHRCQPTGHLPL
7118	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVNLGKGFHSIVRLVAFPCPFASSQVALENANAVSEGUVHEDLR LLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDL SACKAQLGLGHSYSRAKVKFNVRVD NMI IQSISLLDQLDKDINTFSMRVREWYGYHFPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAILINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSL ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRI SRYLANKCSIASRIDCF SEVPTSVFGEKLRQVEERLSFYETGEI PRKNLDVMKBAMVQAE EAAAEITRKLEKQEKRLKKEKRLAALALASSENSSTPEECE EMSEKPKKKKKQKQEVVPQENGMEPPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSI PKRKKSTPKEETVNDPBEAGHRSGSKKKRK FSKEEVPSSGPEEAAGKSSSKKKKKFKHAKSQED
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVNLGKGFHSIVRLVAFPCPFASSQVALENANAVSEGUVHEDLR LLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDL SACKAQLGLGHSYSRAKVKFNVRVD NMI IQSISLLDQLDKDINTFSMRVREWYGYHFPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAILINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSL ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRI SRYLANKCSIASRIDCF SEVPTSVFGEKLRQVEERLSFYETGEI PRKNLDVMKBAMVQAE EAAAEITRKLEKQEKRLKKEKRLAALALASSENSSTPEECE EMSEKPKKKKKQKQEVVPQENGMEPPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSI PKRKKSTPKEETVNDPBEAGHRSGSKKKRK FSKEEVPSSGPEEAAGKSSSKKKKKFKHAKSQED
7120	1991	64	QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYFAEEMKFSKKLSAISLGQGGQP RAEAMMRSSIERGKWNFFQNCPLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPPVSLQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLSLCLPHGNALERRKFGPLGPNIPY EFTDGLDRICISQLKMFLEYYDDIPYKVLKYTAGETINYGGRTVD DWDRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHG LSYIKSLPLNDMPFIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREIIVEDVTQNILKVPPEINLQWVMKYPVLYEES MNTVLVQEVIRYNRLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGLQNFARKFVISIDTISFDFKVMFE APSELTQRPPQVGCYIHGLFLEGARWDFEAPQLAESQPKELYTEM AVIWLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSNTYVI AVEIPTHQQRHWIKRGVALICALDY
7121	2	546	RPLRPWVLSLGSVMGLMTYGRROFQSLDTTMRRLIPPPREASAK LTTLVDADEAFTAYLEAMRLPQNTPEEKDRRTAALQEGRLRAV SVPLTAEVSLWPAQLQELARCGNLACRDLQVAAKALEMGVF GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAQTQAALVLDCL

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7122	2	546	ETRQE RPLRPWVLSLGSVMGLMTYGRRFQSLDTTMRRLIPPPREASAK LTTLVDADEAFAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV SVPLTLAETVASLWLPALQELARCGNLACRSDLQVAAKALEMGVF GAYFNVLINLRDITDEAFKQIHRVSSLLQEAKTQAAALVLDCL ETRQE
7123	1	1092	KPAVPEARSAGTSEAGRSGAEVSCGVSQDGAAMRLTPRALCS AAQAAWRENFPLCGRDVARWFPGHMAKGLKKMQSSSLKLVDCIIE VHDARIPLSGRNPLFQETLGLKPHLLVLNKMDDLADLTEQQKIMQ HLEGEGLKNVIFTNCVKDENVKQIIPMVTTELIGRSHRYHRKENL EYCI MVIGVPNVKGSSLINSLRRQHLRKGKATRVGGEPGITRAV MSKIQVSEERPLMFLDTPGVLPAPRIESVETGLKLALCGTVLDHL VGBETMADYLLYTLNKHQRFQYVQHYGLGSACDNVERVLKSVAV KLGTQKVKVLGTGNVNVIQPNYPAAARDFLQTFRRGLLGSVM LDLDVLRGHPRV
7124	2	382	LPITLLLAAPFAHLILPFGHDQSPCWHPGPALSPGTGLPGLSWAM ANSGLQLLGGYPLALGGWVGIIASTALPQWKQSSYAGDASIQLRS KVFLSEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
7125	166	1127	NCISEKRNYSFSMQKKGRTSRIRRRKLCGSSSESRGVNESHKSE FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLQEGQMIIS LPESCLLT\RDTVIRSYLGAYITKWKPPSPPLALCTFLVSEKH AGHRSLLLEA\YLEILPKAYTCPVCLPEPVNLLPKSLKAKAEQ RAHVQEFFASSRDFSSSLQPLFAEAVDSIFSYSALLWAWCTVNT RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHSHPHVQVKAANE ETHSYEIRTTSRWRKHEEVFICYGPHDNQRLPLEYGFVSVENPH ACVYVSRGWNQLCS
7126	1	733	CRDMAAFIVPSFARRCSQKSLGHLPTQPLWLAAMSFRGQERGT SHSQAREPQRPGRWNLGSLQSSPGTLGQAGTASRRRGCMVQRWV QVATGRRRAVQVPKGLGLALGETSPGASRGMSGGAGGCWALGWA PSPVLPWLLGPPPPWLSIISDSGTQRPSPRRCPARPSPWGPQC WRGGRIASAEASST*TPGSGSRARSRRSPGSRRRSASAPSPPT PTDACA*SCVARPAGSRSSRPAAA
7127	1311	277	GLPAMCST*KAGYEEETEGDCIPKDR*IEKRPFKEI*RRIPRIF AKQKQI*S*NSQKIGASEIDGRKEADCSAPAAARIGAVSVFR RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLLFHTPEQFLAEC ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VLFRI*WLKDCDV *FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*HIMNLLLPM*L CQSSLRDQITIVTWRM*RNYSMFRINMISSL*DGSIHPLKLFY PALIFTLTVPINSCCQRPLPLFAHQSIKTLASSGSPMLACLRLFL LVKKRAFIHTPRSPGCSV*CKHVLVKDNKNNCVGSEV
7128	2	5228	GRVDLWITLLGRSALRELSQIEAELNKHWRRLLEGLSYYKPPSP SSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCYLQE DYRGTRDSVKTVLQDERQSQUALIKIADYIYYEERTCILRCVLHL LTYFQDERHPYRVEYADCVDKLEKELVSKYRQOFEELYKTEAPT WETHGNLMTERQVSRWFVQCLREQSMLEIIFLYYAYFEMAPSD LLVLTKMFKEQGFGRQTNRHLVDETMDFVDRIGYFSALILVE GMDIESLHKCALDDRELHQFAQDGLICQDMCLMLTFGDIPH APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYLTRLQ SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDTA CEVLADPSLPFLFWGTEPTSGLGIILDSVCGMFPHLLSPLQLL RALVSGKSTAKKVVSFLDKMSFYNELYKHKPHDVISHEDGTLWR RQTPKLLYPLGGQTNLRIPQGTVGQVMDDRAYLVRWEYSYSSW TLFTCEIEMLLHVSTADVQHCRVKEPIDLVHKVISTDLSIA DCLLPITSRIYMLLQRLTTVISPPVDVIASCNVCLTVLAARNPA VWNTDLRHTGFLPFVAHPVSSLSQMISAEGBNAGGYGNLLMNSE QPQGEYGVTTIAFLRLITTLVKGQLGSTQSQGLVPCVMFVLKEML

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			PSYHKWRYNSHGVREQIGCLILELTHAILNLCHETDLHSSHTPS LQFLCICSLAYTEAGQTVINIMIGVDTIDMVMAAQPRSDGAE QGQGLLIKTVKLAFSVTNVIRLKPPSNVVSPLAQALSQHGAG GNNLIAVLAKYIYHKHPALPRLAIQLLKRLATVAPMSVYACLG NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\ETQP GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV/VWELIDSQQ QDRYWCPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKFWENLT SPLFGTSPSPSETSEPSILETCALIMKIIICLEIYVVKGSLDQP LKDTLKKFSIEKRFAYWSGYVKS LAVHVAETEGSSCTSLLEYQM LVSARWMLLIATTHADIMHLTDSVVRRLQFLDVLDTGKALLLV PASVNCRLRSGMKCTLLILLRQWKRELGSVDEILGPLTEILEG VLQADQQLMEKTKAKVFSAFITVLQMKEMKVS DIPQYSQVLNV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRDRDQ RDGVCVLGLHLAKELCEVDEDDGDSWLQVTRRLPILPTLLTLEV SLRMKQNLHFTATLHLLTLARTQQGATAVAGAGITQSI CLPL LSVYQLSTNGTAQTPSASRSLDAPSWPGVYRLSMLSMEQLLKT LRYNLFPEALDFGVHQERTLQCLNAVTVQSLACLEADHTVG FILQLSNFMKEWHFHLPLQMRDIQVNLGYLCQACTSFLHSRKM QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPADTE ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLA EYNFLFALSFTPTFDSEVAPSGTLLATVNVALNMLGELDKKK EPLTQAVGLSTQAEGRTRLKSLMFTMENC FYLLISQAMRYLRD PAVHPRDKQRMKQELSELSTLLSSLSRYFRGAPSSPATGVLP SPQKSTSLSKASPESQEPLIQLVQAFVRHMQR
7129	1	1054	FRFRWRRLH*AGPASSAGGSPGEASGTMSGELPPNINIKPR WDQSTFIGRANHFTVTDPNILLTNEQLESARKIVHDYRQGIV PPGLTENELWRAKYIYDSAFHPDTGEXMILIGRMSAQVPMNMTI TGCMMTFYRTTPAVLFWQWINSFNNAVNYTNRSGDAPLTVNEL GTAYVSATTGAVATAGLNLTKHVSPLIGRFVFPFAAANAANCI NIPLMRQRELKVGIPVTDENGNRLGESANAQAQAITQVVSRI MAAPGMAIPPFIMNTLEKKAFLKRFPPWMSAPIQVGLVGFCLVFA TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRVYFNKGL
7130	2	780	HEVPSLQTSDDLPGSVQRCVVVVSQPNKENWCQDHLNLSLGRKG ISAKSPYHRSQSSSVLINSKMSDINYPDSVKGKQLLSLHRS RCESHQDLPLDIADSHQGTGKLSDLTLQDSQKVVVVNRNPLN AQIATQNYFSNFKETDGEDDYVEIKSEDESELELSHNRKRS DSKFVDADFSNVCSGNTLHLSNPRTPKKPVNSKLGSLPYLTP YNDSDKINDYLWRGSPSNQNIQVSLREKFQCLSSSSFA
7131	805	573	AAAEHIEVVFLIEACKVNPFAKDRWGNIPLDDAVQFNHLEV KLLQDYQDSYTLSETQAEAAAEALS KENLES MV
7132	1420	1087	IDMLLSGALVSGPYTLITTAVSADLGTHKSLKGNALHSTVTA IIDGTGSGVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLFLI RLIHKELSCPGSATGDQVPFKEQ
7133	2	3648	QQIPGLLPAHGESGDALRKPRLOKPI TGHLDLFFTLTPSLEKF EEELLEHLHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGFVQ RPQVVVLVPEMDVALTRSASF SRKVVSSTSSGSQALVLRSL RLPEMVGHFAFAVIFQLEYVFSPPAGVDGNAASVTSLSNLCMH MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPASMS SEEVKQVESGTLRFQFSLGSEHLDAPTEPVSGPKVERRPSRKP PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPQHCL ARPTSQPLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLSVLETS IAEQLQELPFTPLHAPIVVGTTQTRSSAGQPSRASMVLLQSSGFP EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS RVAQDCRGTSWPKTVYFTFQFYRFPATTTPRLQLVQLDEAGQPS SGALTHILVPVSRDGTFDAGSPGFQLRYMVGPGFLKPGERRCFA RYLAVQTLQIDVWDGDSLLIGSAAVQMKHLLRQGRPAVQASHE

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			LEVVA TEYEQDNMVVSGDMLGFGRVKPIGVHSVVKGRHLHTLAN VGHPCEQKVRGCSLTPPSRSRVISNDGASRFSGGSLTTGSSRR KHVVQAQKLADVDSELAAMLLTHARQKGQPDVSRSDATRRRK LERMRSVRLQEAGGDLGRRGTSVLAQQSVRTQHRLDLQVIAAYR ERTKAESIASLLSLAITTEHTLHATLGVAEFFEFVLKNPHNTQH TVTVEIDNPESLIVDSQEWDRDFKAAGLHTPVEEDMFHLRGSL APQLYLRPHETAHVFPKFQSFAGQLAMVQASPLSNEKGMNAV SPWKSSAVPTKHAKVLFASGGKPIAVLCLTVELQPHVVDQVFR FYHPELSFLKKAIRLPPWHTFPGAPVGMLEDPPVHVRCSDPNV ICETQNVGPGEPDIFLKVASGPSPEIKDFVVIYSDRWLATPT QTWQVYLHSLQRVDVSCVAGQLTRLSLVLRGTQTVRKVRAFTSH PQELKTDPKGVFVLPFRGVQDLHVGVRLRAGSRFVHLNLVDVD CHQLVASWLVLCCCRQLISKAFIIMLAAGEGKGVNKRITYTNP YPSRRTFHLHSDHPELLRFREDSFQVGGGETYITIGLQFAPSQRV GEEELIYINDHEDKNBEAFCKVIYQ
7134	2115	1111	GGEGFSYPFHVGLSLGTPLDPHYVLEVHYDNPTEEGLIDNSG LRLFYTMDIRKYDAGVIEAGLWVSLFHTIPPMPPEFQSEGHCTL ECLEALEAEKPSGIHVFAVLLHAHLAGRGIRLRHFRKGEMKL LAYDDDFDNFQEFQYLKEEQTILPGDNLITECRYNTKDRAEMT WGGLSTRSEMCLSYLLYPRINLTRCASIPDIMEQLQFIVKKEI YRPTTWPFIKSPKQYKNLSFMDAMNFKWTKKEGLSFNKLVL SLPVNVRCSKTDNAEWSIQGMTALPPDIERPYKAEPLVCGTSSS SSLHRDFSINLLVCLLLSCTLSKSL
7135	2	2072	FVPRVTPRSLSLQGPKEGSEVGSITQPLPSSYLIFRAASESDGRC WLDLELALRCSSLLRLGTCKPGRDGEPTSPDASPSSLCGLPA SATVHPDQDLFPLNGSSLENDADFSDKSERENPEESDTETQDHSR KTESGSDQSETPGAPVRRGTTYVEQVQBELGELGEASQVETVSE ENKSLMWTLLKQLRPGMDLSRVVLPFTFVLEPRSFNLKLSDYHY ADLSRAAVEEDAYSRMKLVLRWYLSGFYKPKGIKKFYNPILG ETFRCCWFHPQTDSRTFYIAEQVSHHPPVSAPFVSNRKGDFCIS GSITAKSRFYGNLSALLDGGKATLTFNLRAEDYLTMPYAHCKG ILYGTMTLELGGKVTIECAKNNFQAQLEFKLPFFGGSTSINQI SGKITSGEVVLASLSGHWRDVFIEKEGSGSSALFWTPSGEVRR QRLQHTVPLEEQTELESERLWQHVTRAISKGDQHRATQEKFAL EEAQRQRARERQESLMPWPKQLFHLDPITQEWYHYEDHSWPDP LKDIAQFEQDGLRRTLQOEAVARQTTFLGSPGRHERSGPDQRL RKASDQPSGHSQATESSGSTPESCPELSDEEQDGFVPGGESPC PRCKEARRLQALHEAILLSIREAQOELHRHLSAMLSSTARAAQA PTPGLLQSPRSWFLLCVFLACQLFINHILK
7136	2	418	DFVPSFRPSPGNTSQTWLLRAATLEKEVAGLREKTHHLDMLK SQQRKVRQMIQQLQNSKAVIQSKDATIQELKEKIAYLEAENLEM HDRMEHLIEKQISHGNFSTQARAKTENPGSIRISKPPSPKMPV IRVVET
7137	2	466	WASGMSTVPGGSRHSLGIQVRGGWGTGGEESLTPVADTWQA GSFKVATQERNPQRAQMLRRQKKGVPVFLGDFLTQLRLDSAI PDDL DGNNTNKRSEKVRVLQEMQLLQVAAMNYRLRPLEKFVITYFT RMEQLSDKESYKLSQCLEPENP
7138	2	466	WASGMSTVPGGSRHSLGIQVRGGWGTGGEESLTPVADTWQA GSFKVATQERNPQRAQMLRRQKKGVPVFLGDFLTQLRLDSAI PDDL DGNNTNKRSEKVRVLQEMQLLQVAAMNYRLRPLEKFVITYFT RMEQLSDKESYKLSQCLEPENP
7139	1	357	SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASSQ LKEHFAQFGHVRRCILPFDKETGFHRLGLGWQFSSEGLRNALQ QENHIIDGVKVQVHTRRPKLPQTSDEDEKDF
7140	1401	1957	RASSLQVLKAWGLIPSSPQQQHTGQYALEELFDLKVYDCFCFSF NMNVSLKQLRPSQPWPRGKCRKTPGWBEARPKAQDLRGDLGKT

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			QAGPAEAHTRGPPRLPAATGCPHPLGLLSGISVDIDPTGLQSQ WTPKGGDPPLMFSEYQKSLLEQYHLGLDQKLKRYVVGELIWNF ADFMTNQCG
7141	124	1073	LDSRSCWLDMELEEDVRFIVDETLDGGLSPSDSREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQSGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP
7142	658	839	LIFLMLHMEKMLSSVTLHIRAFLYWICLKPTSCLIFQNVNLL KK*SRVGVVVVMCRT/YSSDLQGVVIKPWLLLGSDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSIISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA
7143	3	773	SLEMSSDGEPLSRMDESDSISSTIMDV DSTISSGRSTPAMNNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDADHRSIHVDGQRRG VVCLWKGCKVYNTPTSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGRLARHVPHTFSQQNSKVSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI
7144	1	988	FRVNMQDGGPSPAHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPAALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWNVDIVLCCNGKTLISASS DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDELVASAGLDR QIFLWDVNTLTALTASNNTVTSSLSGNKDSIYSLAMNQLGTII VSGSTEKVLRVWDPRCAKLMKLGHTDNVKALLNDRDGTQCLS GSSDGTIRLWSLGGQRCIATYRVHDEGVWALQVNDFAFTHVYSGG RDRKIYCTDLRNPDIRVLICE

TRADOCS:1416260.1(%CSK01!.DOC)

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

- (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

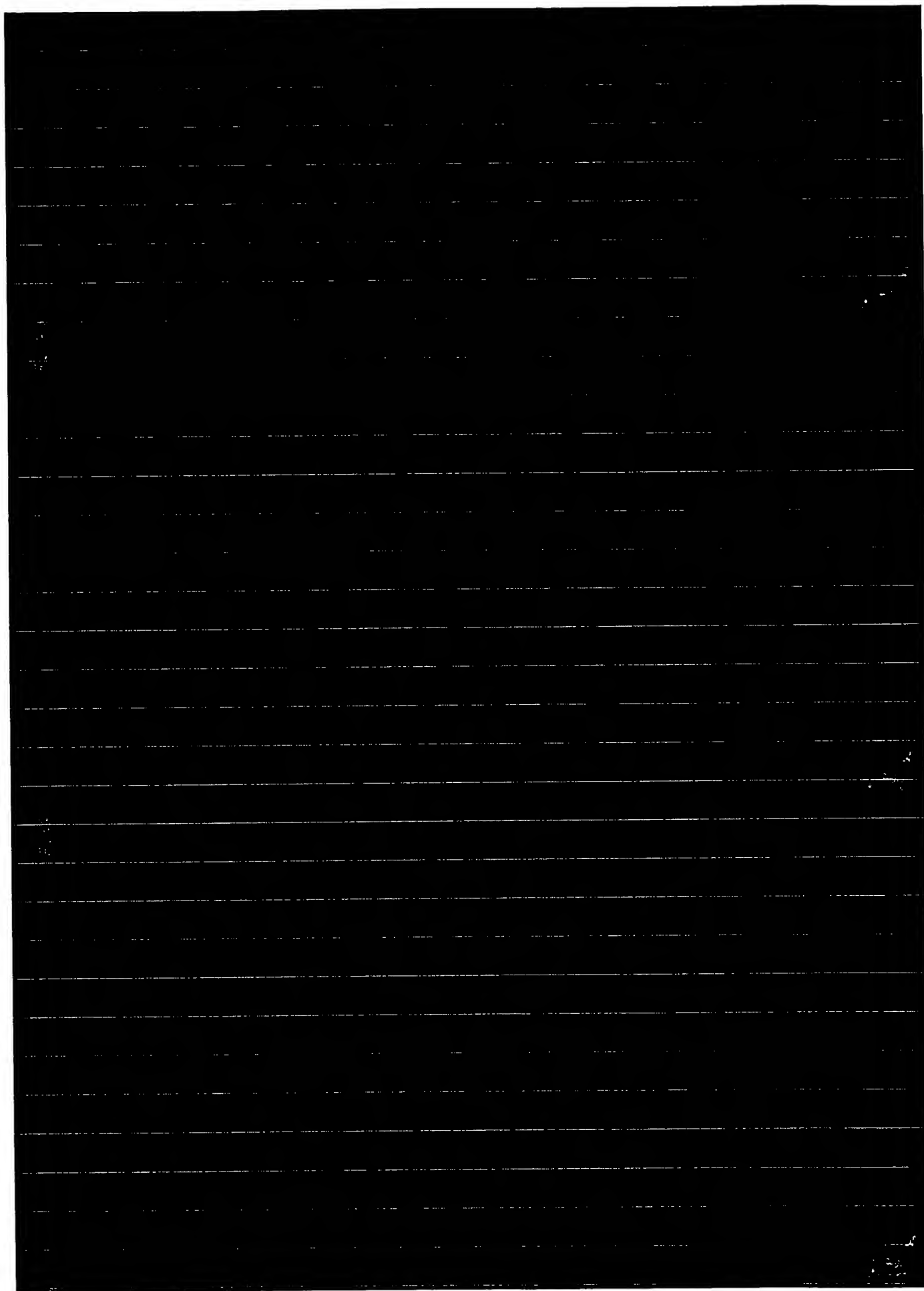
24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.



INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/85; C07K 14/00

US CL : 536/23.1; 435/320.1, 455, 468, 530/300, 350

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1; 435/320.1, 455, 468, 530/300, 350

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
MEDLINE, EAST

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WAJIMA et al. The cDNA cloning and transient expression of an ovary-specific 17beta-hydroxysteroid dehydrogenase of chickens. Gene. 1999, Vol.233, pages 75-82	1-11, 13-16, and 19-26
A	US 5,175,095 A (MARTINEAU et al) 29 December 1992 (29.12.1992), see especially columns 3-18.	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract.	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract.	1-11, 13-16, and 19-26
A	Database PubMed, ID No. 2760883, BEIL et al. Synthesis of polypeptides by the cervix of the baboon (Papio anubis). J. Reprod. Fertil. July 1989. Vol.86. No.2. pages 535-544, see Abstract.	1-11, 13-16, and 19-26
A,P	Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract.	1-11, 13-16, and 19-26

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

Date of mailing of the international search report

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231
Facsimile No. (703)305-3230

Authorized officer
Michael Woodward
Michael Woodward
Telephone No. (703)308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
This includes 4 invention Groups and 3572 sequence species

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group III, claims 17-18, drawn to methods of identifying a binding partner to a polypeptides. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containing same, respectively, and methods of making as well as the first method of use of this subject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

CORRECTED VERSION

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
26 July 2001 (26.07.2001)

PCT

(10) International Publication Number
WO 01/53312 A1(51) International Patent Classification⁷: C07H 21/04,
C12N 15/11, 15/63, 15/70, 15/82, 15/85, C07K 14/00

(21) International Application Number: PCT/US00/34263

(22) International Filing Date:
26 December 2000 (26.12.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

09/471,275	23 December 1999 (23.12.1999)	US
09/488,725	21 January 2000 (21.01.2000)	US
09/552,317	25 April 2000 (25.04.2000)	US
09/598,042	9 July 2000 (09.07.2000)	US
09/620,312	19 July 2000 (19.07.2000)	US
09/653,450	3 August 2000 (03.08.2000)	US
09/662,191	14 September 2000 (14.09.2000)	US
09/693,036	19 October 2000 (19.10.2000)	US
09/727,344	29 November 2000 (29.11.2000)	US

(63) Related by continuation (CON) or continuation-in-part
(CIP) to earlier applications:

US	09/488,725 (CIP)
Filed on	21 January 2000 (21.01.2000)
US	09/552,317 (CIP)
Filed on	25 April 2000 (25.04.2000)
US	09/598,042 (CIP)
Filed on	9 July 2000 (09.07.2000)
US	09/620,312 (CIP)
Filed on	19 July 2000 (19.07.2000)
US	09/653,450 (CIP)
Filed on	3 August 2000 (03.08.2000)
US	09/662,191 (CIP)
Filed on	14 September 2000 (14.09.2000)
US	09/693,036 (CIP)
Filed on	19 October 2000 (19.10.2000)
US	09/727,344 (CIP)
Filed on	29 November 2000 (29.11.2000)

(71) Applicant (for all designated States except US): HYSEQ,
INC. [US/US]; 670 Almanor Avenue, Sunnyvale, CA
94086 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): TANG, Y., Tom
[US/US]; 4230 Ranwick Court, San Jose, CA 95118 (US).

LIU, Chenghua [CN/US]; 1125 Ranchero Way #14,
San Jose, CA 95117 (US). ASUNDI, Vinod [US/US];
709 Foster City Boulevard, Foster City, CA 94404 (US).
CHEN, Rui-hong [US/US]; 1031 Flying Fish Street,
Foster City, CA 94404 (US). MA, Yunqing [CN/US];
280 W. California Avenue #206, Sunnyvale, CA 94086
(US). QIAN, Xiaohong, B. [CN/US]; 3662 Tumble Way,
San Jose, CA 95132 (US). REN, Feiyan [US/US]; 7703
Oak Meadow Court, Cupertino, CA 95014 (US). WANG,
Dunrui [CN/US]; 932 La Palma, Milpitas, CA 95035
(US). WANG, Jian-Rui [CN/US]; 744 Stendhal Lane,
Cupertino, CA 95014 (US). WANG, Zhiwei [CN/US];
836 Alturas Avenue, B36, Sunnyvale, CA 94085 (US).
WEHRMAN, Tom [US/US]; 3210 CCSR Mol Pharm,
269 W. Campus Drive, Stanford, CA 94305 (US). XU,
Chongjun [CN/US]; 4918 Manitoba Drive, San Jose, CA
95130 (US). XUE, Aidong, J. [CN/US]; 1621 S. Mary
Avenue, Sunnyvale, CA 94087 (US). YANG, Yonghong
[CN/US]; 4230 Ranwick Court, San Jose, CA 95118
(US). ZHANG, Jie [CN/US]; 4930 Poplar Terrace, Camp-
bell, CA 95008 (US). ZHAO, Qing, A. [CN/US]; 1556
Kooser Road, San Jose, CA 95118 (US). ZHOU, Ping
[CN/US]; 1461 Japaul Lane, San Jose, CA 95132 (US).
GOODRICH, Ryle [US/US]; 4896 Sandy Lane, San Jose,
CA 95124 (US). DRMANAC, Radoje, T. [YU/US]; 850
East Greenwich Place, Palo Alto, CA 94303 (US).

(74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris,
Glovsky, and Popeo, P.C., One Financial Center, Boston,
MA 02111 (US).(81) Designated States (national): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.(84) Designated States (regional): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— with international search report

[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and
uses thereof.

WO 01/53312 A1



(48) Date of publication of this corrected version:

1 November 2001

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(15) Information about Correction:

see PCT Gazette No. 44/2001 of 1 November 2001, Section II